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- (71) Applicant (for all designated States except US): **HYSEQ, INC.** [US/US]; 670 Almanor Avenue, Sunnyvale, CA 94086 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): **TANG, Y., Tom** [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). **LIU, Chenghua** [CN/US]; 1125 Ranchero Way, #14, San Jose, CA 95117 (US). **DRMANAC, Radoje, T.** [YU/US]; 850 East Greenwich Place, Palo Alto, CA 94303 (US).
- (74) Agent: **ELRIFI, Ivor, R.**; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US).
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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/14827

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468; 530/300

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/320.1, 455, 468; 530/300

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EST, GENESEQ, GENEEMBL, ISSUED_PATENTS, EAST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database SPTREMBL, ID No. Q9TS35, Bailey et al. 01 May 2000. See sequence alignment.	1-9, 19, and 22-26
X	Database Swiss-prot, ID No. P01922, Michelson et al. 21 July 1986. See sequence alignment.	1-9, 19, and 22-26
X	Database Swiss-prot, ID No. P01923, Zucherlandt et al. 21 July, 1986. See sequence alignment.	1-9, 19, and 22-26
X	Database Swiss-prot, ID No. P01924, Matsuda et al. 21 July 1986. See sequence alignment.	1-9, 19, and 22-26

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

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Facsimile No. (703)305-3230

Authorized officer

Shubo "Joe" Zhou

Telephone No. (703)-308-0196

INTERNATIONAL SEARCH REPORT

International application No.

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Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9, 19, 22-26, and SEQ II NO:1

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

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(54) Title: **NOVEL NUCLEIC ACIDS AND POLYPEPTIDES**

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

WO 01/88088 A2

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, circulating soluble factors, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-8051. The polypeptides sequences are designated SEQ ID NO: 8052-16102. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-8051 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-8051. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-8051 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-8051. The sequence information can be a segment of any one of SEQ ID NO: 1-8051 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-8051.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety

of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

5 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-8051 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-8051 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath
10 et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-8051; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-8051;
15 and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-8051. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-8051; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing
20 (*e.g.*, SEQ ID NO: 8052-16102); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.* orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

25 The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-8051; or (b) polynucleotides that hybridize to the complement of the
30 polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably

produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the
5 polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of
10 interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex
15 and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and
20 monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds
25 that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a
30 polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the
35 administration of the polynucleotides or polypeptides of the invention to individuals exhibiting

symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100

nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-8051.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-8051. The sequence information can be a segment of any one of SEQ ID NO: 1-8051 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-8051. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an

eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

5 The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic
10 elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

15 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino
20 acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

25 The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

30 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue
35 may be removed from the protein during processing in the cell. The peptide may be produced

synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural

or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*,

washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less).

Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be

disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. (1990) *Methods Enzymol.* 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

5 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction
10 of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the
15 suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the
20 context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the
25 nucleotide sequences of SEQ ID NO: 1-8051; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 8052-16102; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 8052-16102. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of
30 the nucleotides sequences of SEQ ID NO: 1-8051; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 8052-16102.
35 Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in

receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-8051 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-8051 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-8051 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-8051, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most

preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-8051, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-8051 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-8051 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the

polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-8051, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-8051 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-8051 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are

known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example.

Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pDR540, pRIT5 (Pharmacia).

- 5 Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many
10 suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed
15 (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine
20 kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct
25 transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the
30 periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination
35 signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-8051, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NO: 8052-16102 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-8051 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-8051), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of
10 an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified
15 such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the
20 control of a strong pol II or pol III promoter are preferred.

 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The
25 antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

30 In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit
35 translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-8051). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-8051 (see, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 8052-16102 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-8051 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-8051 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 8052-16102 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 8052-16102 or the corresponding full length or mature protein; and
5 "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.

10 Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 8052-16102.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.
15 U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example,
20 without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where
25 proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

30 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic
35 acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, *e.g.*, Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

5 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either
10 cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 8052-16102.

15 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or
20 deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the
25 molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved
30 systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

35 Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*.

The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked
5 in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal
10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example,
15 Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or
20 artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease
25 states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be
30 inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*,
5 by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and
10 PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If
15 linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to
20 replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or
25 protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene
30 under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally
35 occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals.

Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference.

Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or

5 polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

10 indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation

15 or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

20 protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic

25 disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as

30 an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of

35 the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its
5 receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

10 Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch
15 and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional
20 sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the
25 polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

30 A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one
35 or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

5 HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation,
15 Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
20 include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse
25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin
30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in
35 Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or *ex vivo* is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

5 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and
10 identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be
15 used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In
20 addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated
25 cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al.,
30 Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention
35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In *Culture of Hematopoietic Cells*. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

5 A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the
10 growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
15 WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A
25 protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More
30 specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (*e.g.*, anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

5 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected
10 cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T
15 cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain
20 protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as
25 the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the
30 following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;
35 Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

- 5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1
10 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3,
15 In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:
20 Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation
25 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research
30 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

5 A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention,
10 alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as
15 a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

20 The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci.
25 USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils,
30 T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other
35 trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines
15 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

20 4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events
25 in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

35 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention
5 may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,
10 inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma,
15 acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including
20 bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma,
25 tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically
30 effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, *e.g.* reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a
35 portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

5 Aminogluthethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate
10 (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

15 In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

20 *In vitro* models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30
25 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,
30 *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the
35 invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen
5 recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

10 The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28,
15 Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a
20 ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the
25 present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent
30 molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the
35 novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.* 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

5 Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
10 of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or
15 chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid
20 arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

25 Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic,
30 myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- 10 (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord
15 infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- 20 (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the
25 nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to
30 diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
35 injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, *etc.*, depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, *e.g.*, weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or
5 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other
10 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or
15 entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis
20 and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes
25 possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the
30 polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately
35 adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified
5 nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, *e.g.*,
10 by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model
15 system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant
20 mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and
25 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

30 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

5 The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, 10 lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or 15 complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (*e.g.*, at the same time, or at differing times provided that 20 therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the 25 relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or 30 simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in 35 combination with other therapies such as treatments employing cytokines, lymphokines or other

hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with
5 an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds
10 may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which
15 increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other
20 glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as
25 sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v
30 polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the
35 co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above-mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue
5 regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution
10 and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

15 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of
20 proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include
25 compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in
30 the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of any of the full length proteins of the invention, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention, *e.g.*, a hydrophilic

region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: *MONOCLONAL ANTIBODIES AND CANCER THERAPY*, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (*Bio/Technology* 10, 779-783 (1992)); Lonberg et al. (*Nature* 368 856-859 (1994)); Morrison (*Nature* 368, 812-13 (1994)); Fishwild et al. (*Nature Biotechnology* 14, 845-51 (1996)); Neuberger (*Nature Biotechnology* 14, 826 (1996)); and Lonberg and Huszar (*Intern. Rev. Immunol.* 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab')₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

5 Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

10 Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct
15 bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

20 Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable
25 host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

30 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for
35 increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

5 The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been
10 described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin,
15 mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP),
20 iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a
25 ricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such
30 streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-8051 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-8051 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

5 In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see 10 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA 15 molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

20 The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise 25 contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed 30 polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a 35 polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

- 5 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

- In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

- In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-8051, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

(a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and

(b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see
5 Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into
10 polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the
15 present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid
20 hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-8051. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-8051 can be used as an indicator of the presence of RNA of cell type of such a tissue
25 in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The
30 probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes
35 *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed CovaLink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups ($>NH$) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) *Anal. Biochem.* 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, (1991). In this technology, a phosphoramidate bond is employed (Chu *et al.*, (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, *e.g.*, Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be

Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) *PNAS USA* 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) *Nucleic Acids Res.* 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

- 5 Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic
10 strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader
15 aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon
20 consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

25 5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The
30 inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid
5 Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from
10 a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-8051 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases
15 (*i.e.*, Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score
20 greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-8051) of the present invention are incorporated in the attached Sequence Listing. A subset of the predicted polypeptide sequences contain an unknown amino acid; a stop codon; a possible nucleotide deletion; or a possible nucleotide insertion. These sequences have also been
25 shown in their entirety in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-8051. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to
30 a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers

to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-8051 were obtained by a BLASTX
5 version 2.0a1 19MP-WashU search against Genpept release 123 and Geneset release 200110 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-8051. The nearest neighbor results for SEQ ID NO: 1-8051, having identifiable function(s) are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J.
10 Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the polypeptide sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provides the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide
15 sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1)
pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by pFam analysis for each polypeptide, namely: the name of
20 the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-8051. Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth
25 in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/577,408.

TABLE 1

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
adult brain	GIBCO	AB3001	<p>53-57 119-121 205-206 229-232 311-314 318-320 328-331 340-341 360-361 382-383 398 400 433 444 448-449 455 461-465 467-468 476-479 488 501-504 506 508-513 522-526 533-535 541-542 559- 560 562 637-640 649 654-655 658 679-683 751-752 755 757-764 766 771 780-782 841-849 857 867-869 872-874 879 884-885 890 915-917 945 969 1006-1009 1031-1035 1101-1103 1110 1112 1115 1120-1121 1123 1131 1185-1190 1252 1299-1301 1303-1304 1314- 1316 1338 1355-1359 1361-1363 1382-1387 1395-1399 1447 1458- 1460 1473-1477 1479-1481 1484-1485 1489-1493 1495-1496 1498 1515 1517 1534-1535 1565-1566 1601 1603 1612 1614-1619 1621- 1622 1626 1642-1644 1646 1679 1690-1693 1695-1696 1698-1704 1706-1715 1717-1718 1726 1728-1737 1739-1748 1751-1760 1762- 1763 1768-1771 1782 1843 1847 1862-1863 1877-1880 1882-1886 1895-1901 1904-1905 1922 1976-1991 2023 2034 2171-2174 2182- 2184 2200-2203 2220-2223 2232-2233 2250 2332-2339 2347-2350 2352-2356 2359-2361 2371-2372 2375 2380 2383-2384 2386-2388 2466-2469 2485-2489 2533 2547-2550 2575 2585-2586 2588-2589 2602 2682-2686 2688 2714-2715 2737 2739-2741 2744-2745 2789- 2791 2798-2802 2839-2841 2899 2910-2918 2920-2922 2924 2952- 2955 3043-3050 3095-3096 3101-3102 3104-3105 3109-3110 3116- 3117 3134-3135 3179-3180 3223-3224 3236-3237 3260-3261 3265 3271-3272 3280-3282 3311 3325 3349-3350 3354 3393-3395 3397- 3400 3491-3493 3499-3503 3517-3519 3521-3523 3560 3581-3582 3588-3589 3592-3596 3617-3619 3631 3683 3696 3698-3702 3762- 3763 3801 3805 3834-3835 3837-3838 3850-3855 3866 3944 3955 3967 3979-3985 3990 4017-4020 4081 4098 4100-4103 4126-4127 4189-4190 4193 4226 4266-4269 4271-4272 4298-4301 4303 4320- 4323 4325 4341 4344-4345 4347-4349 4427-4428 4436 4454 4537- 4541 4543 4549-4550 4552-4554 4564-4567 4576 4580-4591 4599 4610 4698 4710 4806-4808 4810 4812 4833 4847-4853 4884-4885 4910 4940-4941 4943-4944 4952 4954-4958 4972 5033-5038 5040- 5044 5056-5060 5062 5105 5116 5137 5141 5158-5161 5163 5166- 5167 5226-5227 5229-5233 5236-5238 5240-5249 5252-5261 5263- 5267 5272 5274 5340-5341 5478-5480 5525 5546-5547 5566-5570 5581 5628-5634 5644 5760 5771 5782 5872 5881-5887 5904 5911 5971-5976 6003 6007 6037-6038 6074 6124-6128 6189 6191-6194 6198 6231-6233 6249-6250 6339-6340 6360 6413-6414 6553-6556 6586-6587 6656 6681 6722-6727 6729-6736 6771 6782 6794 6805 6903 6906 6939-6942 7044-7051 7053 7055-7056 7087-7089 7116 7131 7254-7255 7294 7340 7377-7379 7662 7677 7686 7697 7730 7732-7734 7741 7744-7760 7763 7775 7808-7810 7835-7836 7847 7942 8025</p>
adult brain	GIBCO	ABD003	<p>4-5 28-29 44 47 205-206 211-212 229-232 246-248 250-259 261- 266 282-284 318-320 323-328 338-341 349-354 356-359 368-375 382-383 385-386 397-398 400 404-409 426-427 433 444-449 455 476-479 486-489 492-493 495-497 500-504 506 508-515 517 522- 526 528-529 555-556 584-592 602-604 606-614 616 622 624 627- 633 635-640 649 658 666 668 672-676 679-683 686-688 690-692 704-707 722-723 726 768-769 771 782 841-843 846-849 857 867- 869 872-874 876-881 884-885 890 893-895 900 902 911-917 919- 921 923-927 929 945 960-962 969 973 979-985 991-993 995-1000 1006-1009 1020 1031-1035 1037-1040 1042-1043 1056-1057 1063 1070-1072 1083 1086-1094 1100-1109 1111 1113 1115 1119-1123 1129 1131 1137-1148 1165 1174-1175 1183 1185-1197 1204 1210- 1212 1221-1225 1227-1232 1236-1237 1241-1242 1250 1253 1264- 1265 1267-1270 1272 1279-1281 1286 1291-1293 1303-1306 1308- 1309 1314-1316 1334-1336 1338-1344 1355-1359 1361-1363 1365- 1368 1370 1372-1375 1382-1390 1392-1400 1411-1413 1423 1438- 1439 1442-1445 1447-1449 1451-1456 1476-1477 1484-1485 1489- 1493 1495-1496 1500 1503-1504 1506-1507 1515 1523-1524 1534- 1536 1538 1549 1560 1564-1571 1576-1578 1595-1601 1603 1610 1621-1622 1626 1640-1641 1644 1646 1648-1652 1674 1676-1680 1691-1693 1695-1696 1698-1700 1703-1704 1706 1711-1713 1718 1732-1736 1741-1745 1747-1748 1751-1754 1764 1768-1779 1781- 1790 1792-1805 1807-1819 1821-1826 1828-1837 1839-1844 1850</p>

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
			1852-1855 1861-1863 1870 1874-1880 1882-1886 1904-1905 1922 1931-1935 1992-2000 2002-2008 2010-2011 2013-2022 2024-2033 2035-2036 2039-2041 2052 2065 2076 2081-2083 2085-2091 2098 2103-2109 2113 2119 2130 2137 2139-2143 2146 2155-2160 2168 2171-2174 2179 2185-2200 2206 2216-2218 2227-2229 2232-2242 2244 2247 2253 2265 2276 2320-2321 2345-2350 2352-2356 2359- 2361 2363-2365 2371-2372 2374-2375 2380-2390 2396 2407 2418 2425-2434 2437 2448 2450-2453 2459 2464-2470 2482-2484 2494- 2495 2528-2531 2533 2535-2550 2556 2563-2565 2567 2572-2575 2584 2590-2594 2602-2605 2625-2626 2628-2634 2641-2642 2664- 2665 2667-2670 2674-2676 2678 2682-2686 2688 2695-2697 2706- 2707 2714-2715 2730-2733 2744-2745 2754-2756 2758-2760 2766 2772 2787 2792 2795-2796 2798-2804 2808-2812 2827 2829 2835 2837-2841 2849-2850 2853-2854 2857-2858 2887 2900-2908 2921- 2922 2924-2931 2933-2939 2941-2942 2952-2955 2982-2987 3002 3064 3066-3067 3070 3095 3101-3102 3104-3105 3107-3110 3112- 3113 3115 3120-3121 3126-3132 3144-3146 3149 3156-3158 3179- 3180 3184 3206 3212 3218 3222-3224 3226 3233 3236-3237 3246- 3248 3259 3278-3279 3307 3313 3347 3349-3350 3360-3361 3364- 3373 3375-3384 3386-3388 3397-3400 3402-3406 3408-3417 3419- 3422 3454-3456 3499-3503 3520 3524-3525 3527-3529 3560 3568- 3571 3575-3576 3579-3582 3588-3589 3592-3596 3614-3617 3623 3631 3677 3689 3713-3714 3729 3732 3740-3742 3744 3747 3755- 3759 3761 3770-3773 3777 3805 3832-3835 3844 3873-3880 3882- 3891 3893-3899 3908-3910 3912 3944 3955 3967 3978-3985 3987 3990 3992 3997 4000-4001 4003-4006 4022 4024-4026 4028-4029 4035-4039 4043 4087 4089-4090 4102-4103 4114-4120 4150-4153 4172-4174 4176-4177 4183-4185 4249 4256-4258 4260-4263 4265- 4269 4286 4289 4295 4298-4301 4303 4307 4320-4323 4325 4357 4361 4368 4372-4376 4379 4386 4429 4436 4445 4453 4465 4470 4476 4489 4491-4497 4499-4500 4505-4508 4533-4536 4549-4550 4552-4553 4568 4571-4574 4582-4585 4587 4590-4592 4594-4595 4597 4599-4606 4610 4614-4620 4622 4628-4631 4633-4642 4644- 4649 4651-4653 4655-4658 4703 4728-4729 4737-4739 4745 4753 4755-4756 4774-4775 4791 4802 4806-4808 4810 4845 4847-4853 4884-4885 4899 4906 4948-4952 4954-4958 4963 4978-4984 4986- 4994 5023-5025 5050-5052 5064 5073-5074 5078-5082 5084-5086 5090-5093 5095 5104 5123 5136-5138 5141 5144-5146 5156-5161 5163 5166-5167 5188 5192 5229-5232 5270-5272 5274 5276-5281 5338 5356 5365 5371 5373 5376-5380 5410 5423 5462-5463 5478- 5480 5482 5484-5485 5525 5558 5579 5581 5612-5615 5617-5618 5633-5637 5639-5642 5644-5648 5671 5694 5705 5711 5715 5717- 5718 5720 5757-5760 5771 5782 5786 5793 5803-5805 5811 5814 5825 5836 5847 5858 5873-5874 5881-5887 5914 5916-5917 5927- 5928 5961-5963 5979 5981-5984 5987-5988 5998-6001 6003 6007 6022 6025-6029 6033-6034 6036 6055-6056 6058-6060 6069 6075- 6077 6088 6092 6104-6106 6112 6124-6128 6130 6145 6148-6154 6161-6162 6184-6185 6191 6194-6198 6202-6208 6213-6222 6224- 6226 6231-6233 6235-6243 6245 6249-6250 6260-6265 6267-6274 6276 6278-6281 6333-6336 6341-6342 6344 6352-6353 6356-6358 6360 6368-6369 6398-6399 6410 6412 6415 6430 6441 6454 6494 6530 6540 6551 6565 6586-6587 6601 6612-6613 6624-6625 6628 6656 6658-6660 6662-6666 6702-6703 6721 6726-6727 6732 6737- 6738 6740-6744 6746-6749 6752-6759 6761 6777 6816 6824-6829 6838 6849 6860 6872-6875 6893 6903 6905-6906 6934-6937 6939- 6942 6981 6984-6987 7012-7013 7016 7046-7048 7057-7058 7073- 7075 7077 7098-7107 7109 7116-7117 7176 7186 7194-7195 7197 7220-7221 7229 7232 7297-7301 7340 7346 7368-7369 7377-7379 7411-7412 7440 7482 7541 7551-7553 7587-7589 7619-7620 7624- 7627 7644 7655 7685 7760-7770 7775 7782-7783 7808-7810 7816 7835-7836 7844-7845 7874-7879 7884 7895-7897 7915-7916 7942 7976 7981-7982 7989-7990 7997 7999-8000
adult brain	Clontech	ABR001	27 39-42 53 136-143 145-154 156-163 282-284 297-298 338-339 374 408-409 411-420 422 436-441 476 478-479 528-529 552-554 666 668 703-706 754 773 784 795 806 840-843 859-862 915-917 919-921 929 999-1000 1037-1040 1042-1043 1104-1109 1131 1165 1198-1201 1291-1293 1303-1306 1308-1309 1334-1336 1339-1340

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
			1355-1359 1361-1363 1411-1413 1476-1477 1543-1547 1601 1603 1664 1738 1750 1755-1760 1762 1850 1861 1870 2137 2181 2204- 2205 2207-2208 2220-2223 2289-2294 2347-2349 2435 2463 2558- 2562 2585-2586 2588-2594 2682-2686 2688 2695-2697 2744-2745 2774-2776 2798-2802 3011-3012 3014 3101-3102 3104-3105 3109- 3110 3112-3113 3115 3126-3132 3136-3138 3278-3279 3306 3308 3350 3431-3432 3499-3501 3521-3523 3575-3576 3579-3580 3615- 3616 3740 3747 3823 3834-3835 3851-3852 4035-4039 4042 4298- 4301 4303 4320-4323 4325 4331 4403 4554 4561 4565 4571-4574 4576 4595 4603 4654 4745 4753 4755-4756 4920 4931 4952 4954- 4958 5002-5006 5008-5009 5090-5093 5095 5125-5126 5128-5130 5144-5146 5153-5154 5176 5314-5315 5333-5335 5644 5667-5670 5684-5692 5872 5881-5887 6088 6131-6132 6202-6203 6213-6219 6260-6265 6267-6274 6450-6451 6453 6535 6754 6837 6839-6848 6939-6942 6946-6947 6984-6987 7063 7073-7075 7077 7090-7091 7131 7238 7366 7461 7472 7483 7561 7624-7627 7730 7741 7752 7795-7796 7805 7847 7915-7916
adult brain	Clontech	ABR006	55 122 126-130 136-154 156-163 168-169 178-180 194-195 340-341 360-361 368-373 431 434-435 457-459 476 478-479 495-497 528- 529 584-592 607-612 622 624 649-655 658 674-676 757-764 766 780-781 823-825 867 869 878 880-881 884-885 969 999-1000 1006- 1009 1073-1080 1167-1172 1191 1338 1341-1344 1370 1372-1373 1382-1384 1420 1438-1439 1442-1445 1470-1471 1486-1493 1495- 1496 1503-1504 1506-1507 1543-1547 1596-1600 1615-1619 1621- 1622 1628-1633 1635 1644 1646 1648-1652 1667-1670 1690 1718 1732-1736 1747-1748 1751-1754 1768-1772 1774 1862-1863 1938- 1945 1965-1967 2001 2012 2014-2015 2039-2040 2063 2084 2097 2099-2100 2114-2117 2141 2146 2157 2162-2163 2168 2179 2185- 2187 2196 2200 2206 2217 2228 2234-2242 2244 2253 2265 2285- 2286 2332-2339 2352-2356 2359-2361 2380 2387-2388 2412-2417 2419-2423 2425-2427 2495 2533 2575 2625-2626 2628 2683-2686 2688 2764 2767-2768 2792-2793 2798-2804 2839-2841 2900-2908 2934-2937 2955 3052 3065 3087-3091 3093 3095 3107 3127-3132 3143 3151-3155 3216 3236-3237 3342 3350 3352 3385 3396 3411 3458-3459 3521-3523 3588-3589 3627 3719 3749 3772 3791-3794 3890 3909-3910 3912 3974 3996 4017-4020 4064 4091-4097 4104- 4105 4183-4185 4306-4307 4341 4404-4405 4518-4519 4521 4529 4533-4536 4582-4585 4688-4689 4748 4847-4853 4952 4954-4958 5010-5013 5090-5093 5095 5123 5131-5132 5142-5143 5193-5194 5196 5277-5281 5316 5409 5664 5764-5770 5772-5781 5783-5785 5933 6175 6181-6182 6300-6303 6311-6313 6424-6427 6493 6624- 6625 6658-6660 6662-6666 6735 6871 6882 6888-6889 6899-6900 6939-6942 7063 7397 7493-7494 7504 7515 7526 7535 7546 7558 7569 7587-7589 7616 7677 7686 7697 7725-7726
adult brain	Clontech	ABR008	2 16-17 19 21 45 47 55 58-59 61-66 77-87 89-98 100-110 112-117 122 126-132 134 136-154 156-165 168-169 192-195 208 211-213 221 237-239 249 260 265-266 269 280 282-284 297-298 321 323- 325 328 335-337 340-341 360-361 368-374 382-383 387 389-398 400 404-409 423 428-430 432 436-441 448-449 457-459 476 478- 482 495-497 500 527-529 536-540 550 552-554 567-571 573-580 586-592 602 607-614 616 622 624 627-633 635-640 645 649 654- 655 663-664 666 668 682-683 685-688 690-691 704-707 710-719 721-725 744-745 751-753 755 757-764 766 773 780-781 784 795 806 816 818 823-827 841-849 856 859-862 864-866 872-874 880- 881 883-885 896-900 902 915-917 919-921 929 931 945-948 954 962-965 967-968 979 988 994 999-1000 1006-1009 1015-1017 1031-1035 1037-1040 1042-1043 1054-1055 1073-1080 1101-1110 1112 1119-1121 1123 1152 1155-1160 1163 1167-1172 1174-1175 1177-1179 1181 1192-1193 1195-1196 1198-1201 1210 1221-1227 1231-1232 1236-1237 1241-1249 1251 1266 1273-1275 1279-1281 1283 1287 1289 1299-1301 1305-1309 1328-1331 1334-1338 1341- 1344 1381 1388-1390 1392-1400 1416-1418 1420 1423 1428 1430 1432-1440 1442-1445 1447 1450 1461-1465 1472 1486-1493 1495- 1496 1499-1500 1510-1513 1520 1543-1549 1559-1561 1596-1601 1603-1606 1611-1612 1614-1619 1628-1633 1635 1640-1643 1648- 1654 1657-1663 1671-1672 1686-1693 1695-1696 1698-1699 1703- 1704 1706 1710-1713 1718-1725 1730-1736 1738 1747-1760 1762

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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adult brain	BioChain	ABR012	28-29 432-433 444 455 476 478-479 483 486-487 489 538 618-620 645 753 856 954 979 1299-1301 1654 1703-1704 1706 1732-1736 1749 1849 2016-2022 2347-2349 2425-2427 2898 2909 3212 3222 3233 4952 4954-4958 4978-4980 5645-5648 7771-7772
adult brain	BioChain	ABR013	476 478-482 486-487 489 1133-1135 1305-1306 1308-1309 1701-1702 2024-2026 2347-2349 2425-2427 2621-2624 2682-2686 2688 2898 2909 3056-3063 3134-3135 3743 3772 4952 4954-4958 5272 5274 6545-6546 7771-7772
adult brain	Invitrogen	ABR014	1694 1697 1703-1704 1706 1775-1777 1862-1863 1910 2135-2137 2200-2203 2216 2218 2528 2539 2545 2556 2567 2822 3055 3101-3102 3104-3105 3116-3117 3506 3885-3886 3979-3985 4702 5176 5272 5274 6353 6356-6358 6413-6414 6419 6424-6427 6824-6826 6828-6829 7044 7186 7197
adult brain	Invitrogen	ABR015	202-203 1534-1536 1538 1644 1646 1648-1652 1718 1741-1745 1782 1843 2084 2136 2232-2233 2838 2952-2954 2962-2971 3349 3916-3921 3923-3932 3934-3936 4571-4574 4587 4590-4591 4599 4610 4698 4710 4737-4739 5176 5272 5274 5654-5656 6191 6198 6903 6906 7822-7823
adult brain	Invitrogen	ABR016	28-29 56 1534-1536 1538 1612 1614 1642-1643 1755-1760 1762 1946 1948-1951 2010-2011 2013 2016-2022 2137 2204-2205 2207-2208 2835 2837 2853-2854 2857-2858 2955 3039-3040 3071-3077 3463 3853-3854 3990 4554 4565 4576 4737-4739 5272 5274 5298 6195-6196 6353 6356-6358 6424-6427 6761 6851-6854
adult brain	Invitrogen	ABT004	55 66 77 126-130 144 168-169 201 237-239 265-266 326-327 360-361 368-373 382-383 466 480-482 486-487 489 500 528-529 536-537 540 567-570 593 595-596 607-614 616 654-655 666 668 682-683 744-745 773 782 784 795 806 823-825 846-849 872-874 911-912 919-921 945-948 969 979 999-1000 1073-1080 1119 1152 1163 1177-1179 1198-1201 1221-1225 1227 1299-1301 1326 1338-1340 1346-1348 1350-1359 1361-1363 1369 1374-1375 1381 1388-1390 1438-1439 1442-1445 1462-1465 1484-1493 1495-1496 1529-1535 1572-1575 1587-1588 1601 1603 1615-1619 1628-1633 1635 1640-1641 1686-1689 1691-1693 1695-1696 1700 1703-1704 1706-1709 1718 1747-1748 1751-1760 1762 1790 1792-1795 1806 1823-1824 1862-1865 1887 1895-1901 1904-1905 1914 1925 1930-1935 1974 2002-2008 2087 2097 2099-2100 2114-2117 2185-2186 2250 2276 2289-2294 2328 2330 2332-2339 2347-2350 2374 2383-2386 2396 2407 2418 2425-2427 2429 2437 2448 2459 2466-2470 2482 2500-2502 2528 2539 2545 2556 2567 2572-2574 2590-2594 2679-2681 2706-2707 2718-2721 2723-2725 2750-2753 2764 2766-2768 2777 2784 2803-2804 2849-2850 2853-2855 2857-2858 2900-2908 2919 2936-2937 2955 2962-2971 2989-2990 2992-2993 3003-3008 3070-3072 3101-3102 3104-3105 3107 3112-3113 3115 3118-3119 3121 3151-3158 3195-3196 3209-3211 3213-3215 3223-3224 3260-3261 3278-3279 3310 3322 3356-3357 3389 3436-3437 3449-3450 3452 3511 3581-3582 3584 3620-3622 3732 3741-3742 3745 3772-3773 3775 3782 3791-3794 3806-3807 3809-3810 3813 3839 3856-3859 3861-3865 3867-3871 3881 3888 3958-3964 4009 4024-4025 4087 4089-4090 4114-4120 4128 4183-4185 4193 4218 4220 4227 4233 4309-4311 4373-4374 4377 4415 4433 4443 4486 4491-4493 4531 4537-4539 4542 4551 4622-4624 4671-4672 4753 4755-4756 4765 4774-4776 4787 4798 4809 4821 4832 4838-4841 4843 4845 4847-4854 4861-4869 4872-4880 4884-4885 4905 4917-4918 4921-4926 4940-4941 4943-4944 4952 4954-4958 4964 4969-4971 4975 4995 5010-5013 5056-5060 5062 5082 5125-5126 5128-5130 5168-5169 5216 5218-5221 5272 5274 5307 5333-5335 5400 5537 5539 5579 5599-5603 5678-5680 5747-5748 5928 5979 5981-5982 6022 6025-6032 6043-6045 6047-6048 6104-6106 6112 6143-6145 6148-6152 6178 6197 6249-6250 6333-6335 6450-6451 6453 6455-6456 6604 6627 6629 6639 6650 6656 6687-6688 6693 6709 6711-6712 6733-

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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cultured preadipocy tes	Stratagene	ADP001	25 28-29 36 40-42 123-124 168-169 178-179 229-233 237-239 265- 266 315-320 323-325 352-354 356-359 382-383 423 432-433 444 448-449 455 476 478-479 483 500 518-521 525-526 538 552-554 603-604 606-612 637-640 645 649 654-655 658 666 668 708 730 744-745 753 780-781 833-835 841-845 856 884-885 923-927 949- 950 954 969 987 1015-1017 1019 1024-1028 1156-1160 1165 1181 1192-1193 1195-1196 1236-1237 1264-1265 1273-1275 1299-1301 1305-1306 1308-1309 1322 1355-1359 1361-1363 1374-1375 1424- 1426 1534-1535 1552-1558 1572-1575 1621-1622 1628-1633 1635 1654 1657-1663 1686-1689 1701-1704 1706 1749 1775-1777 1782 1790 1792-1794 1796-1797 1832-1834 1836-1837 1839-1843 1845 1849 1867 1874-1876 1922 1935 2081-2083 2085-2086 2088-2091 2105-2108 2124-2127 2171-2174 2181 2204-2205 2207-2208 2216 2218 2220-2223 2234-2238 2240-2242 2284 2328 2330 2345-2346 2352-2356 2359-2361 2381-2382 2401-2406 2408-2410 2425-2427 2498-2499 2503 2505-2506 2533 2544 2546 2576-2577 2584-2586 2588-2589 2602 2632-2634 2682 2699-2704 2706-2708 2750-2753 2764 2767-2770 2787 2792 2798-2802 2830-2833 2849-2850 2898 2909 3039-3040 3043-3050 3081 3092 3101-3105 3111 3114 3133 3209-3211 3213-3215 3223-3224 3249-3250 3289-3295 3297 3356- 3357 3499-3501 3506 3560 3575-3576 3579-3580 3697 3708 3713- 3714 3717-3718 3720-3722 3732 3749 3782 3788-3790 3796 3802 3916-3921 3923-3932 3934-3936 4002 4083-4085 4087 4089-4097 4138-4142 4144-4146 4172-4173 4176 4256-4258 4320-4323 4325 4357 4368 4373-4374 4379 4537-4539 4571-4574 4582-4585 4633- 4642 4644-4649 4671-4672 4705 4728-4729 4753 4755-4756 4837 4842 4844 4884-4886 4888 4910 5087 5137 5141 5182-5183 5185- 5187 5265-5266 5277-5281 5319-5322 5468-5469 5566-5569 5591- 5593 5595-5596 5638 5644-5648 5654-5656 5694 5705 5747-5748 5910 5918-5919 5934-5935 5937-5938 5961 6022 6025-6029 6055- 6056 6058-6060 6069 6088 6183 6201 6209-6211 6242-6243 6283 6339-6340 6361-6362 6440 6442 6517-6518 6521-6529 6553-6554 6627 6629 6658-6660 6662-6666 6747-6749 7162 7185 7187 7238 7291-7293 7321-7322 7362-7363 7365 7377-7379 7393-7395 7427 7551-7553 7613-7614 7644 7655 7808-7810 7984-7986 7988-7990
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Origin	Source		PCT/US01/14827
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Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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lymph node	Clontech	ALN001	20-21 28-29 34-35 37 40-42 80-87 89-98 100-109 112-117 282-284 335-337 349-351 365 367 387 389-396 432 448-454 456 476-479 488 500-504 506 518-524 536-538 540 552-554 603-604 606 618-620 645 649 747 753 769 846-849 856 923-927 939-943 954 973 979 999-1000 1019 1021 1029-1030 1041 1052 1056-1057 1063 1070-1072 1083 1089 1100 1111 1115-1118 1122 1124-1125 1129 1131 1133-1135 1140 1167-1172 1310-1313 1427 1447 1473-1475 1498 1576-1578 1595 1604-1606 1648-1652 1680 1768-1771 1775-1777 1782 1843 1845 1850 1861 1870 1887 1935 2137 2143 2162-2163 2200 2216 2218 2232-2233 2289-2294 2319 2322-2327 2345-2346 2350 2352-2356 2359-2361 2363-2365 2387-2388 2425-2427 2449 2466-2469 2490-2491 2563 2575 2590-2594 2607-2611 2632-2634 2682 2694 2744-2745 2750-2753 2763 2787 2795 2803-2804 2856 2865 2876 2910-2914 2955 2977 2982-2987 3010 3020-3022 3039-3040 3043-3050 3095 3116-3117 3127-3132 3218-3219 3260-3264 3311 3412-3415 3417 3419 3439 3499-3501 3521-3523 3575-3576 3579-3580 3592-3596 3600 3677 3679 3713-3714 3717-3718 3720-3722 3760 3769 3774 3776 3786 3797 3799 3913-3915 3937-3940 3944 3955 3967 4102-4103 4106-4108 4114-4120 4250-4258 4316 4357 4368 4379 4411 4436 4478 4575 4577-4579 4587 4599 4610 4616-4617 4633-4642 4644-4649 4677-4679 4688-4689 4745 4870-4871 4904 4978-4980 5020 5075-5076 5078-5081 5105 5107-5120 5224 5265-5266 5292-5294 5312-5313 5356 5486-5489 5531-5533 5563 5573 5594 5605 5616 5627 5645-5648 5653-5656 5667-5671 5841-5845 5875-5878 5962-5963 5987-5988 6005-6007 6022 6025-6029 6073 6104-6106 6148-6152 6179 6260-6265 6267-6274 6283-6285 6399 6410 6508 6553-6554 6615 6619-6621 6679 6778 6780-6781 6803 6920-6921 6984-6987 6998 7069-7070 7098-7107 7109 7231 7241 7252 7257-7258 7270 7314-7316 7356 7377-7379 7453-7460 7508 7587-7589 7688 7708 7719 7801-7803 7820 7839 7895-7897 7969-7973 8044-8046
young liver	GIBCO	ALV001	16-17 28-29 118-121 192-193 223-232 268 270-273 282-284 295-301 318-320 326-328 335-337 352-354 356-359 368-374 376 378-381 387 389-397 431 433-435 444 455 477 488 492-493 501-504 506 508-515 517 536-537 540 547-549 551-554 557-558 574-580 586-593 595-596 602 613-614 616 627-629 637-644 650-655 666 668 689 700 708-709 720 722-723 731 742 782 844-845 851 863 872-874 884-885 893-895 900 902 923-927 945 969 973 1006-1009 1037-1040 1042-1043 1101-1103 1110 1112 1115 1124-1125 1136 1165 1177-1179 1191 1213-1214 1216-1218 1226 1228-1230 1236-1237 1246 1264-1265 1267-1268 1279-1281 1294-1295 1297-1301 1339-1340 1346-1348 1350-1359 1361-1363 1365-1369 1374-1375 1416-1418 1424-1426 1447 1450 1458-1461 1472 1476-1477 1486-1493 1495-1496 1498 1514 1523-1524 1570 1589-1590 1592-1594 1601 1603 1612 1614-1619 1640-1643 1690 1698-1699 1703-1704 1706 1715 1717-1718 1782-1789 1798 1809 1823-1824 1845-1846 1862-1863 1867 1874-1876 1881 1891-1901 1907-1909 1935 1938-1940 1992-1995 2039-2040 2105 2114-2118 2120-2127 2143 2177-

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adult liver	Invitrogen	ALV002	68 73 192-193 198 200 211-212 234 265-266 268 270-273 282-284 295-301 326-327 335-337 376 378-381 423 477 480-482 486-489 495-497 536-537 540 557-558 586-592 613-614 616 627-633 635- 636 641-644 650-655 674-676 679-681 707-708 724-725 729 757- 764 766 771 782 823-825 840 844-845 872-874 913 915-917 951- 953 956 969 991-993 995-997 1019 1054-1055 1087-1088 1090- 1094 1116-1119 1124-1125 1146-1148 1165 1177-1179 1191 1202- 1203 1205-1207 1213-1214 1216-1218 1243-1245 1250 1253 1257 1270 1272 1279-1281 1287 1289 1299-1301 1314-1316 1339-1340 1355-1359 1361-1363 1376-1379 1409 1423 1458-1460 1479-1481 1499 1514 1529-1533 1549 1560 1563 1589-1590 1592-1594 1601 1603 1625 1628-1633 1635 1638-1639 1642-1643 1648-1652 1657- 1663 1681-1684 1690-1693 1695-1696 1698-1699 1703-1704 1706 1730-1731 1737 1739-1740 1747-1748 1751-1754 1790 1792-1794 1825-1826 1828-1831 1845 1858-1860 1867 1874-1876 1941-1946 1948-1951 2098 2110-2112 2137 2139-2140 2142 2147-2152 2171- 2174 2177-2178 2180 2188-2195 2197-2199 2220-2224 2234-2238 2240-2242 2284-2286 2319 2345-2346 2380 2466-2469 2515-2516 2518-2527 2533 2564-2565 2629-2631 2638 2682 2690-2693 2710 2712 2716-2721 2723-2725 2730-2733 2750-2753 2769-2770 2777 2784 2795 2814-2820 2849-2850 2856 2859-2860 2865 2876 2921 3016-3017 3073-3077 3081 3092 3096 3103 3114 3151-3155 3244 3256 3267 3274 3285 3296 3331 3358-3361 3364-3373 3375-3384 3386-3388 3433-3434 3499-3501 3560 3562 3584 3587 3590-3591 3620-3622 3624 3635 3646 3676 3760 3769 3776 3786 3797 3825- 3827 3829 3956 3996 4024-4025 4075-4076 4078-4080 4082 4091- 4097 4104-4105 4150-4153 4244-4245 4264 4290 4292-4294 4311 4326-4328 4336-4340 4357 4368 4379 4436 4486 4494-4497 4499- 4500 4537-4539 4560-4561 4618-4619 4671-4672 4707 4737-4739 4753 4755-4756 4777 4817 4827-4831 4842 4844 4847-4853 4872- 4873 4905 4917-4918 4921-4926 4952 4954-4958 4990-4994 5105 5116 5125-5126 5128-5130 5144-5146 5173 5184 5189-5190 5195 5206 5209 5212-5215 5270-5271 5308-5311 5423 5476-5477 5486- 5489 5523 5525 5540-5541 5581 5591-5593 5595-5596 5654-5659 5661-5663 5760 5771 5782 5818-5820 5833-5834 5908-5909 5913 5934-5935 5937-5938 6030-6032 6088 6131-6132 6143-6144 6148-

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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adult liver	Clontech	ALV003	55 299-301 641-644 649-653 872-874 1941-1945 2136 2285-2286 2641-2642 3171-3172 3468-3469 4063 4067-4068 4104-4105 5233 7186 7197 7808-7810 7849
adult ovary	Invitrogen	AOV001	2 4-6 9-11 22-23 27-29 39-42 44 47 55 61-66 68 77 80-87 89-98 100-110 112-118 123-132 134-135 144 168-169 178-179 181-183 196-197 202-203 207-208 215-217 221 229-232 237-239 246-248 250-259 261-268 270-273 282-284 311-314 318-321 323-331 335- 337 340-341 349-354 356-361 368-375 382-383 387 389-398 400 404-409 411-423 426-430 433 436-456 461-468 477 484-489 492- 493 500-504 506 508-515 517-526 533-537 540-542 545-546 552- 554 567-571 573-580 584-593 595-600 602-604 606-614 616 618- 620 622 624 627-633 635-640 646-649 658-664 666,668 670-676 679-683 685-692 700 704-720 722-726 729 731-745 748-749 751- 752 755 757-764 766 768-769 771-772 774-775 780-782 816 818 820-821 823-827 829-832 836-838 840-849 851-855 857-858 864- 869 872-874 876-877 879-881 883-885 890 900 902 905-909 911- 917 923-927 929-930 938 945-948 951-953 956 963-965 967-970 973 979-985 987-988 990-997 1001 1005-1009 1015-1017 1019 1024-1028 1031-1035 1037-1040 1042-1046 1051 1054-1061 1063 1068-1072 1083 1086-1094 1096-1109 1111 1115-1132 1137-1151 1153-1154 1156-1162 1164-1165 1167-1172 1174-1179 1182-1197 1202-1207 1210-1214 1216-1218 1221-1225 1227-1230 1236-1238 1241-1245 1247-1250 1252-1256 1258 1261 1264-1265 1267-1269 1279-1281 1284-1285 1287-1289 1291-1293 1303-1306 1308-1317 1319 1322 1328-1331 1338 1346-1348 1350-1359 1361-1363 1365- 1368 1374-1379 1381-1390 1395-1399 1405-1406 1409 1411-1413 1415-1419 1424-1426 1446-1449 1451-1460 1462-1465 1470-1471 1473-1477 1479-1481 1486-1493 1495-1496 1498 1500-1501 1503- 1504 1506-1507 1510-1513 1515 1521-1522 1525 1529-1536 1538 1541-1542 1549-1551 1559-1561 1563 1565-1569 1571-1582 1591 1595 1602 1604-1606 1611 1613 1615-1619 1621-1622 1624 1628- 1635 1640-1641 1644-1646 1648-1653 1657-1663 1665-1666 1671- 1672 1674 1676-1680 1686-1693 1695-1696 1701-1706 1711-1713 1716 1718-1725 1727 1730-1731 1737-1745 1750 1755-1764 1768- 1771 1773 1775-1777 1780 1782-1794 1796-1798 1807 1809 1820 1825-1831 1843 1845 1847-1848 1850-1855 1857-1861 1864-1865 1867-1870 1874-1880 1882-1887 1891 1893-1902 1904-1913 1915- 1924 1926-1937 1941-1957 1960-1963 1975-1978 1980-1989 1991- 2000 2002-2008 2010-2011 2013 2016-2022 2024-2026 2037-2041 2052 2076 2081-2083 2085-2086 2088-2096 2103-2109 2118-2129 2131-2134 2136-2137 2139-2143 2146-2154 2157 2162-2163 2168 2171-2174 2177-2181 2185-2208 2216-2218 2220-2223 2225-2226 2228 2230-2231 2234-2242 2244 2253 2265 2284 2288 2295 2297- 2306 2308-2316 2319-2327 2331-2339 2341-2346 2350 2352-2356 2359-2365 2369-2372 2374-2375 2381-2410 2418 2425-2435 2437 2439-2444 2446-2454 2459 2466-2470 2480 2482-2484 2490-2491 2494-2503 2505-2506 2509 2511 2515-2516 2518-2528 2533-2534 2539 2544-2554 2556 2558-2565 2567 2569-2577 2584-2586 2588- 2597 2599-2601 2603-2605 2625-2626 2628-2642 2645 2655 2664- 2667 2672-2676 2678-2688 2690-2712 2714-2715 2718-2725 2729- 2733 2737-2741 2744-2748 2750-2753 2757 2762-2764 2766-2772 2774-2776 2781-2783 2785-2795 2798-2804 2806-2812 2814-2821 2827 2829-2835 2837 2842-2843 2846 2853-2855 2857-2858 2898 2900-2914 2918 2920-2922 2924-2931 2936-2939 2941-2942 2945- 2948 2951-2960 2962-2971 2973-2974 2978-2979 2981-2990 2992- 3001 3009-3012 3014-3025 3035 3039-3040 3053-3054 3064 3066- 3067 3073-3077 3087-3091 3093 3095-3096 3098-3100 3106 3109- 3113 3115-3119 3123-3125 3127-3140 3147 3151-3158 3179-3180 3183 3188-3189 3194 3206 3212 3217-3219 3221-3222 3227-3228

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placenta	Invitrogen	APL002	40-42 45 136-143 145-154 156-163 223-228 265-266 382-383 423 426-427 436-443 518-521 541-542 617 627-629 649 658 757-764 766 872-874 887-889 891 905-909 969 973 999-1000 1024-1028 1054-1055 1116-1118 1146-1148 1174-1175 1213-1214 1216-1218 1257 1305-1306 1308-1309 1374-1375 1405-1406 1423 1428 1430 1473-1477 1500 1510-1513 1528-1533 1640-1641 1665-1666 1680 1686-1689 1718 1782 1790 1792-1794 1938-1940 1962-1969 1971- 1974 1992-1995 2002-2008 2027-2033 2035-2036 2063 2098 2136- 2137 2147-2152 2162-2163 2181 2188-2195 2197-2199 2347-2349 2389-2390 2425-2427 2435 2500-2502 2572-2574 2674-2676 2682 2699-2704 2766 2772 2956-2960 3026-3034 3036-3038 3052 3101- 3102 3104-3105 3151-3155 3195-3196 3278-3279 3433-3434 3448- 3450 3452 3615-3616 3796 3937-3940 3944 3955 3967 3972-3973 4016 4024-4025 4064 4150-4153 4181 4287-4288 4326-4328 4415 4459 4490 4537-4539 4571-4574 4723-4729 4734-4735 4765 4776 4787 4798 4809 4821 4832 4843 4847-4854 4865 4874-4880 4884- 4885 4940-4941 4943-4944 5020 5045-5049 5073-5074 5125-5126 5128-5130 5197-5202 5204-5205 5207-5208 5212-5215 5314-5315 5340-5341 5401-5404 5406-5407 5675-5677 5928 6137-6142 6148- 6152 6333-6340 6399 6410 6545-6546 6819-6826 6828-6829 6903 6906 7054 7065 7081-7082 7348 7677 7686 7697 7730 7741 7752 7795-7796 7816-7817 7819 8030 8032
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adult testis	GIBCO	ATS001	55 68 78-79 123-124 168-175 178-179 229-232 237-239 246-248 250-259 261-264 311-314 318-320 335-337 340-341 368-374 376 378-381 397 404-407 428-435 444 448-456 476-479 488 492-493 495-497 501-504 506 514-515 517 528-529 538 567-570 593 595- 596 602 613-614 616 637-640 645 649 666 668 686-688 690-691 704-706 708 722-723 727-728 732-741 743 753 829-832 841-849 851 856 867 869 872-874 880-881 884-885 887-889 891 900 902- 909 913 927 946-948 954 959 963-965 967-968 970 973 979 999-1000 1024-1028 1031-1035 1056-1057 1070-1071 1104-1110 1112 1115 1120-1121 1123 1131 1146-1148 1156-1160 1165 1167- 1173 1210 1231-1232 1247-1249 1264-1265 1284-1285 1299-1301 1303-1304 1307 1323-1325 1341-1344 1355-1359 1361-1363 1365- 1368 1370 1372-1373 1395-1399 1409 1411-1413 1424-1427 1458- 1460 1462-1465 1470-1471 1478-1481 1498 1503-1504 1506-1507 1529-1533 1536 1538-1539 1559 1561 1565-1566 1576-1578 1595 1604-1606 1612 1614 1628-1633 1635 1648-1652 1655 1664 1679 1686-1689 1698-1699 1703-1706 1711-1713 1716 1727 1730-1731 1772-1773 1782-1789 1843 1862-1865 1887-1890 1907-1910 1915- 1918 1923-1924 1926-1929 1974 2009-2011 2013-2015 2065 2114-

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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Genomic DNA from BAC 63118	Research Genetics (CITB BAC Library)	BAC001	2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 7944-7947
Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC002	2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 5056-5060 5062
Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC003	2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 7944-7947
adult bladder	Invitrogen	BLD001	40-42 123-124 329-331 476 478-479 552-554 571 573 682-683 708 710-719 782 816 818 935-936 963-965 967-968 973 1070-1071 1113 1115-1118 1120-1121 1123 1156-1160 1165 1198-1201 1264-1265 1341-1344 1355-1359 1361-1363 1395-1399 1470-1471 1478 1640-1641 1686-1689 1779 1781 1795 1895-1901 1915-1918 1965-1967 1977-1978 1980-1989 1991 2002-2008 2039-2040 2114-2117 2188-2195 2197-2199 2220-2223 2234-2238 2240-2242 2276 2345-2349 2464-2469 2690-2694 2764 2767-2768 2787 2789-2791 2835 2837 2842-2843 2849-2850 2853-2854 2857-2858 2910-2914 2975-2976 3073-3077 3141-3142 3217 3385 3396 3669 3678 3688 3766 3937-3940 3996 4035-4039 4044 4172-4173 4176 4218 4220 4295 4377 4380-4382 4488 4806-4808 4810 4827-4831 4837 4847-4853 5138 5270-5271 5376-5380 5470 5654-5656 5873-5874 5918-5919 6201 6245 6560-6561 6836 6851-6854 6919 6978-6979 7054 7300-7301 7393-7395 7462-7465 7491 7760
bone	Clontech	BMD001	1 22-23 28-29 39-42 44 52 55-56 61-65 67 71-72 74-76 80-98 100-

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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bone marrow	Clontech	BMD002	28-29 123-124 191 223-232 237-239 246-248 250-259 261-264 318-320 326-327 340-341 344 355 366 368-374 377 385-386 388 398-400 404-407 432 450-454 456 477 484-485 488 500 514-515 517 538 545-546 586-592 602-604 606-612 618-620 645 649 654-655 667 678 722-723 747 753 757-764 766-767 773 784 795 806 841-843 856 887-889 891 900 902 939-943 946-950 954 959 963-965 967-968 973 979 999-1000 1036-1040 1042-1043 1056-1057 1095 1115 1156-1160 1181 1191 1264-1265 1279-1281 1299-1301 1334-1336 1341-1344 1355-1359 1361-1363 1371 1377-1380 1391-1394 1402 1410 1424-1426 1432-1437 1447 1473-1475 1541-1542 1552-1558 1604-1606 1611 1628-1633 1635 1642-1643 1648-1652 1664 1690 1701-1704 1706 1718 1782-1789 1798 1809 1867 1881 1887 1892 1907-1909 1911-1913 1915-1918 1922 1938-1940 1992-1995 2016-2022 2037 2081-2083 2106-2108 2135-2137 2143 2155-2156 2158-2159 2185-2186 2188-2195 2197-2199 2201-2205 2207-2208 2232-2238 2240-2242 2246 2285-2286 2289-2294 2322-2327 2345-2346 2352-2356 2363-2365 2381-2382 2391-2394 2412-2417 2419-2423 2425-2427 2449 2454-2458 2460 2466-2469 2494 2496-2497 2503 2505-2506 2553-2554 2558-2562 2595-2597 2599 2617-2620 2625-2626 2628 2682 2699-2704 2744-2745 2764 2767-2768 2771 2803-2804 2822 2828 2836 2853-2854 2857-2858 2898 2909-2914 2982-2987 3003-3008 3010 3039-3040 3043-3050 3055-3063 3087-3091 3093 3116-3117 3179-3180 3209-3211 3213-3215 3223-3224 3262-3264 3358-3359 3416 3448 3473 3577 3728 3730 3732 3743 3893-3898 3913-3915 3937-3940 3954 3992 4003-4005 4016 4048-4049 4053 4066 4174 4191 4207 4209 4218 4220 4282 4316 4320-4323 4325 4329-4330 4336-4340 4392-4395 4516 4582-4585 4604-4605 4696 4814-4815 4847-4853 4872-4873 4884-4885 4892 4899 4928-4929 4940-4941 4943-4944 4948-4951 4978-4980 4985 4996 5010-5013 5069-5070 5099-5101 5107-5115 5117 5333-5335 5401-5404 5406-5407 5410 5531-5533 5645-5648 5654-5656 5667-5670 5694 5705 5752-5754 5807-5810 5841-5846 5848-5850 5861 5875-5878 5934-5935 5937-5938 6131-6132 6177 6181-6182 6198-6200 6206-6211 6231-6233 6256 6311-6313 6337-6338 6545-6546 6567 6698-6700 6709 6735 6849 6903 6906 6915 6917-6918 6920-6923 7002 7007-7010 7031 7098-7107 7109 7118 7121-7122 7231 7241 7251-7252 7321-7322 7377-7379 7393-7395 7440 7443-7445 7453-7460 7462-7465 7469 7479-7480 7517 7542 7659 7664-7665 7708 7719 7771-7772 7774 7808-7810 7821 7893-7894 7987 8024 8034-8035
bone marrow	Clontech	BMD004	7 9-11 178-179 722-723 747 973 2136 2341-2344 2389-2390 2455-2458 2955 4053 4066 4183-4185 4892 5818-5820 6922-6923 7377-7379 7808-7810 7893-7894

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
bone marrow	Clontech	BMD007	28-29 363-364 460 474-475 552-554 1540 2106-2108 2136 2425-2427 2672-2673 2677 2682 2765 2822 4053 4066 5137 5141 5980 5991 6002 6012 6024 6922-6923 7186 7197 7453-7460 7469 8034-8035
adult colon	Invitrogen	CLN001	66 77 311-314 323-327 404-407 476 478-479 484-485 663-664 823-825 844-845 872-874 969 979 1036 1110 1112 1177-1179 1213-1214 1216-1218 1279-1281 1371 1380 1391 1395-1399 1402 1410 1523-1524 1528 1565-1566 1628-1633 1635 1642-1643 1657-1663 1705 1715-1717 1727 1747-1748 1751-1754 1867 1895-1901 1923-1924 1926-1929 1974 2039-2040 2081-2083 2102 2162-2163 2389-2390 2428 2430-2432 2466-2469 2699-2704 2710 2712 2792 2795 2808-2812 2900-2908 2955 3081 3092 3103 3114 3179-3180 3278-3279 3310 3732 3741-3742 3840-3842 3979-3985 4238 4336-4340 4369-4371 4436 4537-4539 4571-4574 4618-4619 4726-4729 4734-4735 4737-4739 4777 4805-4808 4810 4837 4976-4977 5155 5212-5215 5225 5298 5401-5404 5406-5407 5531-5533 5631-5632 5638 5696-5699 5761-5763 5789-5790 5918-5919 5952-5954 6022 6025-6029 6163 6171-6173 6181-6182 6235-6237 6284 6331 6333-6335 6353 6356-6358 6450-6451 6453 6525-6529 6578-6579 6681 6687-6688 6721 6973-6977 6988-6989 7087-7089 7340 7453-7460 7587-7589 7790 7942 7989-7990
mixture of 16 tissues-mRNAs*	various vendors*	CTL016	297-298 426-427 477 488 528-529 552-554 658 722-723 988 994 1037-1040 1042-1043 1124-1125 1146-1148 1904-1905 2284-2286 2563 3039-3040 4526-4527 4659-4663 4952 4954-4958 5594 5605 5616 5627 6755-6758 7377-7379 7808-7810
mixture of 16 tissues-mRNAs*	various vendors*	CTL021	7 28-29 294 376 378-381 436-441 476 478-479 484-485 533-535 552-554 844-845 852-853 1299-1301 1585-1586 2016-2022 2136-2137 2185-2186 2204-2205 2207-2208 2284 2377-2378 2535-2538 2540-2543 3171-3172 3234-3235 3548 3560 4256-4258 4892 4952 4954-4958 5107-5115 5117 5599-5602 5694 5705 6109 6260-6265 6267-6274 6420 6422 6574 6585 6915 6917-6918 6939-6942 7377-7379 7453-7460 7808-7810 7841-7842
mixture of 16 tissues-mRNAs*	various vendors*	CTL028	4017-4020 7808-7810
adult cervix	BioChain	CVX001	9-11 21 28-29 40-44 55-56 66 77 80-87 89-98 100-109 112-117 122-124 178-179 181-183 202-203 215-217 229-232 246-248 250-259 261-264 268 270-273 311-314 318-320 323-325 333 335-339 360-361 374 382-383 398 400 404-409 432 442-443 445-454 456 466 476 478-479 486-487 489 492-493 501-504 506 514-515 517 522-524 538-539 541-542 550 555-556 571 573-582 586-593 595-596 602 607-612 630-633 635-636 645 647-649 658-662 666 668 670-671 704-706 708 722-725 727-728 747 753 768-769 771-772 774-775 780-781 785 816 818 820-821 837 854-856 858-863 867 869 880-881 884-885 905-909 911-912 915-917 923-927 937 939-943 954 959 969-970 973 979 990-993 995-997 1019 1021 1030-1035 1041 1052 1056-1057 1063 1068-1072 1083 1089 1096-1103 1111 1114-1118 1122 1124-1125 1129-1130 1140 1165 1167-1172 1174-1176 1183 1185-1190 1194 1204 1211-1212 1221-1225 1227-1230 1236-1237 1254-1256 1267-1268 1286-1287 1289 1291-1293 1303-1304 1314-1316 1328-1331 1334-1336 1341-1344 1355-1359 1361-1363 1369-1370 1372-1373 1377-1379 1382-1390 1395-1399 1408 1416-1418 1423-1426 1428 1430 1446 1457-1460 1462-1465 1470-1471 1473-1478 1503-1504 1506-1507 1515 1534-1535 1543-1547 1549 1560 1564-1566 1572-1575 1580 1591 1595 1621-1623 1640-1643 1657-1663 1674 1676-1678 1690-1693 1695-1696 1698-1699 1703-1709 1716 1718 1727 1755-1760 1762-1763 1768-1771 1773-1774 1782-1789 1799-1804 1820 1825-1831 1836-1837 1839-1843 1845 1847-1848 1850-1851 1861-1867 1870 1874-1880 1882-1890 1895-1901 1907-1909 1931-1934 1946 1948-1951 1974 2010-2011 2013 2016-2022 2039-2040 2076 2085-2086 2088-2093 2105-2108 2110-2112 2124-2127 2137 2147-2156 2158-2159 2162-2166 2169-2174 2177-2178 2180 2188-2195 2197-2200 2204-2205 2207-2208 2216 2218 2230-2238 2240-2242 2284 2322-2327 2341-2344 2347-2350 2352-2356 2359-2361 2401-2406 2408-2410 2412-2417 2419-2423 2428 2430-2434 2452-2458 2480 2494-2499 2503 2505-2506 2515-2516 2518-2527 2533 2551-2552 2555 2557-2565 2569-2571

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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diaphragm	BioChain	DIA002	229-232 335-337 385-386 436-441 708 923-927 1006-1009 1211- 1212 1299-1301 1498 1541-1542 2806-2807 3560 4250-4255 4884- 4885 6763 7289-7290 7987
endothelial cells	Stratagene	EDT001	9-11 21 24-25 28-29 36 40-45 47 49-51 55-56 66 77-79 168-169 178-179 191-195 215-217 229-233 237-239 246-248 250-259 261- 266 268 270-273 282-284 311-320 323-325 329-331 335-337 340- 341 344 349-361 365-373 375 377 387-400 404-409 423 426-431 433-449 455 461-465 467-468 477 486-489 492-493 500 508-515 517-524 528-529 545-546 552-554 567-570 574-580 584-585 593 595-600 602-604 606-614 616 618-620 622 624 627-629 637-640

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetics Research	EPM001	2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetics Research	EPM003	2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3628-3629 3916-3921 3923-3932 3934-3936
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetics Research	EPM004	2251-2252 2254-2263 2266-2275 2277-2281 2994-2997 3533-3536 3538-3547 3549-3558 3628-3629 3916-3921 3923-3932 3934-3936 4765 4776 4787 4798 4809 4821 4832 4843 4854 4865 4876 5928 7023
esophagus	BioChain	ESO002	28-29 40-42 164-165 477 488 622 624 1110 1112 1115 2232-2233 3567 5752-5754 5918-5919 7289-7290 7808-7810 8024
fetal brain	Clontech	FBR001	178-179 323-325 1116-1118 1202-1203 1205-1207 1395-1399 1409 1428 1430 1486-1488 1694 1697 1701-1702 1737 1739-1740 1782 2024-2026 2147-2152 2710 2712 2899 2919 3023 3025 3087-3091 3093 3116-3117 3150 3322 3585-3586 3717-3718 3720-3722 3732 3867-3870 4021 4329-4330 4341 4805 4884-4885 4906 5641-5642 5760 5771 5782 6702-6703 6934-6937 7587-7589 7790
fetal brain	Clontech	FBR004	40-42 53 658 880-881 1022 1114 1355-1359 1361-1363 1667-1670 1729 1763 1772 1850 1861-1863 1870 1872-1873 1965-1967 2162-2163 2332-2339 2352-2356 2454 2494 2511 2793 2936-2937 3003-3008 3575-3576 3579-3580 3696 3698-3702 3893-3898 3909-3910 3912 3937-3940 4513-4514 4529 4845 4856-4860 5590 6636-6638 7113-7115 7161 7808-7810 8044-8046

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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fetal brain	Clontech	FBRs03	1400 1690 2638 3042 5149 6198 7366 7377-7379 7808-7810
fetal brain	Invitrogen	FBT002	40-42 47 60 69-73 178-179 210-212 237-239 265-266 311-314 335- 337 360-361 374 387 389-397 466 477 486-489 500 541-542 603- 604 606-614 616 627-629 654-655 744-745 826-827 841-845 872- 874 900 902 969 973 979 999-1000 1087-1088 1090-1094 1110 1112 1119 1156-1162 1164 1174-1175 1191-1193 1195-1196 1221- 1225 1227 1241-1242 1264-1265 1305-1306 1308-1309 1314-1317 1319 1338 1346-1348 1350-1359 1361-1363 1369 1376-1379 1381 1395-1399 1405-1406 1415 1428 1430 1432-1439 1442-1445 1479- 1481 1484-1485 1523-1524 1528 1534-1535 1552-1558 1562-1563 1601 1603 1612 1614-1619 1638-1641 1686-1693 1695-1696 1700 1703-1704 1706 1718 1730-1731 1763 1765-1767 1790 1792-1794 1823-1824 1844 1874-1876 1895-1901 1904-1905 1911-1913 1930- 1934 1938-1940 1962 1996-2000 2010-2011 2013 2024-2033 2035- 2036 2041 2052 2094-2097 2099-2100 2106-2108 2128-2129 2131- 2134 2147-2152 2164-2166 2169-2174 2177-2178 2180-2181 2234- 2238 2240-2242 2289-2294 2322-2327 2374 2381-2382 2385 2395- 2400 2407 2418 2429 2437 2448 2459 2463 2466-2470 2480 2482

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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fetal heart	Invitrogen	FHR001	229-232 903-904 1124-1125 1239 1305-1306 1308-1309 1355-1359 1361-1363 1690 2204-2205 2207-2208 2533 2638 3039-3040 3506 4053 4066 4320-4323 4325 4969-4971 5752-5754 7289-7290 7641- 7643 7771-7772 7987
fetal kidney	Clontech	FKD001	9-11 66 71-72 77-79 196-198 200 229-232 246-248 250-259 261- 264 309 335-337 397-398 400 432 450-454 456 476-479 483 486- 489 500-504 506 514-515 517 525-526 538 552-556 567-570 602- 604 606 645 658 726 753 769 856 872-874 884-885 923-927 954 959 973 999-1000 1006-1010 1051 1101-1103 1124-1125 1131 1151 1192-1193 1195-1196 1213-1214 1216-1218 1221-1225 1227 1264- 1265 1286 1318 1327 1338 1355-1359 1361-1363 1371 1380 1391 1395-1399 1402 1408-1413 1462-1465 1470-1471 1534-1535 1559 1561 1563 1648-1652 1680 1694 1697 1768-1771 1904-1905 1936 1947 2016-2022 2076 2102-2105 2110-2112 2137 2177-2178 2180 2200 2204-2205 2207-2208 2284 2322-2327 2350 2359-2361 2455- 2458 2496-2497 2575 2638 2678-2682 2708 2744-2745 2750-2753 2762-2764 2767-2768 2787 2792 2808-2812 2898 2909 2940 2973- 2974 2982-2987 3039-3040 3094-3095 3101-3102 3104-3105 3111 3116-3117 3122 3212 3219 3222 3230 3233 3311-3313 3325 3332- 3333 3439 3468-3469 3499-3501 3521-3523 3575-3576 3579-3580 3583 3600 3695 3713-3714 3726 3749 3763 3777 3799 3817-3819 3890 3900-3901 3956 3998-3999 4055-4056 4091-4097 4231 4260- 4264 4332 4369-4371 4465 4472 4523 4618-4619 4628-4631 4633- 4642 4644-4649 4698 4710 4744 4747 4791 4847-4853 4972 4978- 4980 5124-5126 5128-5130 5149 5151 5162 5204-5205 5207 5216 5218-5221 5233 5336 5338 5356 5399 5510 5540-5542 5590 5594 5605 5616 5627 5872 5875-5878 5918-5919 5956 5961 6022 6025- 6029 6103 6108 6124-6128 6413-6414 6641-6642 6696 6837 6839- 6848 6857-6859 6861-6862 6973-6977 7014 7098-7107 7109 7119 7175 7230 7238 7280 7285 7296 7307 7318 7329 7342 7353 7370 7377-7379 7423 7425-7426 7441 7587-7589 7634-7635 7706 7808- 7810 7839 7841-7845 7967 8012-8016
fetal kidney	Clontech	FKD002	28-29 318-320 385-386 426-430 477 488 552-554 686-688 690-691 1056-1057 1070-1071 1087-1088 1090-1094 1124-1125 1173 1264- 1265 1424-1426 1825-1826 1828-1831 1874-1876 2204-2205 2207- 2208 2359-2361 5051-5052 5654-5656 7377-7379 7425-7426 7808-

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fetal lung	Clontech	FLG001	40-42 335-337 602 617 666 668 722-723 979-985 999-1000 1056-1057 1341-1344 1370 1372-1373 1448-1449 1451-1456 1499 1691-1693 1695-1696 1703-1704 1706 1711-1713 1782 1910 2016-2022 2039-2040 2118 2120-2123 2204-2205 2207-2208 2230-2231 2234-2238 2240-2242 2282-2283 2363-2365 2425-2427 2664-2665 2667 2690-2694 2730-2733 2787 2982-2987 3095 3230 3328 3330 3468-3469 3499-3501 3521-3523 3717-3718 3720-3722 4053 4066 4083-4085 4236 4351 4473 4575 4577-4579 4628-4631 4633-4642 4644-4649 4703 4745 4847-4853 4892 4917-4918 4921-4926 4948-4951 5455 5613-5615 5617-5618 5628 5694 5705 5873-5874 6035 6046 6057 6413-6414 6515 6681 6984-6987 7289-7290 7367 7425-7426 7437-7438 7839 8010-8011 8044-8046
fetal lung	Invitrogen	FLG003	19 201 237-239 309 311-314 329-331 338-339 360-361 426-427 433 444 455 545-546 658-662 708 710-719 757-764 766 844-845 883 892 900 902 946-948 979 1001 1031-1035 1073-1080 1165 1177-1179 1243-1245 1355-1359 1361-1363 1395-1399 1408 1462-1465 1549 1560 1562 1604-1606 1640-1641 1657-1663 1705 1716 1727 1755-1760 1762 1773 1775-1777 1843 1974 2016-2022 2039-2040 2124-2129 2131-2134 2136 2284 2345-2349 2363-2365 2389-2390 2428 2430-2432 2528 2539 2545 2556 2567 2638 2682 2706-2708 2730-2733 2750-2753 2787 2808-2812 2898 2909 3039-3040 3078-3080 3082-3086 3101-3102 3104-3105 3151-3155 3209-3211 3213-3215 3356-3357 3457 3468-3469 3628-3629 3738 3741-3742 3764-3765 3791-3794 3806-3807 3809-3810 3913-3915 3937-3940 4016-4020 4053 4066 4091-4097 4114-4120 4136-4142 4144-4146 4150-4153 4157-4162 4164-4171 4218 4220 4307 4351 4377 4606 4659-4663 4667 4837 4847-4853 4872-4875 4877-4880 4917-4918 4921-4926 4981-4984 4986-4989 5090-5093 5095 5131-5132 5142-5143 5212-5215 5807-5810 5862-5868 5870 5977-5978 5987-5988 6147 6304 6404-6406 6413-6414 6454 6491 6850 6899-6900 6913 6933 6973-6977 6991 7012-7013 7016 7087-7089 7126 7186 7191 7197-7203 7256 7377-7379 7570 7600 7602 7609-7610 7676 7678-7680 7696 7698-7700 7808-7810 7874-7879 7954
fetal lung	Clontech	FLG004	265-266 476 478-479 552-554 1056-1057 1165 1365-1368 1424-1426 1552-1558 1690 2699-2704 3260-3261 7118 7121
fetal liver-spleen	Columbia University	FLS001	1 3 7 9-12 14 26-30 39 45 47 49-51 55 66 71-72 77-87 89-98 100-109 112-117 119-121 123-124 144 155 166-167 178-179 199 201-207 210 215-217 222-234 237-243 246-248 250-259 261-266 268 270-279 281-284 295-301 309 311-314 318-320 323-337 340-341 344 349-361 363-383 385-400 404-407 411-420 422 426-456 460 466 476-483 486-489 495-497 500-504 506-515 517-526 528-532 536-538 540-549 551-558 567-571 573-580 584-593 595-604 606-616 618-624 627-645 649-655 658-666 668 672-676 679-681 686-688 690-694 704-708 722-723 729-730 751-753 755 757-764 766-768 771-775 779-785 795 806 816 818-827 829-837 840-849 854-863 867-869 872-874 876-879 883-885 887-891 900 902 905-909 911-913 915-917 919-921 923-927 929-930 932 934 939-943 945 949-950 954 960-961 963-970 973-976 978-985 990-993 995-997 999-1013 1015-1019 1023 1031-1035 1037-1040 1042-1043 1049-1050 1053-1057 1063 1070-1072 1083-1086 1089 1095 1100-1103 1111 1114-1125 1127-1129 1131-1136 1140 1146-1148 1156-1162 1164-1165 1167-1172 1174-1179 1182-1191 1194 1198-1201 1204 1208-1209 1211-1214 1216-1225 1227-1232 1250-1251 1253-1257 1263-1265 1267-1268 1279-1281 1284-1285 1287 1289-1295 1297-1301 1303-1306 1308-1317 1319 1322-1325 1328-1331 1334-1337 1339-1344 1346-1348 1350-1359 1361-1363 1365-1368 1377-1379 1381-1387 1392-1400 1404 1408 1411-1415 1420-1421 1423-1428 1430 1438-1440 1442-1445 1447 1458-1460 1462-1465 1470-1471 1473-1477 1479-1481 1486-1493 1495-1496 1498-1499 1503-1504 1506-1509 1514-1515 1517 1520 1523-1524 1529-1533 1536 1538 1540-1542 1548 1552-1559 1561 1564-1569 1571 1576-1601 1603-

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fetal liver- spleen	Columbia University	FLS002	12 22-23 27-29 40-42 44 66 71-72 77-79 122 136-143 145-154 156- 163 170-175 192-193 205-207 215-220 223-232 237-239 246-266 268-277 280 295-301 311-317 326-328 332 334 340-341 349-354 356-361 365 367-375 382-383 385-387 389-398 400 404-407 411- 420 422 432 436-443 445-449 466 476 478-479 495-497 508-515 517-521 528-529 538 541-542 547-549 551 555-556 567-570 574- 580 586-593 595-600 602-604 606-612 618-620 627-633 635-645 649-653 657-662 666 668 677 679-683 686-688 690-692 707-708 722-725 727-728 730 732-741 743 748-749 753 757-764 766 772- 775 779-782 784-785 795 806 816 818 820-821 823-825 833-835 837 841-843 846-849 851 856-857 868 872-874 876-879 884-885 890 905-909 911-912 915-917 923-930 932 934 945-948 954 960- 961 963-965 967-968 972-973 980-985 991-993 995-1000 1005- 1009 1015-1017 1029 1031-1035 1037-1040 1042-1043 1049 1053 1081 1087-1088 1090-1094 1113 1116-1119 1127-1128 1131-1132 1136 1146-1148 1156-1160 1167-1172 1174-1176 1182 1184-1191 1202-1203 1205-1207 1211-1214 1216-1218 1221-1225 1227-1230 1236-1238 1241-1242 1246-1250 1253 1257-1258 1261 1263-1265 1279-1281 1283 1286 1290-1293 1303-1304 1323-1326 1328-1331 1338-1344 1369-1370 1372-1373 1377-1379 1381-1387 1419-1420 1423-1426 1447 1458-1460 1473-1478 1484-1485 1499 1501 1510- 1515 1517 1528-1533 1543-1547 1552-1559 1561 1564-1569 1571 1580 1589-1595 1601 1603 1611-1612 1614 1621-1622 1625 1628- 1633 1635 1638-1641 1645 1648-1652 1654 1657-1663 1671-1672 1674-1680 1691-1699 1705 1707-1709 1716 1718 1727 1730-1731 1741-1749 1751-1763 1768-1771 1774-1777 1782-1790 1792-1794 1796-1804 1806 1809 1823-1826 1828-1831 1843 1846 1848-1851 1857-1861 1867-1870 1877-1880 1882-1886 1888-1891 1893-1901 1903 1907-1910 1915-1918 1921-1924 1926-1934 1937-1940 1946 1948-1951 1962-1964 1968-1969 1971-1972 1976-1978 1980-1989 1991-2000 2002-2008 2010-2011 2013 2023-2037 2039-2040 2042- 2051 2053-2063 2066-2075 2077-2083 2085-2086 2088-2091 2105 2110-2112 2114-2117 2128-2129 2131-2134 2138 2141 2143 2146 2155-2159 2162-2163 2168 2171-2174 2177-2181 2187-2200 2204-

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fetal liver- spleen	Columbia University	FLS003	7 28-29 223-228 268 270-273 299-301 376 378-383 557-558 844- 845 923-927 1355-1359 1361-1363 2136 2284 2584 2699-2704 2795 3123-3125 3468-3469 3560 3562 4053 4066 4091-4097 4183-4185 6364-6365 6367 7116 7186 7197 7263 7274 7850 7852-7861 7893- 7894
fetal liver	Invitrogen	FLV001	7 49-51 55 78-79 223-228 237-239 265-266 282-284 295-301 309 311-314 335-337 363-364 375-376 378-383 387 389-397 433 444 455 460 474-475 480-482 495-497 536-537 540-542 586-592 613- 614 616 650-655 666 668 679-681 707-708 724-725 744-745 757- 764 766 816 818 822-825 840-845 872-874 900 902 919-921 945 963-969 979 999-1000 1011-1013 1047-1048 1051 1110 1112 1151- 1152 1163 1174-1175 1177-1179 1191-1193 1195-1196 1211-1214 1216-1218 1299-1301 1338-1340 1346-1348 1350-1359 1361-1363 1381 1405-1406 1514 1552-1559 1561 1585-1586 1589-1590 1592- 1594 1601 1603 1628-1633 1635 1642-1643 1698-1699 1703-1704 1706 1747-1748 1751-1754 1763 1775-1777 1850 1861 1870 1895- 1901 1904-1905 1923-1924 1926-1929 1938-1940 1962 1977-1978 1980-1989 1991 2063 2106-2108 2124-2127 2136 2177-2178 2180 2185-2186 2284-2286 2380-2382 2389-2395 2397-2400 2425-2428 2430-2432 2435 2476-2478 2480 2494 2503 2505-2507 2528 2533 2539 2545 2556 2567 2600-2601 2682 2730-2733 2787 2994-2997 3015 3039-3040 3043-3050 3052 3100 3151-3155 3173-3177 3244 3256 3266-3267 3274 3285 3296 3299-3302 3355 3436-3437 3449- 3450 3452 3468-3469 3506 3562 3610-3612 3620-3622 3743 3745 3829 3849 3944 3955 3967 4053 4064 4066 4087 4089-4097 4104- 4105 4138-4142 4144-4146 4150-4153 4172-4173 4176 4183-4185 4234-4235 4326-4328 4357 4368 4379 4445 4459 4491-4493 4516 4533-4539 4544-4546 4659-4663 4693 4728-4729 4806-4808 4810 4814-4815 4847-4853 4874-4875 4877-4880 4953 4981-4984 4986- 4989 5010-5013 5073-5074 5144-5146 5189-5190 5197-5202 5204- 5205 5207 5216 5218-5221 5270-5272 5274 5401-5404 5406-5407 5416 5427 5531-5533 5677 5703-5704 5747-5748 5760 5771 5782 5934-5935 5937-5938 5961 5987-5988 6030-6032 6104-6106 6145 6199-6200 6300-6303 6333-6335 6339-6340 6377 6388 6399 6410 6412 6420 6422 6450-6451 6453-6454 6470-6471 6499-6501 6607 6618 6654 6656 6704-6705 6755-6758 6765 6869 6872-6875 6922- 6923 6959 6968 6973-6977 6982 6984-6987 7012-7013 7016 7063 7069-7070 7118 7121 7186 7194-7195 7197 7262-7263 7274 7310- 7311 7393-7395 7427 7462-7465 7467-7468 7543-7544 7677 7686 7697 7771-7772 7795-7796 7808-7810 7837-7838 7847 7874-7879 7949-7952 7963 7993-7995 8041
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fetal liver	Clontech	FLV004	28-29 61-65 78-79 184-187 189-190 299-301 385-386 547-549 551 602 650-653 658 722-723 748-749 939-943 999-1000 1006-1009 1124-1125 1589-1590 1592-1594 1596-1600 1698-1699 1701-1704 1706 1782 1938-1945 2027-2033 2035-2036 2136 2177-2178 2180 2200 2204-2205 2207-2208 2215 2220-2223 2234-2238 2240-2242 2285-2286 2332-2339 2380-2382 2391-2394 2584 2600-2601 2714- 2715 2803-2804 2925-2929 2938-2939 2941-2942 2982-2987 3116- 3117 3122 3133 3171-3172 3506 3937-3940 4060-4062 4104-4105

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fetal muscle	Invitrogen	FMS001	237-239 246-248 250-259 261-264 318-320 323-325 332 334-337 363-364 382-383 476 478-479 518-524 555-556 571 573 654-655 666 668 674-676 710-719 724-725 744-745 757-764 766 782 876-878 887-889 891 903-909 930 963-965 967-968 1058-1061 1073-1080 1087-1088 1090-1094 1104-1109 1115 1119 1165 1177-1179 1202-1203 1205-1207 1213-1214 1216-1218 1266 1287 1289 1303-1306 1308-1309 1339-1340 1355-1359 1361-1363 1374-1375 1381 1448-1449 1451-1456 1462-1465 1484-1485 1529-1533 1563 1595 1671-1672 1705 1714 1716 1718 1727 1747-1748 1751-1754 1765-1767 1850 1857-1861 1870 1888-1890 1910-1913 1930 1959 1974 1977-1978 1980-1989 1991 2016-2022 2063 2092-2093 2137 2164-2166 2169-2170 2224 2284 2289-2294 2425-2427 2533 2682 2694 2708-2709 2726-2728 2750-2753 2762 2787 2795 2852-2854 2857-2858 2900-2908 2910-2914 2930-2931 2973-2974 2998-3001 3039-3040 3052 3134-3135 3156-3158 3212 3222 3233 3288 3356-3357 3385 3396 3431-3432 3444 3499-3501 3506 3548 3560 3588-3589 3683 3745 3788-3790 3836 3993-3994 4063-4064 4067-4068 4083-4085 4133 4336-4340 4357 4368 4379 4436 4486 4491-4493 4526-4527 4532 4571-4575 4577-4579 4616-4617 4761 4827-4831 4837 4847-4853 4892 4969-4971 5056-5060 5062 5078-5081 5125-5126 5128-5130 5137 5141 5149 5155 5228 5239 5282-5283 5285 5436 5478-5480 5537-5539 5566-5569 5671 5684-5692 5694 5705 5752-5754 5821 5854-5857 5900-5901 5908-5909 5998-6001 6030-6032 6083-6084 6143-6144 6181-6182 6294 6420 6422 6440 6442-6446 6454 6605 6681 6763 6851-6854 6872-6875 6939-6942 6948 7007-7010 7087-7089 7191 7194-7195 7256 7289-7290 7298 7358-7359 7377-7379 7551-7553 7587-7589 7664-7665 7673-7675 7771-7772 7808-7810 7899-7900 7943 7987 8024
fetal muscle	Invitrogen	FMS002	4-5 477 488 666 668 887-889 891 923-927 929 1056-1057 1266 1299-1301 1305-1306 1308-1309 1428 1430 1686-1689 1782 2063 2204-2205 2207-2208 2232-2233 2284 2425-2427 2956-2960 3052 4064 4508 5752-5754 7771-7772 7808-7810
fetal skin	Invitrogen	FSK001	7 9-11 16-17 40-42 55 66 77-79 123-124 136-143 145-163 166 178-179 237-239 246-248 250-259 261-264 309 311-314 323-325 335-339 368-374 376 378-383 387 389-396 404-407 423 432-433 444 450-456 476-482 488 501-504 506 514-515 517 522-526 538 552-556 559-560 562 574-580 584-585 607-612 622 624 645 647-649 654-655 658 666 668 684 686-688 690-691 704-706 708 710-719 722-723 753 767 771 780-782 785 829-832 840-845 856 864-867 869 872-874 887-889 891-892 900 902 911-912 923-927 935-936 945-948 954 963-965 967-969 979-985 988 994 1015-1017 1022 1031-1035 1051 1056-1061 1063 1072-1080 1083 1089 1100 1110-1112 1114-1119 1122 1129 1132 1140 1151 1161-1162 1164-1165 1177-1179 1211-1212 1221-1225 1227-1230 1264-1265 1287 1289 1305-1306 1308-1309 1317 1319 1328-1331 1355-1359 1361-1363 1374-1375 1381 1395-1399 1428 1430 1447 1458-1460 1470-1471 1484-1485 1489-1493 1495-1496 1514 1539 1541-1542 1550-1558 1572-1578 1580 1591 1601 1603 1621-1622 1625 1644-1646 1655 1657-1663 1665-1666 1674 1676-1678 1681-1684 1690-1693 1695-1696 1701-1709 1716 1727 1738 1746-1748 1750-1754 1765-1767 1782 1790 1792-1797 1843 1845 1857-1860 1866 1874-1876 1888-1890 1895-1901 1904-1905 1910 1922 1931-1934 1937 1964 1974 1977-1978 1980-1989 1991-1995 2002-2008 2010-2011 2013 2023 2027-2036 2039-2040 2063 2081-2083 2085-2086 2088-2093 2109 2114-2118 2120-2123 2137 2141 2146-2152 2157 2164-2166 2168-2170 2177-2180 2187-2199 2204-2208 2216-2218 2224-2226 2228 2234-2242 2244 2253 2265 2282-2284 2319 2331 2352-2356 2359-2361 2380-2382 2387-2388 2450-2451 2463 2480 2494 2498-2499 2528 2533 2539 2545 2556 2564-2565 2567 2599 2613-2615 2627 2629-2631 2639-2640 2646-2654 2656-2663 2679-2686 2688 2706-2709 2729 2738 2746 2750-2760 2762 2774-2777 2784 2792 2794 2806-2812 2822 2846 2849-2850 2855 2859-2860 2938-2939 2941-

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fetal skin	Invitrogen	FSK002	21 123-124 164-165 196-197 205-206 360-361 374 398 400 477 488 525-526 545-546 708 757-764 766 841-843 915-917 923-927 949- 950 973 1192-1193 1195-1196 1231-1232 1382-1384 1458-1460 1552-1558 1595 1611 1655 1657-1663 1690 1703-1704 1706 1711- 1713 1730-1731 1747-1748 1751-1754 1852-1855 1881 1892 1904- 1905 1911-1913 1946 1948-1951 1992-1995 2039-2040 2081-2083 2141 2143 2146 2157 2168 2179 2187 2196 2204-2208 2217 2228 2234-2242 2244 2253 2265 2319 2374 2385 2396 2407 2418 2429 2437 2448 2459 2470 2482 2496-2497 2584 2587 2598 2792 2798- 2804 2842-2843 2900-2908 2989-2990 2992-2993 3009 3064 3066- 3067 3071-3072 3101-3102 3104-3105 3122 3134-3135 3307 3325 3696 3698-3702 3904-3905 3937-3940 4022 4024-4025 4320-4323 4325 4549-4550 4552-4553 4621 4632 4643 4654 4734-4735 4806- 4808 4810 4837 4884-4885 4920 4931 5099-5101 5216 5218-5221 5338 5342-5349 5351-5352 5644 5962-5963 6148-6152 6249-6252 6720 6765 6872-6875 7038-7039 7291-7293 7377-7379 7791-7793 7839 7953 7955-7957
fetal spleen	BioChain	FSP001	28-29 385-386 450-454 456 552-554 593 595-596 649 730 1056- 1057 1264-1265 1498 2185-2186 2232-2233 2345-2346 4516 4554 4565 4576 5416 5427 6161-6162 6735 7231 7241 7252 7808-7810 7966
umbilical cord	BioChain	FUC001	7 28-29 40-42 55 71-72 123-124 155 166 178-179 194-195 223-232 237-239 246-248 250-259 261-266 302 309 323-325 329-331 335- 337 363-365 367 382-383 387 389-397 404-409 411-420 422 432- 433 442-444 455 460-465 467-468 476-479 488 500 514-515 517 522-524 538 571 573 584-592 597-600 602-604 606 618-620 627- 633 635-640 645 647-649 654-655 658-662 666 668 686-692 700 707-709 720 731 742 753 757-764 766 771 833-835 841-843 856 859-862 867 869 872-874 880-881 892-895 905-909 911-913 923- 927 929-930 935-936 954 963-965 967-969 973 979 987-988 994

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Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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induced neuron cells	Stratagene	NTD001	40-42 246-248 250-259 261-266 335-337 411-420 422 428-430 555- 556 567-570 613-614 616 703 771 854-855 858 872-874 915-917 969 1006-1009 1018 1056-1057 1063 1072 1083-1085 1089 1100 1111 1122 1129 1140 1264-1265 1291-1293 1382-1384 1395-1399 1529-1535 1615-1619 1657-1663 1701-1702 1718 1772 1783-1790 1792-1794 1843 1847 1864-1865 1996-2000 2016-2022 2024-2026 2081-2083 2105-2108 2204-2205 2207-2208 2220-2223 2322-2327 2332-2339 2345-2346 2350 2363-2365 2369-2370 2575 2625-2626 2628 2638 2641-2642 2672-2673 2679-2682 2742-2743 2792 2798- 2802 2835 2837 2919 2938-2939 2941-2942 3011-3012 3014 3039- 3040 3056-3063 3096 3116-3117 3123-3125 3134-3135 3150-3155 3230 3354 3395 3560 3617 3889 3958-3964 3977 3990 4017-4020 4087 4089-4090 4256-4258 4289 4329-4330 4406 4446-4449 4547- 4548 4571-4574 4623-4624 4664 4666 4781-4784 4802 4811 4827- 4831 5137 5141 5272 5274 5448 5563 5566-5569 5631-5632 5644 5654-5656 5694 5705 5791-5792 5794-5799 5908-5909 6022 6025- 6029 6092 6186-6188 6191 6198 6260-6265 6267-6274 6294 6360 6413-6414 6424-6427 6658-6660 6662-6666 6727 6883 7049-7051 7130 7146 7328 7375 7377-7379 7386 7441 7641-7643 7790 7808- 7810 7996
retinoic acid- induced neuronal cells	Stratagene	NTR001	9-11 28-29 178-179 323-325 431 434-441 477 486-489 559-560 562 666 668 844-845 949-950 969 1070-1071 1146-1148 1174-1175 1264-1265 1299-1301 1355-1359 1361-1363 1783-1789 1843 2200 2345-2346 4102-4103 4748 4791 5272 5274 7291-7293 7771-7772 7808-7810
neuronal cells	Stratagene	NTU001	28-29 71-72 80-87 89-98 100-109 112-118 340-341 368-373 477 488 501-504 506 552-554 584-592 666 668 686-688 690-691 707 826-827 841-845 854-855 858 872-874 900 902 911-912 919-921 949-953 956 963-965 967-968 1006-1009 1011-1013 1015-1018 1056-1057 1124-1125 1156-1160 1243-1245 1264-1265 1299-1301 1303-1304 1346-1348 1350-1359 1361-1363 1438-1439 1442-1445 1458-1460 1552-1558 1572-1575 1587-1588 1601 1603 1621-1622 1703-1704 1706 1747-1748 1751-1754 1845 1862-1863 1895-1901

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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pituitary gland	Clontech	PIT004	66 77 318-320 382-383 461-465 467-468 518-521 613-614 616 649 666 668 980-985 1056-1057 1165 1202-1203 1205-1207 1228-1230 1257 1284-1285 1303-1304 1576-1578 1648-1652 1654 1701-1702 1711-1713 1749 1783-1789 1849 1857 1977-1978 1980-1989 1991 2002-2008 2039-2040 2106-2108 2234-2238 2240-2242 2345-2346 2350 2533 2553-2554 2563-2565 2575 2629-2631 2638 2682 2787 3096 3151-3155 3212 3218 3222 3233 3422 3499-3501 3521-3523 3560-3561 3602 3613 3732 3788-3790 3867-3870 3902 3976 3996 4024-4025 4035-4039 4391 4445 4549-4550 4552-4553 4625 4664 4666 4668-4669 4703 5125-5126 5128-5130 5136 5203 5452-5454 5478-5480 5681 5987-5988 5998-6001 6130 6183 6220-6221 6862 7062 7186 7197 7790 7871-7872 8044-8046
placenta	Clontech	PLA003	205-206 282-284 385-386 552-554 844-845 1124-1125 2124-2127 2204-2205 2207-2208 2955 3026-3034 3036-3038 3732 4091-4097 4326-4328 5654-5656 5841-5845 6319-6320 6322-6330 6450-6451 6453 7808-7810
prostate	Clontech	PRT001	40-42 214 233 282-284 318-320 408-409 426-427 436-441 450-454 456 500 518-521 567-570 581-582 584-585 593 595-596 618-620 637-640 647-649 658 672-673 707 726 732-741 743 872-874 969 1005 1031-1035 1037-1040 1042-1046 1056-1057 1086 1101-1103 1115 1165 1167-1172 1191 1221-1225 1227-1230 1258 1261 1305- 1306 1308-1309 1355-1359 1361-1363 1365-1368 1382-1384 1411- 1413 1416-1419 1447 1473-1475 1500 1541-1547 1550-1551 1559 1561 1580 1591 1612 1614-1619 1644 1646 1674 1676-1678 1686- 1689 1737 1739-1740 1775-1777 1783-1789 1823-1826 1828-1831 1843 1862-1863 1887 1904-1905 1910 1922 1941-1945 1968-1969 1971-1972 2010-2011 2013 2084-2086 2088-2091 2118 2120-2123 2136-2137 2144 2201-2203 2216 2218 2345-2346 2350 2359-2361 2389-2390 2425-2428 2430-2432 2450-2451 2464-2465 2480 2495 2500-2502 2533 2544 2546 2549-2552 2558-2562 2584-2586 2588- 2589 2627 2706-2707 2742-2745 2787 2789-2791 2795 2823-2824 2842-2843 2922 2924 2943-2944 2955 2982-2987 3095 3116-3117 3227-3229 3271-3272 3303 3305 3313 3398-3400 3436-3437 3485 3499-3501 3517-3519 3585-3586 3588-3589 3631 3679 3681 3732 3736-3737 3739 3755-3757 3766 3777 3783-3784 3802 3828 3851- 3852 4063 4067-4068 4072-4074 4183-4185 4286-4288 4341 4355- 4356 4358-4360 4387 4392-4395 4401 4404-4405 4433 4443 4464 4466-4467 4473 4505-4508 4628-4631 4650 4699-4701 4703 4753 4755-4756 4774-4775 4937-4939 4959-4962 4997-4998 5002-5006 5008-5009 5056-5060 5062 5090-5093 5095 5137 5141 5171-5172 5174-5175 5399 5420 5435 5457 5526 5573 5583 5610-5611 5949 5962-5963 5966-5967 6004 6007 6069 6198 6202-6203 6235-6237 6292 6333-6335 6443-6446 6479 6612 6687-6688 6735 6771 6782 6794 7087-7089 7238 7248 7284 7286-7287 7377-7379 7462-7465 7482 7499 7624-7627 7667 7738-7739 7928-7930 7932-7933 7987 8001 8034-8035 8044-8046
rectum	Invitrogen	REC001	40-42 123-124 265-266 282-284 323-327 387 389-396 404-409 411- 420 422-423 476 478-482 484-487 489 500 518-521 559-560 562 586-592 617 674-676 744-745 747 823-825 841-843 892 896-899 969 979 990 1022 1036 1115-1118 1120-1121 1123 1213-1214 1216-1218 1447 1479-1481 1563 1572-1575 1580 1591 1604-1606 1612 1614 1640-1643 1657-1663 1679 1686-1697 1703-1704 1706

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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salivary gland	Clontech	SAL001	2 55 110 178-179 181-183 221 237-239 246-248 250-259 261-264 282-284 321 323-325 328-331 335-337 340-343 345-348 476-479 484-485 488 508-513 545-546 552-554 649 663-664 708 747 773 784 795 806 838 844-845 859-862 872-874 1019 1036 1049 1081 1133-1135 1165 1202-1203 1205-1209 1211-1212 1303-1304 1328-1331 1346-1348 1350-1359 1361-1363 1427 1462-1465 1498 1657-1663 1681-1684 1698-1699 1730-1731 1772 1782 1843 1845 1877-1886 1892 1895-1901 1931-1934 2010-2011 2013 2039-2040 2136 2141 2146 2157 2168 2179 2187 2196 2206 2217 2228 2232-2242 2244 2253 2265 2352-2356 2359-2361 2363-2365 2504 2510 2517 2544 2546 2549-2550 2555 2557 2564-2565 2575 2600-2601 2638 2682 2690-2693 2699-2704 2787 2842-2843 2846 3011-3012 3014 3039-3040 3043-3050 3095 3116-3117 3160-3168 3179-3180 3212 3222 3233 3323 3398-3400 3425-3428 3431-3432 3560 3575-3576 3579-3580 3626 3639-3645 3647-3656 3658-3667 3670-3672 3696 3698-3702 3749 3799 4002 4009 4035-4039 4207 4209 4218 4220 4265 4357 4368 4379-4382 4389 4400 4487 4598 4625 4696 4726-4727 4737-4739 4745 4796-4797 4814-4815 4817 4884-4885 4976-4977 5082 5166-5167 5270-5272 5274 5337 5455 5482 5484-5485 5501-5504 5506-5509 5537 5539 5645-5648 5654-5656 5761-5763 5833-5834 5873-5874 5934-5935 5937-5938 6163 6293 6411 6443-6446 6547-6548 6771 6782 6794 6851-6854 7453-7460 7487-7489 7512 7779-7780 7808-7810 7922-7923 7993-7995
salivary gland	Clontech	SALs03	484-485 613-614 616 887-889 891 1355-1359 1361-1363 2510 2517 6684 6695 7377-7379 7580 7590 7601 7612 7622 7633
skin fibroblast	ATCC	SFB001	903-904 1355-1359 1361-1363 1874-1876 2533 2638 2682 2744-2745 3212 3222 3233 3260-3261 3417 3419 4526-4527 4561 6198 6260-6265 6267-6274
skin fibroblast	ATCC	SFB002	584-585 903-904 1058-1061 1317 1319 1355-1359 1361-1363 1621-1622 2395 2397-2400 2638 3212 3222 3233 4102-4103 4369-4371 4526-4527 4745 5694 5705 6198 6260-6265 6267-6274
skin fibroblast	ATCC	SFB003	477 488 584-585 1231-1232 1355-1359 1361-1363 2016-2022 4526-4527 5918-5919 6198
small intestine	Clontech	SIN001	80-87 89-98 100-109 112-117 210 476 478-479 484-485 501-504 506 514-515 517 552-554 584-585 617 686-688 690-691 707 722-723 726 732-741 743 747 829-832 841-843 872-874 878 887-889 891 900 902 905-909 915-917 962 969 980-985 1005 1070-1071 1176 1247-1249 1286 1339-1340 1346-1348 1350-1354 1392-1394 1409 1420 1473-1475 1681-1684 1690 1703-1704 1706 1737 1739-1740 1775-1778 1796-1797 1848 1851 1881 1892 1895-1901 1935 2016-2023 2034 2137 2230-2231 2352-2356 2359-2361 2401-2406 2408-2410 2494 2564-2565 2613-2615 2708 2750-2753 2774-2776 2803-2804 2839-2841 2851 2855 2930-2931 2938-2939 2941-2942 2955 3020-3022 3144-3146 3149 3217 3255 3299-3302 3362 3385 3396 3422 3499-3501 3520 3560 3605 3614 3639-3645 3647-3656 3658-3667 3670-3672 3675 3717-3718 3720-3722 3732 3777 3803 3904-3905 3988-3989 4002 4201-4202 4271-4272 4281 4341 4433 4443 4445 4461 4490 4554 4565 4576 4607-4609 4611-4613 4628-

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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skeletal muscle	Clontech	SKM001	7 178-179 229-232 246-248 250-259 261-264 323-325 332 334 404-407 428-430 476-479 488 627-629 744-745 748-749 771 773 784 795 806 863 878 880-881 887-889 891 900 902-904 911-912 919-921 990 1146-1148 1273-1275 1299-1301 1370 1372-1373 1395-1399 1498 1517 1596-1600 1714 1730-1731 1755-1760 1762 1845 1887 1895-1901 2027-2033 2035-2036 2105 2188-2195 2197-2199 2234-2238 2240-2242 2425-2427 2452-2453 2466-2469 2529-2531 2584 2716-2717 2744-2745 2950 2961-2972 2980 2991 3276 3430-3432 3468-3469 3548 3560 3581-3582 3615-3616 3937-3940 4010-4011 4016 4172-4173 4176 4244-4245 4320-4323 4325 4373-4374 4446-4449 4455 4650 4708 4711 4728-4729 4737-4739 4847-4853 4897 4969-4973 5441 5478-5480 5591-5593 5595-5596 5752-5754 6040-6042 6092 6443-6446 6553-6554 6601 6605 6715-6716 6933 7123-7125 7190 7289-7290 7512 7517 7551-7553 7738-7739 7779-7780 7987 8024
skeletal muscle	Clontech	SKM002	584-585 887-889 891 903-904 1888-1890 3548 3592-3596 6260-6265 6267-6274
skeletal muscle	Clontech	SKMS03	584-585 887-889 891 903-904 1888-1890 7551-7553
skeletal muscle	Clontech	SKMS04	887-889 891 903-904 1198-1201 1888-1890 2638 4847-4853 7098-7107 7109
spinal cord	Clontech	SPC001	9-11 40-42 53 66 71-73 77 80-87 89-109 112-117 123-124 133 178-179 194-195 246-248 250-259 261-264 282-284 311-314 328 335-337 375 382-383 397 411-420 422 426-427 433 444-447 455 476-479 488 500 508-515 517 528-529 545-546 552-554 584-585 597-600 602 630-633 635-636 647-648 659-662 666 668 686-688 690-691 708 729 771 780-781 876-877 923-927 929 959-961 969 973 979 988 994 999-1000 1002-1003 1006-1009 1031-1035 1063 1072-1080 1083 1089 1100 1111 1114-1115 1122 1124-1125 1129 1136 1140 1202-1203 1205-1207 1241-1242 1299-1301 1305-1306 1308-1309 1341-1344 1346-1348 1350-1359 1361-1363 1365-1368 1395-1399 1448-1456 1461 1472 1484-1485 1499 1525 1528 1534-1535 1612 1614 1621-1622 1648-1652 1657-1663 1665-1666 1698-1704 1706 1718 1732-1736 1738 1747-1748 1750-1760 1762-1763 1775-1777 1783-1789 1836-1837 1839-1843 1845 1862-1863 1866-1867 1874-1876 1895-1901 1910 1923-1924 1926-1929 1935 1938-1940 1965-1967 1977-1978 1980-1989 1991 1996-2001 2010-2013 2016-2023 2034 2039-2041 2052 2063 2118 2120-2123 2136 2143 2153-2154 2216 2218 2220-2223 2234-2238 2240-2242 2276 2289-2294 2319-2321 2345-2350 2352-2356 2359-2361 2466-2469 2494 2509 2534-2538 2540-2543 2551-2552 2558-2562 2564-2565 2575 2579 2584-2586 2588-2589 2632-2634 2638 2679-2686 2688 2690-2693 2714-2715 2772 2787 2798-2804 2813 2823-2824 2839-2841 2856 2865 2876 2921 2930-2931 2933 2946-2948 2950-2951 2955 2961-2972 2980 2982-2987 2989-2993 3020-3022 3039-3040 3052 3056-3063 3078-3080 3082-3091 3093 3095 3101-3102 3104-3105 3116-3117 3120 3150-3155 3183 3194 3203 3221 3223-3224 3234-3235 3246-3248 3299-3302 3347 3350 3363 3374 3393 3433-3434 3454-3456 3499-3502 3506 3521-3523 3560 3605 3681-3682 3713-3714 3762 3791-3794 3806-3807 3809-3810 3814 3832-3833 3853-3854 3856-3859 3862-3865 3867-3870 3887 3909-3910 3912 3986 3990 3998-3999 4010-4011 4064 4102-4103 4126 4183-4185 4193 4230 4241 4248 4287-4288 4373-4374 4396 4429 4464 4466-4467 4473 4483 4490 4549-4550 4552-4553 4587 4590-4591 4599 4610 4633-4642 4644-4649 4651-4653 4655-4658 4732 4749 4838-4841 4847-4853 4884-4885 4893-4896 4899 4906 4952 4954-4958 4978-4980 5002-5006 5008-5009 5094 5118-5120 5138 5144-5146 5156-5161 5163 5173 5184 5195 5206 5216 5218-5221 5223 5228-5232 5236-5240 5329-5330 5333-5335 5376-5380 5435 5441 5452-5454 5462-5463 5478-5480 5497 5534-5536 5631-5632 5634 5636 5667-5670 5694 5705 5707 5713-5714 5786 5862-5868 5870 5872 5979 5981-

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thymus	Clontech	THMc02	6 9-11 20-21 55 61-66 77 80-87 89-98 100-109 112-118 122-124 164-165 196-197 223-233 246-248 250-259 261-266 318-320 360- 361 368-374 387 389-396 432 448-454 456 476-479 488 495-497 501-504 506 514-515 517 525-526 533-535 538 545-546 552-554 586-593 595-596 607-612 645 649 658 663-664 670-671 686-688 690-691 704-706 708 710-719 732-741 743 753 757-764 766 771 780-781 822 844-845 856 884-885 900 902 919-921 929 949-950 954 973-976 978-985 988 994 1005 1024-1028 1031-1035 1049 1054-1055 1065-1067 1087-1088 1090-1094 1115 1120-1121 1123- 1125 1127-1128 1133-1135 1156-1160 1174-1175 1183 1192-1196 1198-1201 1204 1210 1221-1225 1227 1231-1232 1264-1265 1279- 1281 1284-1285 1314-1316 1334-1336 1355-1359 1361-1363 1365- 1368 1371 1380 1382-1384 1391-1394 1402 1410 1422 1424-1426 1428 1430 1448-1449 1451-1456 1462-1465 1486-1488 1498 1501 1503-1504 1506-1507 1510-1513 1543-1547 1552-1559 1561 1572- 1578 1587-1588 1595 1611 1640-1641 1648-1653 1680-1684 1686- 1689 1703-1704 1706-1709 1711-1713 1737 1739-1740 1782-1789 1807 1820 1827 1836-1837 1839-1842 1862-1863 1872-1873 1881 1892 1895-1901 1904-1905 1914 1925 1935 1975 2010-2011 2013 2024-2033 2035-2036 2039-2040 2081-2086 2088-2091 2110-2112 2128-2129 2131-2134 2143 2147-2152 2171-2174 2188-2195 2197- 2199 2204-2205 2207-2208 2230-2231 2234-2238 2240-2242 2285- 2286 2288-2294 2345-2349 2352-2356 2359-2361 2374 2385 2387- 2394 2396 2407 2412-2423 2425-2427 2429 2437 2439-2444 2448 2454 2459 2464-2465 2470 2482 2490-2491 2504 2511 2515-2516 2518-2527 2558-2562 2595-2597 2607-2611 2613-2615 2617-2626 2628-2631 2635-2636 2641-2642 2668-2670 2682-2686 2688 2690- 2693 2708 2718-2721 2723-2725 2729 2738 2742-2743 2746 2757 2764 2767-2768 2772 2781-2783 2785-2786 2798-2804 2808-2812

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thyroid gland	Clontech	THR001	28-29 44-45 55 144 178-179 205-206 229-233 246-267 269 280 318- 320 323-327 332 334-337 340-341 349-354 356-361 365 367 374 376 378-381 385-387 389-398 400 408-409 428-432 434-443 445- 449 461-465 467-468 476 478-479 514-515 517 522-526 528-529 536-540 550 552-554 559-560 562 574-582 586-593 595-596 602 607-612 617 622 624 630-633 635-640 645 647-649 654-655 657- 658 666 668 670-676 685 704-707 710-719 722-723 747 753 768 770-772 774-775 780-782 840-845 851 854-856 858 872-874 878 880-881 884-885 900 902-909 911-912 914-917 923-927 929 938- 943 954 963-965 967-970 973 979 999-1000 1002-1003 1005-1009 1015-1020 1031-1035 1037-1040 1042-1043 1054-1057 1063 1068- 1069 1072 1081 1083 1087-1094 1100-1103 1110-1112 1115 1119- 1123 1129-1130 1136 1140 1165 1167-1173 1176 1183 1192-1196 1204 1210 1213-1214 1216-1218 1228-1230 1236-1237 1246-1249 1257 1283 1291-1293 1303-1304 1314-1317 1319 1322 1328-1331 1341-1344 1349 1355-1359 1361-1363 1370 1372-1375 1382-1390 1395-1399 1404 1411-1413 1415-1419 1424-1426 1446-1449 1451- 1456 1458-1460 1462-1465 1476-1477 1486-1488 1498-1499 1503- 1504 1506-1507 1510-1513 1515 1536 1538 1562 1565-1566 1580 1591 1595 1601 1603 1611 1627 1653 1657-1663 1679 1690-1693 1695-1696 1698-1699 1701-1706 1711-1713 1716 1727 1730-1731 1738 1750 1755-1760 1762-1763 1772-1773 1775-1777 1779 1781- 1790 1792-1794 1796-1797 1820 1825-1831 1843 1845 1857 1871 1877-1880 1882-1887 1895-1901 1904-1905 1911-1918 1922-1929 1931-1935 1962 1974 1992-2000 2002-2008 2010-2011 2013-2022 2024-2033 2035-2036 2039-2040 2081-2083 2085-2086 2088-2091 2102-2109 2114-2117 2136-2138 2143 2147-2156 2158-2159 2162- 2163 2171-2174 2181 2188-2195 2197-2203 2209-2214 2216 2218 2220-2223 2225-2227 2229-2238 2240-2242 2251-2252 2254-2263 2266-2281 2289-2294 2328 2330 2332-2339 2341-2344 2350 2352- 2356 2359-2361 2371-2372 2375 2381-2384 2386 2391-2394 2425- 2428 2430-2432 2435 2439-2444 2449-2454 2464-2465 2476-2478 2480 2490-2491 2507 2512-2514 2529-2531 2533 2535-2538 2540- 2543 2551-2554 2563-2565 2569-2571 2576-2577 2584-2598 2600- 2601 2629-2631 2635-2636 2639-2642 2672-2676 2679-2682 2695- 2697 2708-2709 2716-2717 2750-2756 2758-2760 2763-2764 2767-

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
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trachea	Clontech	TRC001	<p>19 54 56 178-179 360-361 365 367 450-454 456 484-485 500 586-592 603-604 606 613-614 616-617 657-658 663-664 674-676 747 782 837 872-874 893-895 914 938-943 980-985 1070-1071 1101-1103 1115-1118 1137-1139 1141-1145 1156-1160 1174-1175 1219-1220 1236-1237 1291-1293 1303-1304 1338 1411-1413 1419 1424-1427 1450 1461 1472 1604-1606 1621-1622 1694 1697 1796-1797 1845 1856 1990 2010-2011 2013-2015 2102 2118 2120-2123 2136 2155-2156 2158-2159 2220-2223 2289-2294 2345-2346 2350 2363-2365 2439-2444 2492 2498-2499 2555 2557 2580-2583 2585-2586 2588-2589 2612 2632-2634 2674-2676 2694 2744-2745 2774-2776 2830-2833 2982-2987 3024 3035 3039-3040 3095 3097 3116-3117 3159 3170 3181 3183 3212 3222 3233 3262-3264 3313 3322 3332-3333 3491-3493 3520 3682 3732 3799 3815 3968 3978 3987 3997 4006 4114-4120 4135 4138-4142 4144-4146 4183-4185 4207 4209 4232 4237 4243 4249 4273 4287-4288 4373-4374 4380-4382 4422</p>

Tissue Origin	Tissue/ RNA Source	Library Name	SEQ ID NO:
			4533-4536 4587 4598-4599 4610 4628-4631 4650 4691-4692 4726-4727 4745 4777 4795 4813 5362-5364 5376-5380 5478-5480 5853 5872 5875-5878 5943-5945 5983-5984 6099 6134 6222 6224-6226 6242-6243 6260-6265 6267-6274 6295-6298 6755-6758 6827 6855 6893 6905 7038-7039 7122 7328 7595-7596 7895-7897 7993-7995
uterus	Clontech	UTR001	2 30 74-76 110 155 166 213 221 233 318-321 323-325 335-337 411-420 422 477 488 514-515 517 528-529 555-556 584-593 595-596 618-620 647-649 659-662 769 840 854-855 858 880-881 896-900 902 915-917 923-927 973-976 978 1018 1024-1028 1056-1061 1063 1072 1082-1083 1089 1096-1100 1111 1115 1122 1124-1125 1129 1131 1140 1166 1176 1183 1185-1190 1194 1202-1207 1284-1285 1303-1304 1355-1359 1361-1363 1395-1399 1423-1426 1476-1477 1505 1525 1611 1642-1643 1648-1652 1674 1676-1678 1690 1701-1702 1719-1725 1741-1745 1765-1767 1775-1777 1783-1789 1796-1797 1825-1826 1828-1831 1862-1863 1930 1992-1995 2010-2011 2013 2081-2083 2136 2153-2154 2177-2178 2180 2216 2218 2371-2372 2375 2381-2382 2428 2430-2432 2436 2438 2500-2502 2528 2539 2545 2556 2564-2565 2567 2572-2574 2585-2586 2588-2589 2682 2713 2774-2776 2781-2783 2785-2787 2795 2910-2914 3095 3226 3236-3237 3265 3328 3330 3347 3443 3485 3499-3501 3524-3525 3527-3529 3568-3571 3585-3586 3683 3758-3759 3761 3821-3822 3950 4024-4025 4147-4149 4172-4173 4176 4264 4287-4288 4298-4301 4303 4357 4368 4373-4374 4379 4392-4395 4424 4465 4473 4490 4575 4577-4579 4616-4617 4667 4673-4674 4747 4796-4797 4856-4860 4897 4978-4980 5078-5081 5099-5101 5138 5155 5204-5205 5207 5236-5238 5240 5376-5380 5401-5404 5406-5407 5418 5428-5430 5462-5463 5833-5834 5918-5919 6022 6025-6029 6055-6056 6058-6060 6069 6189 6245 6251-6252 6368-6369 6412 6545-6546 6675-6676 6732 6772 6983 7179-7180 7271 7326 7400-7405 7437-7438 7462-7465 7494 7504 7515 7526 7535 7546 7558 7569 7814 7829 7839 8034-8035

TABLE 2

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Met h o d	SEQ ID NO: in USSN 09/577,408	Nucleotide location corresp. to first residue of peptide sequence	Location of first nucleotide of codon corresp. to last residue of peptide sequence	Amino acid sequence (X= Unknown; *=stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion)
1	8052	A	1	2	424	
2	8053	A	10	67	373	FCDCHHFI LMFKSPHIWPGIFSSWLLCF FWACLHHSLSIALLSCTKRYSGLILYFLC SSFEITVSSKSSVSF*RRMVFRNQVLGSR CACCC*GVAAPRPFP
3	8054	A	100	404	1072	ARACKIPNTASDRPII VALQRKSSPKMT QSAAGTCPTSCMIK/IDSHKCGDDRELFA QAPVDQFPGTAVESVTDSSRYFVIRIEDG NGRRAFIGIGFGDRGDAFDNFVALQDHF KWVKQQCEFAKQAQNPDPQPKLDLGF KEGQTIKLNIANMKKKEGAAGNPRVRP ASTGGLSLLPPPPGGKTSTLIPPGGE/PVG CGGIPRPASSCSQFRSTSSQTQPGTGW
4	8055	A	1000	2	333	ACPFNKSAEDLLNL/RQGLTAGQLPFLP WWNIVLDSP/SLTSIPATSFSTSLATARAR SASEVPIWKTLFCSLSQVRKTRRSSGAT KSTVLSTSLTLLH*IILRSISSSQ
5	8056	A	1001	292	945	
6	8057	A	1002	46	493	
7	8058	A	1003	2	406	
8	8059	A	1004	192	548	
9	8060	A	1005	1	528	DNELLDYEDDEVETAAGGSMS/EAPAKK DVKGSYFSIHSSGFRDFLKPELLRAIVD CGFEHPSEVQHECIPQAILGMDFLCQAK SGMGKTAVFVLATLQQLPVTGQVSVL VMCHTRELAFQTR*KTRPFWNVTVCPSG EDTRVGVKETLLPPPLTAPTPWLPSFASP PLLNPHF
10	8061	A	1006	807	1034	
11	8062	A	1007	136	1520	LFTPCFHLFCENPSRSPFPSSPAGPVMAE NDVDNELLDYER*MRWETAAGGDGAE APAKKDVNGLLCLPSHSSGFRDFLKPE LLRAIVDCGFEHPSEVQHECIPQAILGN GMSCARAKSGSGERQAVFVLATLQGLE PVTGQGV CAG*CCHTRELAFQISKEYER FSKYMPNVKVA VFFGGLSIKKDEEVLKK NCPHIVVGTGRILALARNKSLNLKHIKH FILDEC DKMLEQLDMRRDVQEIFRMTPH EKQVMMFSATLSKEIRPVCRKFMQDPM EIFVDDET KLT LHLGLQQYYVKLDNEKN RKLFDLLDVLEFNQVVIFVKS VQRCIAL AQLLVEQNFP AIAIHRGMPQEERLSRYQ QFKDFQRRILVATNLFGRGMDIERVNIAF NYDMPEDSDTYLHRVARAGRFGTKGLA ITFVSDENDAKILNDVQDRFEVNISELPD EIDISSYIEQTR
12	8063	A	1008	92	191	
13	8064	A	1009	219	422	
14	8065	A	101	2	477	IVSPEVRWAPGVAMEESGYESVLCVKPD VHVYRIPPRATNRGYRAAEWQLDQPSW SGRLRITAKGQMAYIKLEDRTSGELFAQ APVDQFPGTAVESVTDSSRYFVIRIEDG NGRRAFI*IGFGDRGDAFDNFVALQDHF KWVKQQCEFAKQAQNPDPQG
15	8066	A	1010	215	416	
16	8067	A	1011	261	486	GFLGKVLQSPATTVVRTLNDRSSIVMGE PISQSSSNSQ*FFFFKENSRLFC LG*CAVE QHFSSIFHCVD FYII

17	8068	A	1012	31	2697	
18	8069	A	1013	306	439	
19	8070	A	1014	149	404	
20	8071	A	1015	2	343	
21	8072	A	1016	172	341	
22	8073	A	1017	73	408	
23	8074	A	1018	53	237	
24	8075	A	1019	51	480	
25	8076	B	102	118	419	XLFCVDIDECSIMNGGCETFCTNSEGSYE CSCQPGFALMPDQRSCTDIDECEDNPNIC DGGQCTNIPGEYRCLCYDGFMASEDMK TCVDVNECDLNPNICLX*
26	8077	A	1020	49	399	
27	8078	A	1021	564	651	
28	8079	A	1022	2	366	SLPASDRPPISSPLATSGTIFSAISCFWDLF APFLWLAPSCQPTMSSQIRQNYSTDVEA AVNSLVNLYLQASYTYLSLQDIKKPAED EWGKTPDAMKAAMALEKKLNQALLDL HALGSART
29	8080	A	1023	18	781	EICPSRPKNSARRGGPAGLSLASTVFGRN RSGDWASSLRPPSDFLLRLQPPGSPYRPS PASGTCQHRFLWLAPSCQPTMSSQIRQ YSTDVEAAVNSLVNLYLQASYTYLSLG FYFDRDDVALEGVSHFFRELAEEKREGY *RLKMQNQVRGGRALFQDIKKPAEDEW GKTPDAMKAAMALEKKLNQALLDLHA LGSARTDPLCDFLETHFLDEEVKLIKK MGDHLTNLHRLGGPEAGLGEYLFERLTL KHD
30	8081	A	1024	217	608	
31	8082	A	1025	147	430	
32	8083	A	1026	489	700	
33	8084	A	1027	899	1097	QPAGPSLTRCATAQALCTTLPCCLVKQ DGSTIHIRYREPR/QQCWRMPIDDLTSP EERRARLRKR
34	8085	A	1028	59	426	
35	8086	A	1029	1	2148	
36	8087	A	103	59	450	CLGVTVKDVNQEFVRALAAFLKKS KLKVPEWLDTVKLLAKHKELAPYDEN WFY/SREFVRNLASTARHLVLRGGRWG LAPLTKIYGGDVQRKRAFIAPAFSRGSK SVARRVLQALIEGLKMVEKDQD
37	8088	A	1030	193	564	GDSGGSPWPDEKPKGEVKTENNDHINLK VAGQDGSVVQFKIKRHTPLSKLMKAY CEKQGLSMRQIRFRI*PGNPIHETDTPAP VGKWKDERYQLMVFFQARPGGVYLKK GTCFFYSKNSVSF
38	8089	A	1031	216	372	
39	8090	A	1032	566	787	
40	8091	A	1033	2	401	
41	8092	C	1034	379	453	
42	8093	A	1035	2465	2795	
43	8094	A	1036	1264	1385	
44	8095	A	1037	1249	1457	
45	8096	A	1038	146	438	
46	8097	A	1039	2	2387	
47	8098	A	104	583	1526	PHLILQVTKAMCPFESGRESFLVVSICIYF KPDSSASFSPDPYSVQC*PQLEPPPHCST SIYFPK/PTLPHIPFPPLTKHPKEDLELA GWTSSGCFYFSLPSTKLGENWSLHPQSH VYRSGDLVGSF*LLSQLHNRNPSICSL KGPPPREGLGNDPVSTNTAPYPRNLP*DL QRTIFSSPSIFYPGPPGAPSGES*NP*ELEG ILEVF*LELCPT/VH*HQPGLVFPPPSGLF SSFPPQKILTHRFLVQASKPTPLPLRLC PI.WSPSHYPSSILAPSSSLEFGPGSPOKTL

						PLWSPSHYPSSLAPSSSLEFGGSPQKTL E*PPLPKKQTD RHAPGPE
48	8099	A	1040	1	1329	
49	8100	A	1044	3	581	
50	8101	A	1045	1	741	PLTRAAGIRHEDSQSVGNSSPEIPVLPEPA YQLGPLCQVLP RRAGSSCLPVMTRTVKL WDKSSRECVHSYCEHGGFVTYVDFHPS GTCIAAAGMDNTVKVWDVRTHRLLQH YQLHSAAVNGLSFHPSGNYLITASSDSTL KILDLMGRLLYTLHG HQGPATTVAFSR TGEYFASGGSDEQVMVWKRNF DIGDHG EVTKVPRPPGTLASSMGNLTVSILEQRLT LTEDK LKQCLNQQLIMQRATP
51	8102	A	1046	526	1272	
52	8103	A	1047	57	307	
53	8104	A	1048	1669	1820	
54	8105	A	1049	212	547	
55	8106	A	105	1283	1648	SSGASVAPTSWTSNRFPF*SWVPSSF*RT HGPRPSGPPRRERKPRAPGQEPKGT PRES VCLNDLPCPGLLGICRPILQTSP/CHGHH GILSVNV LKGD KPSRSLGLPVFHNH HFRDLSVL
56	8107	A	1050	670	1296	
57	8108	A	1051	243	335	
58	8109	A	1052	1	1170	
59	8110	A	1053	1	1122	
60	8111	A	1054	1	392	
61	8112	A	1055	47	296	
62	8113	A	1056	1	315	
63	8114	A	1057	1	579	
64	8115	A	1058	87	507	
65	8116	A	1059	866	1002	
66	8117	C	106	263	304	MLKLSVRNRETFL*
67	8118	A	1060	385	573	
68	8119	A	1061	328	530	
69	8120	A	1062	6	664	LPGRPTRAPTRPAEHSIVGTRLVSCQLQP SQPNADQGKLT TMRIAVICFCLLGITCAI PVKQADSGSSEEKQLYNKY PDAVATWL NPDPSQKQNL LAPQTLPSKSNESHDMMD DMDDEDDDDHVDSQDSIDSNDSDDVDD TDDSHQSDSHHSDESDELVTDFPTDL PATEVFTPVVPTVDTYDGRGDSVVYGLR SKSKKFRRPDIQYPDATDEDITS
70	8121	A	1063	2	613	PRVRPRVREEAEHSIVGTRLVSGQLQPSQ PNADQGKLT TMRIAVICFCLLGITCAIPV KQADSGSSEEKQLYNKY PDAVATWLN DPSQKQNL LAPQNAVSSEETNDFKQETL PSKSNESHDMMDMDDEDDDDHVDSQ DSIDSNDSDDVDDTDDSHQSDSHHSDE SDELVTDFPTDLPATEVFTPVVPTVDTY DGRGDSVG

71	8122	A	1064	1	1073	TDCRVDPVIRVRVEHSIVGTRLVSCQ LQPSQPNADQGKLTMMRIAIVICFLLGIT CAIPVKQAESIGSSEEKQLYNKYPDVA TWLNPDPSQKQNLAPQVTLPSKSNESH DHMDMDMDEDDDDHVGRTARDSIGLG TTLDGCRMDTGWIFHQF*WSLHHFWME SGWNWSLDFSPRDLAQATEVFQFQFVP TVDTYDGRGDSVVYGLRSKSKFRRPDI QYPDATDEIDITSHMESEELNGAYKAIP VGPDPA PSDWDSRGKDSYETSQDDQ SAETHSHKQSRLYKRKANDESNEHSDVI DSQELSKVSREFHSHEFHSHEDMLVVD KSKEEDKHLKFRISHELDSASSEVN
72	8123	A	1065	1	1128	LETPIDSPRNRPGNPGATHASGRQSTAS SGPDSVSGQLQPSQPNADQGKLTMMRIA VICFLLGITCAIPVKQADSGSSEEKQLY NKYPDAVATWLKP*PIFRRQNLGPTW LCPLKETNDFKQGGPFPS*GPTERPWT WDDMG*WKVDGWTMWDSQDSIDSND SDDVDDTDDSHQSDSHHSDESDELVT GFSTDLPA TEVFTPVPVTVDTYDGRGDS VVYGLRSKSKFRRPDIQYPDATDEHITS HMESEELNGAYKAIPVAQDLNAPSDWD SRGKDSYETSQDDQSAETHSHKQSRL YKRKANDESNEHSDVIDSQELSKVSREF HSHEFHSHEDMLVVDPKSKEEDKHLKF RISHELDSASSEVN
73	8124	A	1066	514	1000	
74	8125	A	1067	1	1098	
75	8126	A	1068	2388	2658	FYKVTFMWKS VKSLGDNFVLGSVVP FLFFFFFLRWSLALLPRLECSGAISAHCI LCLPGSSNS/PASASQVVGITGTCHHAWL IFLYF
76	8127	A	1069	788	1000	
77	8128	A	107	426	1519	AWRRRRSGTSGKATWWCSGLRRASPTP SRRVQSWATAVMWKPSPPSSPASWE/PA LPREPHRAVSEQRQ*GR*PCKPELTAPLC LEPVHRPEGPMGT/YSRCCSPLHRP/PGP VGTFPV/SPEPVHRPQDPWHIPGVPEPVH RPQDPWHIPGVPEPVHRPQDPWHIPGV EPVHRPQDPWHIPGVPEPVHAPTGPVAL ASVGASSRDGLLPAHAAACTLHETAGQ TRTSRLSPS*GLGLPFCRRSRQPWTPAL GHSKTSGEWRGGARPGPCGC*CCMLSPT QQPLPGGHPQRRARASPRAGEG*TSRAYL AVHAAATLWKLPLPEDPPPLLDARISAH RPLCPSGRHRKVSFLTLTFSISCEARKIG
78	8129	A	1070	306	1195	
79	8130	A	1071	3	715	FVAHTKGVRGLPSMRRSPDCGRMELAA GSFSEEQFWEACAEQQPALAGADWQL LVETSGISYRLLDKKTGLYEYKVFGVLE DCSPTLLADIYMDSDYRKQWDQYVKEL YEQECNGETVVYWEVKYFPMSNRDY VYLRQRRLDMEGRKIHVILARSTSMPO LGERSGVIRVKQYKQSLAIESDGKKGSK VFMYYFDNPGGQIPSWLINWAAKNGVP NFLKDMARACQNYLKKT
80	8131	A	1072	1	1128	
81	8132	A	1073	3	862	
82	8133	A	1074	1	912	MTDNILELAQNMDKYTKYEMTTTSILSQ PSSSQREQDQGQFQELTVTSEMFRKGKG SFCSHPHPEKFLRTFNEIETYLIGNFQDLE LESSDDLPRGCTNEKARKTYDPKKLPLP YT/VRPCWILASKLHI*ESYG*RQ*A**CH Q*TPWPRPVWWSLHTEAHEIWCRRSDQ GTSLGSRIPCPPVLC*ERSTYDLR/PQTD QPSKHLTNLKSASTPPYPNFITSPHTRS GLQFRSTSSPPAPAQQFTLKKVAEAKGIV KVNAPESI.SDI.SOISVRI.GSFIKYEKSSPV

						KVNAPFSLSDLSQISVRLGSGFIKYEKSSPV HGSFGSNPETLYSPRP
83	8134	A	1075	611	817	
84	8135	B	1076	1	1500	MRTREVSITGADFTALLVDIIGNSTSYLT EIFKSTSILSVNQSNESDCIFCVMTGKSG RNLSDFWIEEEKYPIINYFTTSGLSGV LAL LLTQSLFGGLFTRTRMKFGAVTRIGGPPL GNQSPSSCSLLHEKDPPTSGPQTDQPKK HLTNFKSGTEEAMNTTSLAPAAEIMAT PGSPSQASPTSGAFTHGTQTPSPTKATAP RYPQTGAQSRPRRRFRPPAGAAPKAAA PRHPHPRGTAPPPRRISPESIRPHPPPLDR GPRPPVTPFLIVLGCLILAVLTTKEYETV SGDWLLLLLETFAIFIGAFAFALRIWAAGC CCRYKGWRGRCLKFARKPLCMLDIFVLIA SVPVAVGNQGNVLATSLRSLRFLQILR MLRMDRRGGTWKLLGSAICAHSKELITA WYIGFLTILSSFLVYLVEKDVPEVDAQG EEMKEEFETYADALWWGLITLATIGYGD KTPKTWEGRLIAATFSLIGVSFFALPAGIL GSLALK*
85	8136	A	1077	606	1065	LVARTERLSVSQGLFPWCTGRIRSHVGL ENECKVLLSGSSSQKMGKPEGRWFS PGV GPPPCLAAPALLRLPWKSPHPTGGWPA SVPVPVGVLFQCRAPLDDQLVCWPAR VLEKRYWQPPLS*LCPSCAHMHMNGYGS GAYVWVLTELTVDFAFWA
86	8137	A	1078	1	822	MWNAVTLWQQRESCIEEIEIGTLETKE THFIRGPKTLAPVTDWEGSLPLVFNQCR DASLIHPRFKGFRPRRDACLGPSPLAASP AFLGKGQAAPRQAE LGPNSSSASAPPY NPFITSPHTWSGLQFHSMTSPPPPAQQF PLKKVAGAKGIVKRLKTDARLPWKPP DHRRRRASGNHSGRVQPP/CPAAFVGS C*VSQAFFGARCKLSVDLPFDLEDVRV FMCVRVKRPPNRLCVSNMAVYFTWVQL LQAIWAYTCKSQGMRLGLGSEA
87	8138	A	1079	38	639	MTLIKSPIVIWTIRSRLKWSQMEMRNLL GTGAKRQRRHVLSVDPKLRWSRTGKA AFPWCLIIAGRPALVLHP*QVLLSWGR GKI*LTSPSRCTIIEKSCNSWPPL*DKPQP HLQHTRTSKRLNRSQGAFQLNLLPQELA TSTRN/PDHQAKECLQPRIPPKPCPICAGP HWKLDLCSTHLAATPRAPGTLAQGS LTDS FSA
88	8139	A	108	1	537	RRCCCRHTRSPCLALLLEIVSLFSFAVPQ SPDSSPLVFTYFARTHDPDPSLLPLPAQL WQRTMWTMKLLDYER*MRWETAAGG DGAEAPAKKDVKGSYVS/LSHSSGFLDF LLLL*VLPSIVHCAFEHSTHFRHECISQAI LGKDALFPALLDIFLTGVFFLTIFSPVLRV LLRCLFCLS
89	8140	A	1080	1	1611	

90	8141	A	1081	17	1173	MADSRIKRTWMRMKFGAVTRIGGTSLG RSIPCPALCSVKIHLRPRVLRPTSPRNI SPILN/TARFKRIKACYSPATAWPFKAY KLPLQFPHT/WS*NQTRLTA*FS*KHTCS P*LSSPANLPNPNFYKTTTFLPRHG**G QILTQELGPRPIAFLSKQLDLTVLTQPS LHAAAAAAILLKALKITKYAQLTLYSS HNFQNLFSYLMHILSAPWLLQLYSLF VESPTITIVPGTDFNPASHIILDTTPDPHD CISLIHLTFTPFPRISFFVPHPNHIWFDG SSTRPKCHSPAKAGYAIVSSTSIEATALP PSTTSQQAELVALTQALTLAKGLCVNIY TDSKYAFHIVHHHARSFLTQKGSSINPS LIKTLNAA
91	8142	A	1082	324	548	SFYHLPSSHWVLLTVSFRD*PSPTCPAIYS *KGGWSQRHSQGACYKCQKSGHWAKE CPQPRIPKLRPICVGPCH
92	8143	A	1083	760	1260	HTDGVLVWMSFLFVSFSPNSQDPQLQLC WSLLEVHSRSCPLPGYQQWRLSWKCRNH SSASLTLRAVDWCSYSAILEPRWYCL LYFIQSIILKKHRGRRWIFLMEQRTGGQR IDLPRGGPPI*VTAPNLMHVRVKRPPNRL CVSNKAVYFTSKSGPLSQDVVTVVIH
93	8144	A	1084	908	1192	
94	8145	A	1085	1	420	
95	8146	A	1086	287	515	LFTHVSKELATSARNLTTRPRTAGSPGFL LSHVPVWDPTANRTVQLTWQPLPEPLE ISGPRLSD*LLPRSSRLSG
96	8147	A	1087	1	5127	
97	8148	A	1088	3	721	
98	8149	A	1089	144	408	
99	8150	A	109	1	457	AGGGCSPKGRPEAKSGQRDWELVAGGP PGISRREGTCCSRFPSRLSQPFRSAQQLQ LAASLPANLSNFCQGSEMPITSRPALDV KGGTSPAKEDARPEKSTLGQ/YSTLLVID NQVSSKTR*PDESANQYYASDTFIILSRT YNRYILVHLSK
100	8151	A	1090	265	769	RQKRHVLSVDPKLRWSRTGKAAPWC LIIAGRPALVLHP*QQVLLSWGRGKI*LT SPSRCTIIEKSCNSWPPL*DKPQPHLQHTR TSKRLNRSGQAFLLQNLQPQLATSTRN/P DHQAKECLQPRIPKPCPICAGPHWKLD CSTHLAATPRAPGTLAQGSLTDSFSA
101	8152	A	1091	69	634	KQKRSTYNLRSSDPPAQETSHQFQIRDK GDTFYLTQNSGAAHGLGRQPSLDV*S LQGHLSDYSPMFPRCQTMQGRLP*SFTL SGKSRFSGEGASTPQPLHLP*WQVPLFW GRGKYPSTPSSPLVASPAFLGKGQKPPRP SRMPSTFG
102	8153	A	1092	1	655	MGATHPFELLTKMTSQGSDISGDLPEI NPLSSCSLLHEKDPPTTSGPQTDQPKKHL TNFKSETKETHFIRGPKTPVLVDWEGR LPLVFNHSRDASLIHPRFRGVRPRRDAC LGPSPLAASPAFLEEGQVPQPLLSMLTP SLLFWRRGKKPSTPSSPLAASPAFLEEGQ VPQPHIS/GA/LDPLFLHPNLL*LCTPTFPF LFWKTVRKYSNNQKGE
103	8154	A	1093	756	878	LSQWRSDNGPAFISQITQAVSQAPGIQ*N LYIPYHPQSSGK
104	8155	A	1094	781	1194	FPKGGPPI*VIAPNFMVRVRKPPNRLCV SNKAVYFTWVQVGALCRLGA/PAPCIPA APVP/VHGSEGRYNSSRCLAEKLP*ALA ASMWYLSLKALGIESGRVSITAILINISSA RKA/SCVPLGSRILESLMLSTVRALR
105	8156	A	1095	400	686	RQVLLFWGRGKYPSTPSPSPLAASPTFLG QGQELVTSARNLTTRPRNACGPGFLLSH VPSVRDPTGNRTVQLTWQPLPEPLEISGP

					RLSD*LLI
106	8157	A	1096	1	883
					MASSAQLLGSSQETYNHSKRQRGGEMS HMAGARRKRERGEMLHTFKQPDLMRW SSVCRKNKEKVGNSRKRNRVRYCFSRK FNGTSKVFEWQVVVVGEINSHVAHTKP VRWSLHTDAHEIWCRSDRRTSLGRSIP CPPVLCMRKIHLQAQVLRPTSPRNISPIL NRRKRHHVLSVDPKLRHRSWTREGSLPL VFNLCRDASLIHPGFRGVRPRDTCCLGP SPLAASPTFLGEGARACYKCQKSGHQAK ECLQPRIPPKLCPIWRDPAGNRTVQLTW QPLPKPLELWPKVL
107	8158	A	1097	2	551
					CGKVWNFLETFSMALTKMLIMIWTMFK RLRSSQMEMRNLLGTGISLETWCPAS*P L*P*LKGDKIQLRPWLQRVQGSIGSFQE VLGPWVLRNQLRFGNLCYFAGCMEK PVCPRGSLLOQGF/PWYVPVAVVGAK VHDVNLHMLSFPKWKLHTCMKFGAVT WIRGPPLGDQSPVLLLFAP
108	8159	A	1098	1436	1699
109	8160	A	1099	1099	1250
					LVYLKVTGRMEPSWKTLCRILSRRTSPI* QGRPTFRFRKYREHHKDTPRD
110	8161	A	11	366	795
					AWVEQSKVLIKEGGIQLLLTIVDTPGFGD AVDNSNCWQPVIKYFDSKSDIYLNES QVNRQCMGPNRVHCCLYFIAPSGHGPL HN*RLPPSGRIG*YMFVTTWHCLLLRLK PLDIEFTKHLHEKVNIPLIAKADTLMPEE C
111	8162	A	110	232	376
					FPTTKSLG*DSFTSEFCQTFKAELIPILS/R LFQKLEQYVTLPPFYEA
112	8163	A	1100	303	1413
					VRRQRSDRERSDARMVRFNLYM*RKN PFILH*LFR*TLRQTKPDSSA/V*MCQNL MTHSKSTEWKITK/QIFDGDGKTYQNVQ QFIDEQNYTSGDNHILRDPHYVEDKGH KYLVEANTGTENGYQDSAHLHPGEINS HVAHTKPVWWSLHMDAHEIWCRSDR GTSIGRSIPRPALCSVRKIHLQPQVLRPT SPRNISPISNPGFCFRNHHQTGFSPAGA NQRGPLAATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFINAAGTT GFPTGKRAVSATQLMDFADFGTTTKQD FRLGQTSVDRLLQLSQQAQVKGQNLPL VSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLESGQ
113	8164	A	1101	846	1825
114	8165	A	1102	2141	2384
					AEQWPSVKILRQELATSARNLATRPRNA RSPGFLSCVPSVWDPTGNQTVQLTWQP LPEPLESGPRLSD*PLPRCSRLSS
115	8166	A	1103	305	1148
116	8167	A	1104	2779	3182
					DKTQPHLLHTGTSKCLNCSGQAFLQNL LQELATSARNLATRPGNSCSPGFLSHVP SVDPDTGNRTVQLTWQPLPEPLELWPKV LSRVMDYI*MVY*STIPQNSAIVLTDLL GVYIPSESKHARPKVVLWAH
117	8168	A	1105	2286	4921
118	8169	A	1106	1	761
119	8170	A	1107	1	969

120	8171	B	1108	1	2175	MVNPDTGYINYDQLEENARLFHPKLIH GTSCYSRNLEYARLRKIADENGAYLMA DMAHISGLVAAGVVPSPFEHCHVTTTT HKTLRGCRAGMIFYRKGGMAPLGTATL LQALFSLFLSKSRDVPGTGADPGVMYV KRRPRGTDSCGCVLEPRRFLPSGMAFTK EEEEEEEPYNEPALPEEYSVPLFPFASQG ANPWSKLSGAKFSRDFILISEFSEQVGPQ PLLTPNDTKVFGTFDLNYFSLRIMSDY QASFVGHPPGSAYPKLNFVEDSKVVLGD SKEGAFAYVHHLTYDLEARGFVRPFC MAYISADQHKIMQQFQELSAEFSRASEC LKTGNRKAFAGELEKKLKDLDYTRTVL HTETEIQKKANDKGFYSSQAIEKANELA SVEKSIIEHQDLLKQIRSYPHRKLKGHDL CPGEMEHQDQASQASTTSNPDESADTD LYTCRPAYTPKLIKAKSTKCFDKKLKTL EELCDTEYFTQTLAQLSHIEHMFGRDLC YLLTSQIDRALLKQQHITNLFEDFVEVD DRMVEKQESIPSKPSQDRPPSSSLEECPI KVLISVGSYKSSVESVLIMEQELGDEEY KEVEVTELSFDPQENLDYLDMDMKGSI SSGESIEGLGTEKSTSVLSKSDSQASLTVP LSPQVVRKAALLQHPNPHTHLRSSSM EYKPDPPHRFSEPWPNEPEANLSSPAVK DSVTKEQTARPSREQT*
121	8172	A	1109	2	964	DIIPLVMPNPDTGYINYDQLEENARLFHP KLIHAGTSCYSRNLEYARLRKIADENGA YLMADMAHISGLVAAGVVPSPFEHCHV TTTTTHKTLRGCRAGMIFYRKGVKISVG SPRLGKEILYNLESLINSAVFPGLQGPH NHANAGVAVALKQAMTLEFKVYQHGV VANCRALEALTELGYKIVTGGSDNHLI LVDLRSKGTGGRAEKVLEACSIACNKN TCPGDRSALRPSGLRLGTPALTSRGLLEK DFQKVAHFIHRGIELTLQIQSDTGVRATL KEFKERLAGDKYQAAVQALREEVESFA SLFPLPLPDF
122	8173	A	111	515	909	LPLFIMNMTVELVWPDTTSLNPRNSEILS SPTRPNQLFVCLFLGSPSLRLEYKWYSQ SSL*PQNPGLK*SSPSASYVAKTTDMCH HAWLIFLFLQTEGL/NYIAQVG/VQTPGF KQSSCLTLPKC*DYRHEPP
123	8174	A	1110	172	375	
124	8175	B	1111	827	1276	MATAAWSSSLEKSYELPDGQVITIGNER FRCPETLFQPSFIGMESAGIHETTYNSIMK CDIDIRKDLYANNVLSGGTTMYPGIADR MQKEITALAPSTMKIKIIPPERKYSVWI GGSILASLSTFQQMWISKQEYDEAGPSIV HRKCF*
125	8176	A	1112	144	261	
126	8177	C	1113	122	253	MGWVGTATSPHPVAWRTRRPSLSRLPS VRALVVRTERRVPCG*
127	8178	A	1114	50	368	RQAILTAAPRRAAAARAVERSRHGGARA LSPGMEQRRRRRTTWSLLQPRRRRWA ARRPRGRRAQVARRTARRICPCGRPPV RAPAADPWARRAWSTSRSPAGTE
128	8179	A	1115	336	689	
129	8180	A	1116	164	370	
130	8181	A	1117	974	1111	
131	8182	A	1118	179	404	FSSSIGSLRRQRRGMKTPFGKAAAGQRS RTGAGHGSVSVTMIKRKAHKKHRSRP PSQPRGNIVGCIIQHGWKDG
132	8183	A	1119	1	1698	
133	8184	A	112	40	351	LKIPMQFLHSGFWFSFFVFFGF*KFGFGP QGGRQGGANKTKGEKLPPGSSSLPGPNP QENREKKGPPKTLKKFNLSSSGKTRG

						PRGEKNSDPRGTPGQNPNGN
134	8185	A	1120	264	799	
135	8186	A	1121	231	351	
136	8187	A	1122	1	3654	
137	8188	A	1123	1376	3462	TKPKTKTLLSQ*MQKKPLTKFNNPSC* KLSIN/IVLEVLARAIQKKEIKGIQLGKE EVKLSLFADDMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTKNRQTE SQIMSELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVG RINIVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQKNKV GGITLPDFKLYYKATVTKTAWYWYQNR VIDQWNRKEPSEITPHTYNYLIFDKPEKN KQWGKDSL FNKWCWENWLAICRKLKL DPFLTPYTKINSRWIKDLNVRPKTIKTLE ENLGITIQDIGMGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRVNRQPTT WEKIFTYSSDKGLISRIYNELKQIYKKK TNNPIKKWVKDMNRHFSKEDIYAAKKH MKKCSSSLAIREMQIKTTMRYLTPVRM AIKKSGNNRQTGSGVDLKQTPDLKLR DLTVRRKMKNQKEIASTSTKRTSTPNPT CRSVGPKDCSSLGAMEQSWTENDFDKL TEKKALEENQEEMDKFLDTYTLPRLNQE EVESLNRPTGSEIEAIDSIPTKKYPGPDG FTAKFYERIKVFCTESLAKWIKWTHTKT FIMEFHTIGNAKILQASSFTEVKTKTKTL EHRLESIMALTSQ
138	8189	A	1124	485	2347	TEPKTKTT*LSQ*MQKRPLTKFNNTSC*K LSIN/IVLEVLARAIQKEIKGIQLGKEE VKVSLFADDMIVYLENPTVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNNRQTE RQIMSELPFTIASKRIKYLGIQLTRDVKDL FKENNKPLLKEVKEDTNEWKNIPCSWV GRINIVKMAILPKVIYRFNAIPIKLPMTFF TELEKTTLKFIWNQKRACIAKSIFSQKNK AGGITLPDFKLYYKATVTKTAWYWYQNR RDIAQWNRTEPSEIMLHIYNYLIFDKPEK NKQWGKDSL FNKWCWENWLAICRKVK LDPFLTPYTKMNSRWIKDLNVRPKTIKT LEENLGITIQDIGVGKDFMSKTPKAMAT KAKIDKWDLIKLSFCTAKETTIRVNRQP TTWEKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDVNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMRYHLTPV RMAIKKSGNNRKIQ/GGIWCDRIL*R*TT CRVAKEIQLS*RRI/WKRLQRTLSIPVLDA V*PPMF*ASVIDTMTI*CFEARDTCFTLTL ESFWDMMHRCLAASKGIGLLC*PLIWHM SLMGVKSPPFVFSCLWTS AVRPTT
139	8190	A	1125	1	2784	
140	8191	A	1126	1	3000	
141	8192	A	1127	1	3045	
142	8193	A	1128	1	2736	MIISIDAEKAFGKVQQPFMLQTLNKLIGID GSYLKIIIRAVYDKPTANITLNGQKLEAFP LKTGTRRGCPSPLLFNIVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKRIKY LGIHLTRDMKDLFKENYKPLLNEIKEDT NKWKNI PCSWVGRINIVKMAILPRFNAI PIKLPMTFFTELEKTTLNFIWN/Q
143	8194	A	1129	1	2955	

144	8195	A	113	307	1429	CTATQSGWLC LHRPCPAWRCTWRTTW CIRYK GEMVKVSRNYFSKLWLLYRYS DDSAFERFLPRVWCLLRRYQMMFGVGL LTRGTGLQGFAACMSLRPSTDSLASVS ECFASPLNCYFRQYCSAFPDTDGYFGSR GPCLDFAPLSGSFEANPPFCEELHGCHGL SL*ETA*ELTGAPVPSSVFIPEWAGNPQH QRSPA WKQ/MPLQTPPVDPACL*A*VPQ WLP AHLQEGGNALQGR PQHGCALPTE/P TLALPSGRRRLTGCRS*VLPTGSPGP/PAT ALVLP HRSYLGGPRTGIRGREQGPKPRA SPHLTYSCGEEGAPGVLSLDLLGLGPLGP QRDPGCH*HMKIMVLPGLPSLPVPKSSP QTPSKSHVYRS
145	8196	B	1130	1	3105	MGKKQNRKTGNSKEQSTSPPPKECSSSP AREQSWTENDFDELREEGFRRSNYSELW EDIQTKGKEVENFEKNLEECITRITNTKK CLKELMELKTKARELREECRNLRSRCDQ LEERQINETESQQGYPIELSSAPSGPNT HLQNSPPQINRIYIFSAPHHTYSKTDHILG SKALLSKCKRTEIITNYLSDHSAIKLELRI KNLTQSRSTTWKLNLLNDYVWHNE MKA EIKMFFETNENKDTTYQNLWDAFK
146	8197	A	1131	1	2826	MEYYAAIKNDEFMSFAGTWMLKGITILS KLPQGQKTKHHMFSLTAPHHTYSKIDHII GSKALLSKCKRTEIITNYLSDHSAIKLELR IKKLTQNRSTTWKLTNLLNDYVWHNE MKA EIKMFFETYENKDTTYQNLWDAFK AVCRGKFIALNAHKRKQKRSKIDILTSOL KELEKQEQTHSKANRRQEITKIRAELEI ETQKTLQKINESRSWFFERINKIDRPLAR LIKKKREKNQIDA KNDKGDITDPTD
147	8198	A	1132	1709	2973	TEPKTKTT*LSQ*MQKRPLIKFSNASC*K LSIN/IVLDVLARAIQEKEIKGIELGKEE VKLSLFADDMIVYLENPIVSAQNLLKLIS NFNKVSGYKINVQKSQAFLHTNNRQTES QITSELPTIASKRRKYLGIQLTRDMKDL FKDNYKPLLNEIKEDTNKWKNI PCSWVG RINIMKMAILPKATVTETAWYWYQNRDI DQWNRTEPSEIMPRIYHYLIFEKPDKNK QWKGDSL FNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKTIKTEE NLGNTIQDIGMGKDFMSKTPKAMATKA KIDKWDLIQLKSFACTAKETTIRVNRQPIE WEKIFANYSSDKGLISRIYNELKQVYKK KTNNPIKKWAKDMNRHFSKEDIYAVANR HMKKCSRSLAIREMQIQTMMRYHLTPV
148	8199	A	1133	1	2856	
149	8200	B	1134	1	3786	MVKGSIQQEELTILNIYAPNTGAPRFIKQ VLSDLQRDLDSHTLIMGDFNNPLSTLDR SMRQKVNKDTQELNSALHQVDLIDIYRT LHHKSTEYRFFSAPHHTYSKIDHILGSKA LLSKCKRTEIITNYLSGHSAIKLELKIKNL TQNRSTTWKLNLLNDYWIHNEMKAE IKMFFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSOLKELE KQEQTHSKAGRKEITKIRAQLKEIETQ
150	8201	A	1135	1	3276	
151	8202	A	1136	1	3042	
152	8203	A	1137	1	3663	
153	8204	A	1138	1	3144	

154	8205	B	1139	1	3380	MVKGSIQQEELTILNIYAPNTGAPRFIKQ VLSDLQRDLDSHTLIMGDFNNPLSTLDR SMRQKVNKDTQELNSALHQVDLIDIYRT LHHKSTEYRFFSAPHHTYSKIDHILGSKA LLSKCKRTEIITNYLSGHSIAKLELKIKNL TQNRSTTWKLNLLNDYWIHNEMKAE IKMFFETNENKDTTYQNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLTSQLEKE KQEQTHSKASRRINKIDRPLARLIKKKR
155	8206	A	114	161	218	
156	8207	A	1140	1	3345	
157	8208	A	1141	1	3429	
158	8209	A	1142	1	3030	
159	8210	A	1143	1	4170	MNSLEQNPRSKWELLHRGTMELWPTM WADEEEQGLKAVLALSAKKFVPGARSK TGLTDCMGVGGGLLPAPPHIPGKRDSH NPLWNITPENQSPTPTVAMERSSSPATEQ SWMENDFDELREEGFRRSNYSELQEEIK TKGKEVKNFEKNLDECITRITNTEKCLKE VMQLKAKARELREECRSLRSRWNLLEE RVSVMEDEMNEMKREGKFREKRIKRNE QSLQEIWDYVVKRPNLRLIGVPESDGENA TRLENT
160	8211	A	1144	1	3921	
161	8212	A	1145	1	2884	MVKGSIQQEELTILNIHAPNTGAPRFIKQ VLSDLQRDLDSHTLIMGDFNTPSTLDRS MRQKVNKDTQELNSALHQADLIDIYRTL HPKSTEYTFFFSLPHHTYSKIDHIVGSKAL LSKCKRTQIITNYLSDHSAIKLELRIKTLT QSRSTTWKLNLLNDYWVHNEMKAEI KMFFETNENKDTTYQNLWDAFKAVCRG KFIALNAHKRKQERSKIDTLTSQLEKEK QEQTHSKASRRQEITKIRAELEKETETQ
162	8213	A	1146	1454	3917	
163	8214	A	1147	11537	15574	
164	8215	A	1148	115	450	
165	8216	A	1149	278	885	
166	8217	A	115	116	565	EPTGTASRAATMPNFSGNWKIIRSENFQE LLKVLGVNVMLRKIAVA AASKPAVEIK QEGDTFYIKTSTTVRTTVEINFKVGEEFEE QTV DGRPCKSLVKWESENKMOVCEQKLL KGEGPKTSWTREL TNDGELITMTADDV VCTRVYVRE
167	8218	A	1150	2	378	
168	8219	A	1151	172	464	ASHRVGLLQPFNLWPSGCSTVLAKMK SVLVATEGAEVLFYWTDQEFEE SLRLKF GQSENEEEVGLLML*AR*PHPTPPVLS GLNEGKKKSNFIT
169	8220	A	1152	164	528	
170	8221	A	1153	1	1122	
171	8222	A	1154	1	558	
172	8223	A	1155	1	495	
173	8224	A	1156	51	579	LRSSSPATEQSWTENDFDKLEEGFR*SN YSELQEEIQTGKEVENFEKNLEECITRIT NTEKCLKDLMELKAKARELHEECRSLRS RCDQLEERVSVMEDEM NEMKREGKFRE KRIKRNEQSLQEIWDYVVKRPNLHLIGVPE SDGENGTLENTLQDIIQENFPNLARQA NIQIQ
174	8225	A	1157	286	456	FCHLSSTSWGGADGTCREGGPLGGFMG PSHQ*ESSPVPEAASSRFTKSSAVSQSPL

175	8226	A	1158	1	1758	MDDIPQEARQYRHQAYAYSIIQGDGAE DDDERIVRFHTRVTVDSDTLASDAARLT CRHGLGNQDRSSSPAMEQSWTENDFDE LTEVGFRRSVITNFSSELKEDVRTHRKE HSAIKLELRIKKLIQNLTTTWKLNLLLN DYRVNNEMKAEIKMFFETNENKDTTYQ NLCDTFKAVCRGKFIALNAHKRKQERSK IDTLTSQLKELEKQEQTHSKACRRQEITK IQAELKEIETQKTLQKINESRSWFEKINK IDRPLARLIKKKREKNQIDAIAKNDKGYIT TNPTEIQTIREYYKHL YANKLENLEEM DKFLDTYTLPRLNQEEVESLNRPIGFEIE AIINSLPTEKRPVDPGFTAKFYHSSADCT RSMAPAPASGEALRLLPLMGEGEGELTC RDHIAREEAQECSSSPATEQSWMENDFE ELGEEGFRRSVITNFSSELKEDVQTHFKEA KNLEKRLDEWLTRINSVEKTLNDLM*LK TVA*ELRDTYTSFNSRFDQVEERVSVIED QMNEMEREKFKREKV*RNEQS/LQEIW NYVKRPNLHLIGVSEIDRENGTKLENTL QDIFQENFTYLARQANIQQ
176	8227	A	1159	138	324	
177	8228	A	116	343	528	
178	8229	A	1160	1	525	
179	8230	A	1161	319	1035	EWSSVRRSLVEKRALRRPHQPCLCFRMK TILASNQTCRPFPEINVITLKGRTVIVKGP /REGTLRRDFNHINVELSLLWKEKKRGF RVDK\WWGNRKELATGRD*FVSHVQN MIKGCYT GASGYKMKVLWYAHFPIQRL LFQGELGPSLLKSRNFLGGWKNTSRRVS G*GPGCLLVSVSQGPRKDEINPLKGNDI ELVSKFQRALIQQ\ATTVKNGKVRKFFG WVSMSLEKGTVPGLIE
180	8231	A	1162	232	338	
181	8232	A	1163	474	647	
182	8233	A	1164	1	413	
183	8234	A	1165	2	2545	
184	8235	A	1166	1364	1618	SQHSGRPRQADHLRSGVRDQPGQHGEIL SLLKIQKLAGRAGSRL*SQLLERLRYHR TPA*VTE*DMASKNKKKPHRIQARKYF
185	8236	A	1167	3	342	LTQELPGAEAHACNPSTLGGQGGQIMRS GARDQPGQHSGTPSLLKIQKLAGRGGT HL*SQLLRRLRQENRLNLGSGGCSELRL RHCTPAWVTDSVSKKNELEKESYLIFSSL T
186	8237	A	1168	2	232	WAGRGG SRL*SQHFGRPRRADHERWKN TWELRQLNLGQAPCSRNGMRRYGERRH HPDEPGQPSVEGFLRVLSMCIC
187	8238	A	1169	1294	1624	GQLYEKLGRRGPGAVAHACNPSTLGG GGWITRSGDRDHPG*HGETPSLLKIQKK\ LAGRGGGHL*SQLLGRRLRQENGVPNGA/ RGCSELRSCYCTPAWGTERDSVSKKKK K
188	8239	A	117	296	629	FKLTSSRNVPPTGPGAVAHACNPQHFR PRQVDHLRSGV*DQPGQHGETPSLLKIQ KLAGHGGVHL*S*LLRRLRQENRLNLGG GGCSEPRSHHCTPAWTTG*DSASKKKK
189	8240	A	1170	427	730	
190	8241	A	1171	6497	6788	SQRFRPGQANCLSSGV*DQPGQYGETL SLLKIQKLGCGGTCL*S*LLGWLRLQEN HLNLGDGGCSEPRMCHCTPPWTTEGGS A*KLKKKKKKRKYL
191	8242	A	1172	173	395	
192	8243	A	1173	239	404	

193	8244	A	1174	126	915	SACVSCNPAALLLALRSAGPPSFLPPHPA RGSAGCVTLSHPTHQAPAGQHGWTVKL EVFSLPQCKVEDAEWYTPMRREMQUEI LPGFLGPYSSAMKKQDPSLLAVSSHG QENEFLLTRVQSCHGGFYPHDLNLKLI IFQRLHHHILGLPVLQKHGITHIICIRQNE ANFIKPNFQQLFSAAFVIAYIMETFGMKY RDAFAYVQERRFCINPNAGFVHQLQEYE AIYLAKLTIQMMSP/LRDRKVIICSFYWH RQFEENT
194	8245	A	1175	1	924	
195	8246	A	1176	441	707	
196	8247	A	1177	109	437	NQRRKWRRSRTQLQTLQEQALKAEIQGH QKLAAQMKQDPQNADL*KQLYELQAKI TALSEKQKRVEQLRKNLIVKQEQPDKF QIQPLQSDNKLRTAQQQLQQLQQQQ
197	8248	A	1178	343	670	
198	8249	C	1179	130	390	MAEQSLISGGPKPKSVNSLRWINLXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSWVDK*
199	8250	A	118	74	396	GQILALMPKGGGGGGILTYPNPPLPG*N NFPGLTPPRTGJINGLGPGRVNFQIFKKK GGFPPGARGV*NPGRGASSPGFPKGRG *SPPP/QGPFKPLKRFPDLPIFPR
200	8251	A	1180	238	435	
201	8252	A	1181	615	945	
202	8253	A	1182	232	564	
203	8254	A	1183	3	487	LPNMAQSINITELNLPQLEMLKNQLDQE VEFLSTSIAQLKVVTQKYVEAKDCLNVL NKSNEGKELLVPTDGVLCMSPGKLHDV EHVLID\VGTYGYVKKTAEDAKDFFKR KINDFLTQKMEKIQPALQEKHAMKQAV MEMMS\QKIQQLTA\GEAQATAKA
204	8255	A	1184	187	423	
205	8256	A	1185	539	871	
206	8257	A	1186	158	1330	SVDLVIHPLWPPEVLGLQQQPTQFINPET PGYVGFANLPNQVHRKSVKKGFEFTLM VVGESGLGKS/TLS*NSLFLTDLYPERVIP GAAV*FFSRKN*KELVQIEASTVEILRAR GSSLRLASG*DTPGYG*PLFNCRDCF*G QFISYYLMRQF*GGYLHDESG/LNRRHII DNRVHCCFHFISPFHGHLQPLDVAFMK AIHNKVNI PVIAKADTLTKERERLKKR ILDEIEEHNIKIYHLPDAESDEDEDFKEQT RLKASIPFSVVGSNQLEAKGKKVRGRL YPWGVVEVENPEHNDFLKLRTMLITHM QDLQEVTDQLHYENFRSERLKRGRKV ENEDMNKDQILLEKEAELRRMQEMIAR MQAQMQMQMQGGDGDGGALGHHV
207	8258	A	1187	405	632	
208	8259	A	1188	111	375	
209	8260	A	1189	428	574	
210	8261	A	119	454	777	ADPMSPSSKSPNMEAVLWIPDTNIVL*SL KVYPSS*TIKSWLGT/CGSRL*CQHFRP RRVDHEVKRLRPS*PTWRTPSLL/RTTKIS RAWWHTSVVPATREAEAGESLE
211	8262	C	1190	216	458	MNRDRTSRNRCVCDVFRNAVKGQTVLG RQLFIGRVRVPVRPGEGFLPWGFLPVSP WCPSWGLSTHALWWAEAVPGRALVH*

212	8263	A	1191	1	594	RTRGRTRGLLPSCAFEPAAAGSATAPRG CKNPGAKGGLLAAMAGRODIFHAIVKA DERFHGEGYREGYEKGSILGVKEGRQHG TLHGAKIGTEIGRYQRFPAWKCLLHVA PLRRTA*T*RS*HAWIGRIQIFPYDDPTYD KLHEDLDKIRGKFKQVRALCVSSC*EHLI APFPGGAHSGRRCGNGLGLRAPRNC
213	8264	A	1192	482	788	
214	8265	A	1193	572	676	
215	8266	A	1194	1	394	KGGSMHMYAKNFYGGNGIVGAQQQIFE AYNMAALWKLPCIFICENNRYGMGTSV ERAAPSTDYYKRGDFIPGLRVDGMDILC VREATRFAAAYCRSGKGPILMELQTYR YHGHSMSDPGVSYRTREEIQE
216	8267	A	1195	641	722	
217	8268	A	1196	354	1145	KQISCINRKLFFVSVTCVMVRKLAVWA WRPASTPQTISSQPTGLTALLSPGAFSE KFSQSLQDEKEVVLKKGEDRCTCMPRTS TGAMASWERRCPWAAGIALACKYNGK DEVCLTYGDGAANQQQIFEAYNMAAL WKLPCIFICENNRYGMGTSVERAAASTD YYKRGDFIPGLRVDGMDILCVREATYI GRAYCRSGKGPILMELQTYRYHGHSMS DPGVSYRTREEIQEVRSKSDPIMLLKDR MVNSNLASVEELKGI
218	8269	A	1197	2	506	
219	8270	A	1198	1	1455	
220	8271	A	1199	509	839	
221	8272	A	12	105	702	AGSSVSLGFCPAAAAHKPRGGALRLPVF RRRAQQGPDYALAGVARQPACTRRRC NRSHCRAEDPQWPTPAAAPAAHSPHMS LGESGLGKLILINSLFLTDLYSPEYGPSSQ RIKKPVQVYILVFLIDDKLE*Y*YTQSTC CNFHYASQSWQPAINYIDSKFEDYLNAE SRVNRQMPGNRVQGCLYFIAPSGHGPL HN
222	8273	A	120	133	359	RHCSSGMEIPTNYPASRADLVAQNYIN YQHGTPHRVFEVHNAYRVIMQDMSG* GHLVSPSSRFFLHSFATSLFE
223	8274	B	1200	109	267	MEETPCRELEEEEEWGSSEDASKKDG VESISVPDMVDKNLTCPEEEDTVKV*
224	8275	A	1201	856	1030	VPNLQVGDEKQDSPNGEHWGQEDST AEPAEVKAMMSVAVV*KNLTTPPPLG RSSV
225	8276	A	1202	67	264	
226	8277	A	1203	3	1251	
227	8278	A	1204	1403	3362	
228	8279	A	1205	388	1711	ACALGMAPQRKRRKQLSMKTGYSQRS SFQRRKRPQGQGRSRNSAPSGATLSLGA LAWHLEWLSVIQLWHYLFIGTLNLLTN MAGGDMARVSTYTNAFAFTQFGVLSAP WNGLLMDRLKQKYQKEARKTGSFNIRG PHSLYFPNHHLPHATYRDKAKMKLPLLL ALLFGAVSALHLRSETSTFETPLGAKTL PEDEETPEQEMEETPCRELGGRGREW LWEVEDASQERWGLFESILQCPDMGGT KTFTCS*GKEGHQLKVGWGPGGCPRPA RYLPG*ESLSRRFSSKLWFYFARSCYRG QTWVFHSTTFQY*LSESKCSVIALNQG QVWIGRITGSGRICRRFQWVDGSRWA NFAAYWGAHQPWASRGGHCVALCTRG GYWARAHCLQKNFPFICFPLSWSQPAV QVVPSPGQLPPLLCLPSLPPPCNNNGFY
229	8280	A	1206	97	441	
230	8281	A	1207	19	432	
231	8282	A	1208	165	257	

232	8283	A	1209	80	1239	GAVVGGGGRRRRITYKCLPKLDPKPK FQEGERVLCFHGPLL YEAKCVKVAIKDK QVKYFIHYRGWNKNWDEWVPESRVLK YVDTNLQKQRELQKANQEYAEGKMR GAAPGKKTSGLQQKNVEVKTCKNKQK TP\GN\GDGGSTSETP\QPPRKKRARDP TV\ENEETFMRNVEVKVPIEELKPWL DD\WD\LTRIQKQLFYLPKKNVDSILED YANYKKS/RVGNTDNKEYA/VLNEVVAG D*KNTFNV\MLG\TQLLYKFERPQYAEIL ADHPDAPMSPGVWSAQHLEIIWYRIGA MLAYTPLDEKISLALLLNLYLHDFLKyla KNSATLFSASDYEVAPPEYHRKAVWKS TLTHLCLDLRKHIFVLSLSPWYKPMC FE DVS
233	8284	A	121	3	1671	SSGARWRFRAGSMGLFCQRKHSS/SHPV LQKPSVFGNDSDDDDSVSESLQREAA KKQAMKQTKLEIQKALAEDATVYEYDSI YDEMOKKKEENNPKLLGKDRPKYIH NLLKAVEIRKKEQEKRMEKKIQREME KGEFDDKEAFVTSAYKKKLQERAEER EKRAAALEACLDVTQKDLSGFYRHLL NQAVGEEVVKCSFREARSGIKEESRG FSNEVSSKKQNTTREMHSFKLM*K*REN PDADSYFDAKSSPDDK*KKLELTAEGK RS*RPLRMTSSTTGVTTLGHLVKEGT VPGTTRKDHERREDMRKGKISTSRNPE TKRTITLTVITGKKGILIGTERPVIEPIGR GMNRKINQGRGTKEKEVTEYKGRKIG RNIPKENKKEIDNKMIRTDVPRKERRR KAKQRKRAYESKGGKVLKLLINTEIEKN ER*VFS/ASERNQDQKGKQPKFQQRINF LTNLDFIQNGETWQRTKERNQEKPSNSE SSLGAKHRLTEEGQEKGEQERPEAVS KFAKRNNEETVMSARDRYLARQMASG
234	8285	A	1210	31	1029	WWNSEVPHGPFMRKAAVLT/APVLFSD G*ARRRHFVQGG*SPRAAWDRV\K\DL ATRPWTVLKEQRTETYVSQFEGRLGE NS*TLKLL\DNW\DSVDLPFSKLREHSF GPC*PRDFLGINLGKRETRGALRQGR LR QRIFGRRLKGPRLQP*LGDDFPRKKLAR KEIGALTRQKGWSRLRARTSKKGARPE S LHELARRSLSPLGEAVSRPRARPMWDAL RTHLAPYSDEMSQRLGARLGLALRENG GARMGQYHA\QATE\HLSTLSEKAKPAL ED\LRQGLLPVLESFVSFLSALEEYTKK LNTQLRRPPPPYPVLRINVSKVGKKKK KK
235	8286	A	1211	3	450	QTQREPTMVLSPADKTNVKAAGWKVG AHAGEYGAEALERMFLSFPTTKTYFPHF DLSHGSAQVKGHGKKVADALNAVAVH VDDMPNALSALSDLHAHKLVRDPVNF K LLSHCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR
236	8287	A	1212	9	675	NSARATDSERTHHGARLLPDKTNVKA V WGKVG AHAGEYGAEALERMFLSFPTTK TYFPHFDLASHGSAQG*RAHGKKVADA LTNAVAVHVD\MPQTALSALSGPATAH KL\RVDPVQLSSS*SHLPCWWTLGRPTSP SEFNPWRLHAFPGTKFPGLLVEAPLLEPS KLPLKLGSLRVGHAFAPLGLPPRALLPF PGTRNPVGLLNKILNWGGKKKKKKKIF
237	8288	A	1213	1	645	KIFLSDCLACDSCMTAEKGVQLSQQNAK DFFRVLN/LNKKCDTSKHKVLVSVCPQ SLPYFAAKFNLSVTDASRRLCGFLKSLG VHYVFDTTIAADFS/H/RWRMLKWQRPS PDSRRTCG*GPAAADGRHLR*HPCAASG VQCKRAGAVPGVAGGDQLPQGPGRGAA YHVPEPGAWHTQPGHQVVKSGQGLPAA LGARAKSISVEGGAALSGVITIKKT

						LGARAKSLSVEGGAALSGVLKTLKKT
238	8289	A	1214	193	564	
239	8290	A	1215	211	1795	TPLGRRRRRKTHDKRKPGQGPMPGAEC SKKTK\ADDQENV\SADAPSPAQENGEKG EFHKLADAKIFLSDCLACDSCMTAEEGV QLSQQNAKDFRVLNLNKKCDTSKHKV LVVSVCPQSLPYFCWLNFNLSVTD\ASRR LCGFLKSLGVHYVFDTTIAADFSIL\ESQ KEFVRRYRQHSEGGNAPCMLTSACPG L\WVRYAGAGCWGRPITG\HTFLAPPKSP QQVMGSLVKDYFARQQNL\SPEKIFPRS LVAPIC\YDKKL\EALQKPFPLALHG\SR GRLTCVLTSGEICFKLMEQGDLSVRDA AVDTLFGDLKKDKVTRHDGASSNGHLA HIFRHAAKELFN\ERDVEEVTYRTLNRQ RFPQKVTLLEEPKRWW*TFVLEPYAFRNI PET*SLKPLKKGKVPFFHFVEGSSPCAIG GCLNGKRPKPKIQDGHGDKAPAAGRM EGIY\SLDIPVRRPES\SAHVQEL\YQEWL EG\NSPKARKVL\HTTYQS\Q\ERGTHSLG HSSWLKFRPGPSSCSWGQSQEPLSRGRG LP
240	8291	A	122	170	339	IMKLITILFL*CRLLLSLTQESQSAEIDLLD NDLFLAEEA\GLYRYIMQIQTNPRI
241	8292	A	1222	1	456	RPRRPQREPTMVLSPADKTNVKA\AWGK VGAHAGEYGAEALERMFLSFPTTKTYF PHFDLSHGSSQVKGHGKKVADALTNV GHVDDMPNALSALS\DLHAHKLRVDPVN FKLLSHCLLVTLAAHLPAEFTPAVHAFL DKFLASVSTVLT\SKYR
242	8293	A	1223	2	435	QTQREPTMVLSPADKTNVKA\AWGKVG AH\AGEYGAEALERMFLSFPTTKTYFPHF DLSHGSAQVKGHGKKVADALTNV\EH VDDMPNALSALS\DLHAHKLRVDPVN\FQ APKATGLLVDPGPAHFPGRVSPRLQGF LGTKFLGFC
243	8294	A	1224	9	390	NSARATDSERTHHGARLLPDKTNVKA\AA WGKVGGAHAGEYGAEALERMFLSFPTTK\ TYFPHFDLSHG\SAQVKGPTAKKVAER ADQTPWRNVDDMPKRRCP*SDLHAH KL\RVDPVQLSSS*SHLPCW
244	8295	A	1225	3	452	
245	8296	A	1226	26	636	NSTDERTHHGARLLPDKTNVKA\AWG KVGGAHAGEYGAEALERMFLSFPTTKTY FPHFDLSHG\SAQVKGHGQKVADALT NAV\AHVDDMPNALSALS\DLHAHKLR VGPGSTFKLLKPLALLG*TLGRPPSPAEF QPLGGCKASLGTKFLGFLVEAPLLEPSKL PLKLGSLRLAML\SLPLWAPPAPPLSCT RTPVVFEIKS
246	8297	A	1227	17	233	AFGTRELQCCVFLASMLGVPIPTVQGF QWTLRGTDVETSPFGAPRATSHGVGQM KSCQIPQLKIRMVKQNNIPGETQILLRF TGWESKVN\AKKQPPVGKCEPMDQNE QTGGHETDGHGIGSVV\SAATQECLI*N TTRNVWTQ*TKSNLTRCGPNEELPDPTA LEDKDGQTK
247	8298	A	1228	1	433	
248	8299	C	1229	312	443	MHKRNFHRAGRSQAVQDNWKELNNIYP VSPARLQALLPPAAPC*

249	8300	A	123	23	307	RQTRWCPVVRLSHYRTLGGCCHLRRGR GVA*VRGPQSGTISSVENTPPWRRVSCFP APNITCKDSSGNETHFTGNEVGFFKPISC RNVNGYSYK
250	8301	A	1230	1	94	
251	8302	A	1231	2	122	DLLCPQMG*GWKLTALSLQCSLQDGIER SRAKASQCCLSI
252	8303	A	1232	3	53	
253	8304	A	1233	1	2679	SAVGSDHIFHNIPDSTSSATNVSMVVSAG PWSSEKAEMNILEINEKLRPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKYKYEE CKDLIKFMLRNERQFKEEKLAEQLKQAE ELRQYKVLVHSQERELTQLREKLREGRD ASRSLNEHLQALLTPDEPDKSQGGDLQE QLAEGCRLAQQLVQKLSPENDEDEDED VQVEEDEKVLLESSAPREVQKAESKVPE DSLEECAITCSNSHGPCDSNQPHKNITF EEDKVNSTVVVDRKSSHDECQDALNILP VPGPTSSATNVSMVVSAGPLSSEKAEMN ILEINEKLRPQLAEKKQQFRSLKEKCFVT QLAGFLAKQQNKYKYEECKDLIKSMLR NELQFKEEKLAEQLKQAEELRQYKVLV HSQERELTQLREKLREGRDASRSLNEHL QALLTPDEPDKSQGGDLQEQLAEGCRLA QHLVQKLSPENDEDEDEDVQVEEDEK LESSSPREMOKAESKVPEDSLEECAITC SNSHGPCDSNQPHKNITFEEDKVNSSL VVDRESSHDECQDALNILPVPGPTSSATN VSMVVSAGPLSSEKAEMNILEINEKLRP QLAEKKQQFRSLKEKCFVTQVACFLAK QQNKYKYEECKDLIKSMLRNELQFKEE LAEQLKQAEELRQYKVLVHSQERELTQL REKLREGRDASRSLNEHLQALLTPDEPD KSQGGDLQEQLAEGCRLAQHLVQKLS ENDNDDDEDVQVEAEKVQKSSSPREM QKAEEKEVPEDSLEECAITCSNSHGPYDS NQPHRKTITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQ ESEEEVPQESWDEGYSTLSIPPERHRW DQVKKEDQEATGPRLSRELLA
254	8305	B	1234	33	2996	MLRNERQFKEEKLAEQLKQAEELRQYK VLVHAQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGGDLQEQLAEGC RLAQHLVQKLSPENDNDDDEDVQVEVA EKVQKSSAPREMOKAEEKEVPEDSLEEC AITCSNSHGYPYDSNQPHRKTITFEEDKV DSTLIGSSSHVEWEDAVHIIPENESDDEE EEEKGPVSPRNLQSEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQV CM
255	8306	B	1235	16	1041	MVKQNNIIPGETQILVRFTGWESKVNAK KQPPVGKCEPMDQYEECKDLIKSMLR NERQFKEEKLAEQLKQAEELSMVVSAGP WSSEKAEMNILEINEKLRPQLAENKQQF GNLKERCFVTQLAGFLANQKKYNYEE CKDLIKFMLRNERQFKEEKLAEQLKQAE ELRQYKVLVHSQERELTQLREKLREGRD ASRSLNEHLQALLTLDEPDKSQGGDLQE QLAEGCRLAQHLVQKLSPENDEDEDED VQVEAEKVQKSSAPREVQKTEESKVPE DSLEECAITCSNSHGPCDSNQPHKNITF EDEVNSTLVVDRESSHDECQDALNILP ACMTE*

256	8307	A	1236	1	2219	MSQSVQDNLKELNNIYPDHSSSPAMEQS RMENDFDELTEVGFRKLVTNFSELKED VRTHRKEAKNLEKRLDEWPTRMNSVEK TLNDLMELKTMARELRDACTSFSSQFDQ VQETPLKIRMVQKQNNIISAESQILVRFTS WESNVNAKKQLPVGIKCEPMDQECIPGS RACTLLVRFSSNGGPPMDPGSERKDLLQL GGELARTSRAVQEAGLGLSTGLWLAESR AKAALEKQALLQAQLEEQLRDKDLAQ QQMQSDLDKADLSARVTELGLAVKRLQ KQNPEKDQVNTDLTEKLEALVQMLPLES QLPIPTSGTLTPPGYSLVWSPLCVGPGLG SRSGSPIDCVTWGKTDSTMQAHEDAQR EVQRLRSAKELLRRLSGMLMEVEEPEVL QDSLDRCYSTPSMYFELPDSFQHYRSVF YSFEEQHISFALDVD/E*VSYFDGNKSP GLPDGSHIPTPRTAGQARLLHARRRIPQ ERTTTPKVSQLASWVSLG/RQYLHPAGS LRWL*TTLPPTSSSMFPLCPQ/YPSEDSRE AGIKKDQEEEEEDQGPPCPRLSRELLEAVE PEVLQDSLDRCYSTPSSCLEQPDSCLPYG SSFYALEEKHVGFSLDVGGYLELTDSCQ PYRSAFYILEQQRVGWALDMDEIEKYQE VEEDQDPSCPRLSRELLDEKEPEVLQDSL DRCYSTPSGYLELPDLGQPYRSVYSLE EQLGLALDVD/E*VPYYEDEETEAQRSE DTGAGSHSW
257	8308	A	1237	3	1270	
258	8309	C	1238	160	267	MGPLTLSSSSLHTETFLCPILTQGHQSCQ CENRRL*
259	8310	A	1239	1	1233	
260	8311	C	124	35	91	MSPPQNKGPFPKSPGWF**
261	8312	A	1240	401	2582	
262	8313	A	1241	946	2562	FPLAYSLLFPP/CSRLSRELLEVVEPEVLQ DSLDRCYSTPSSCLEQPDSCQPYGSSFYA LEEKHVGFSLDVGEIEKKGKGKRRGR STKKRRRRGRKEGEEDQNPPCPRLSREL LDEKGPEVLQDSLDRCYSTPSGYLELTD SCQPYRSAFYILEQQRVGWALDMDEIEK YQEVEEDQDPSCPR*L*AITDA*FCVDTW RCQVQKQECVQFHVFNEG*ITPTDIAV GFHCSRCLGFHFFLPLSFTHLL*VDHTSK AVWQLHGILSKFMENY*AHSFHDHCSLC VPRALTQSVL*PLHQCVRPIR*AHFLLS LSLPLPVFLFHSFLPGPGLSQHKGNNSLP H*WICPFSF*TVPYVSHEI*LGLCGF*FPL AYSLLFPT/CSRLSRELLDEKEPEVLQDSL DRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEEDQGPPCP LSRELLEVVEPEVLQDSLDRCYSTPSSCL EQPDSCQPYGSSFYALEEKHVGFSLDVG EIEKKGKGKRRGRRSKKKKKGRP
263	8314	A	1242	442	5178	HQELPDPTGPCGGRLLSLTIHGVTRYHA LLWARGPIMSKSQVLGEWEPVQGGKSS ENDKWTMSDPGAAPTCSRAASGVDKE QQGRWQGLWNSHIKPLKIRMVQKQNNIIP GETQILLRFTGWESKVNAKKQLPVGIKC EPMQDQENEQTGGHETDGHRIVSVLHFP LISILSYATWGLSLECIPIGSPVCTLLVRF SNVGTRWSLEVRGSPCGFGSNKVCVGM TPEIKMVCVCEGKAGKAVGSGGVEGTK EVST

264	8315	A	1243	1	3242	MDKPRPGKTFVIMVSPLPAPYTSPTFH MVTCPAHPRAFLALTHSWDPQVRPAVL NPLPRHGSSFVVKQPVAKQOPLRLIYIE VALSVMSPTAPSSSRSPWKRPLRPGFE QPGGSREAERLVGSRDGSSRSLHSLHPV REPVPSSLRIRGAAELPLSSDPAFGTG APPGQGSWQYKVLVHAQERELTQLREK LREGRDASRSLNEHLQALLTPDEPKSQ GQDLQEQLAEGCRLAQHLVQKLSPEND NDDD
265	8316	A	1244	148	197	DPLGFL*QKRNQQEDD
266	8317	A	1245	1333	2383	RMKKEHVLHCQFSAWYPFRGVTIKSVI LPLPQNVKDYLLDDGTLVVSGRDDPPTH SQPDSDEAEIEQWSDDENTATLTAPF P*SLPLKVQGSYQIPLGGQVSFPKV*FGS APRDIAIWAMNSSLCKCTLSDIFLLFKS SDFITRDFTQPFHCTDDSPDP\CIEYELVL EKWCEMIPGG\EFRCFVKENKLIGISQRD YTQYYDHISKQK\EEIRRCIQDFFK\KHIP VQIL*MKDLVFDIYR\DSRGKVWLIDFN PFGEVTDSSLFTWEEL\SEN NFRRFLV KVDAQE QD SP SFVAQTSEVTVQPPLIC SYRL\PKDFVDSL\TGEDAHKLIDFLKLLK RNQPEGR
267	8318	A	1248	66	703	RRRLPSVAIMIILPGPSSSHDEMFSDIY KIRGDRGRGLCLEGGGRWVSRTEAGTI D\DSLIGGNA\SAESPRGAKGTERHK*ST GV\DIVMNHHLPGNKFSQKEASKKVHQR ITMKS\K\GKP*KNRRPRKSKTFL*QGAA EQIKHILANFKKLQF/YFIGENMNPRWA WVLLLDY*RDGVPP\YMIFFK\DG\LEME KMLTNVAIILDLSPCHP
268	8319	A	1249	1	521	MKNRSRNGKNVWQAEGRSKRSVKGQ RPSKAKIPSGDKNGVSLTHNEVINNDNP LESNDEKEGQEATCSRPIVP/EFQQ**LF RPE*WRRASGNLQIPKKRVSAGTRGSP SKKGERVRRDAQQTATW*TRSPASGCF QICEGNKQDEACDVRGLQHCHERHSLAG PREYMP
269	8320	A	125	50	230	NLKGPLRRPVSGIIHVISLPLYQKCSKNE KKIPWRQMEM/C*NVPSANNPPLGLLKN IVF
270	8321	A	1250	3	168	
271	8322	A	1251	3	249	
272	8323	A	1252	23	2669	
273	8324	A	1253	97	1609	GGKMAGGGGDLSTRRLNECISPVANEM NHLPAHSHDLQRMFTEDQGVDDRLLYD IVFKHFQR\NKVEISNAIKKTFPFLEGLRD RDLITNKMFEDESQDSCRNLVPVQRVVY NVLSELEKTFNLPLVLEALFSDVNMQEYP DFKFHIYKGFENVIHDKLPSPRKVEEEE KGRRGLGLPTKSLNKG TGENSFRKPDFG PPSGFPHPPCLGTTPE/NMGLSEHPCETE QINAKRKDTTSDKDDSLGSQQTNEQCAQ KAEPTE SCEQIA\VOVNMGDAGREMPCP LPCDEVESPRGKSLHNHWNPKFNSLVLC ELVDIKKEKPFNSKVE\CAQARTHN QASDIIVISSEDEGSTDVDEPLEVFISAPR SEPVINNDNPLAESNDEKEG\QEATCSRQ IVPE\PLIFRKLFT\FRESFRKRVIG/QKTHD FSESQ*GGGAPQEASSGGTEEARHGEKA PIDF*EVHLTWEEYPSR\KETFP\AVSDFSD PE*MGERAFQETC\SSSLRRGLG
274	8325	A	1254	3	274	FFASLLESPVSPRLAMPNCSCAAGVSC TCAGSCKCKECKTSCKKSECEAISMVW GCG*GCCSCCP/AAASKCAQGCVCCKGAS EKCSOCD
275	8326	A	1255	788	1173	

276	8327	A	1256	80	231	IRPLPPRFKTESRSLPGPCLQPGTFLWSRN RRVLGFPSMNGEDMGLLFLCSEWERSSE GWLCTEKGEVDTQLNPTAVPSCISLTAH CVFLFLVGGSTCAGSCKCKECKCTSC KKSECG/CH/PPGIWGC*GAWFSQHEW RGHGASLPLL
277	8328	C	1257	81	476	
278	8329	A	1258	3	452	
279	8330	A	1259	9	486	NSARATDSERTHHGACLLPDKTNVKA WGKVGAHAGEYGAEALERMFLSFPTTK TYFPHFDLSHGSAQG*RAHGK\KVA\DA LTKRRGATWDDM/PQTALSALSDLHAH KL\RVGPGSTFKLL\SQLPCLGEPWAAHL PAEFQPLAVARLPWNKVSWGFC
280	8331	A	126	814	1292	GISPFYIFGQDMGLEKNPTSFPKMCFC PLESLPSYVGCWKTGNMSCVVCTVNW LRSVIYFWIFTNLSHFVLAALKRLLAPG GGGNMPPRVL*CCRRTTGHQRVWPSRP PEQTDQTARRPPSWRPTL/CSPLPLPPPR SGREKGNRARFLKGPRIG
281	8332	A	1260	3	497	PTLLVPTDSERTHPWLLSPADK\TNVKA AWGKVGAHAGEYGAEALERMFLSFPTT KTYFPHFDLSHGSAQV*GPRARKVADA L\TNAVAQRGT DIAQRACPLSDLHAHK L\RVGPGSTFKLLKATC/HCLGEPWAAHL PAEFQPLAVARLPWGQSFLGLLKQRC
282	8333	A	1261	1	1077	MLSGVGGFVLGLLFLGAGLFIYFRNQKA EESFVSALSIDLSGGNMALLSMVCLKF PGG\SCMAALT\TLMVLSSPLALAGDTR VPPVRLRKTEDEPLGCVLSGLRVGPDSVF PGGRFCNRIVLVPPARFLEQVKHECHFF NGTERVRFLDRYFYHQEEYVRFDSDVG EYRAVTELGRPDAEYWNSQKDLLEQKR AAVDTYCRHNYGVGESFTVQRRVYPEV TVYPAKTQPLQHHNLLVCSVNGFYPGSI EVRWFRNGQEEKTG VVSTGLIQNGDWT FQTLVMLETVPRSGEVYTCQVEHPSLTS PLTVEWRARSESAQSKMLSGVGGFVLG LLFLGAGLFIYFRNQKGHSGLOPTGFLS
283	8334	A	1262	3	825	LFSSMVCLKLPGGSSLAALT\TLMVLSS RLAFAGDTRPRFLELRKSECHFFNGTER VRYLDRYFHNQEEFLRFDSDVGEYRAV TELGRPVAESWNSQKDLLEQKRAAVDN YCRHNYGVGESFTVQRRVHPQVTVYPA KTQPLQHHNLLVCSVSGFYPGSIEVRWF RNGQEEKAGVVSTGLIHNGDWTFTL VMLETVPRISEEVYTCQVEAPRA*QAPL TVE\WRARSESAQSKMLSGVGGFVLGLL FLGAGLFIYFRNQKGHSGLOPTGFLS
284	8335	A	1263	11	885	DLPASLAPGPVLFSSMVCLKLPGGSCMT ALT\TLMVLSSPLALAGDTRPRFLWQP KRECHFFNGTERVRFLDRYFYNQESVR FDSDVGEYRAVTELGRPDAEYWNSQKD FLEDRRAAVD TYCRHNYGVGESFTVQR RVQPKVTVPSTQPLQHHNLL/VFCSV SGFYPGSIEVRWFLNGQEEKAGMVSTG LIQNEGDGPFQTLVMLETSFGVERVNT SQVEHPKCARP\TVE*RARSESAQSKML SEVGGFVLG\LLLPLGPGLFIYFRNQKG HSGLOPTGFPELKCR
285	8336	A	1264	25	628	EFHRLRENPPWCLSPADKTNVK/APAWG KVG AHAGEYG\SEALER\MVLFPPPTPKP YFPHFDLSHGSAQV*GPRARKVADAL TNAVAQRGT DIAQRAVPPLSDLHAHKL RVGPGSTFKLLKATC/HCLGEPWAAHLPA AEFQPLAVATSSLGTFPGFLVEAPLLTF QITFKGWKLWLAIVFLPGLPPSPSPFL HPYPRGL

286	8337	A	1265	1	625	CKFIRVMAHTRLRLPLRRKKAHLMEIQ VNEGTVAEKLDWATERLEQQVPVNQVF GQDEMIDVIGVTKGKGYKGVTSRWHTK KLPRKTHRGLRKVACKDGLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVML KGCVVGTKKRVLTLRKSLLVQTKRRAL EKIDLKFIDTTSKFGHGRFQTMEEKAF MGPLKKDRIAKEEGA
287	8338	A	1266	1	1251	
288	8339	A	1267	1	903	
289	8340	A	1268	1	1131	
290	8341	A	1269	1	1345	WALPAGFDGVMShrkfsAPRHGSLGFL PRKRSSRHrgkVKSFPKDDPSKPVHLTA FLGYKAGMTHIVREVDPRGSKVNKKEV VEAVTIVETPPMVFGVGVYVETPRGLRT FKTVFAEHMSDECKRRFYKNWHKSKKK AFTKYCKKWQDEDGKKQLEKDFSSMK KYCQVIRVIAHTQMRLPLRQKKAHLM EIQVINGGTCARESWDWGPREGKQQV PVKPSVLGRDEMIELHRG*PKGQKAYK GGHPVVWHTQESCPRKD/HHPRACAKV ACIGA\FHPARVAFSVARAGQKGYHPR TEINKKIYKIGQG\YLIKGGKLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVM LKG\CVVGTKK\RVLT\LRK\SLLVQTKAA GLWRRITLKFIDTTSKFGHGRFQTMEEK KAFMGPLKKDRIAKEERSLMPGTDFAV GGVSIKVIFH
291	8342	A	127	191	482	DSSGQVQWLKPIIPVLGNLRQADHLRSG VQDQHVQHGETPSLLKIQKKLARHGGA CL*SQLLGRLR/QETH*NSGSRGCSEPR RHCTLA*ATEGDSI
292	8343	A	1270	3	451	
293	8344	A	1271	9	487	NSARATDSErTHHGARLLPDKTNVKAIA WGKVGAHAGEYGAEALERMFLSFPTTK TYFPHFDLASHGFCPRLKGPRQRRWPDA LTK\AVAHVDGHAQTALSGPEATLHGA QSFQVDPVQLSSSLSHCLLG*PWAHL RPSSTPGGWNAFPGTKFPWVSC
294	8345	A	1272	197	821	RLFHSNQTVdHSQKNVDITLKG\RPNSR VRAPKGTLR\DFNPHQM*NSALLGKEQ QRGFRVDKWWGYQKGNWPTRSGLFGS HVQDMIKGWLPLGLPVT\KMR\SVYAHF PHPTLLSRENGVSLKSRNFLG\EKYIPQ GFRMKTRVLLCQYLKAQKR*N*SLEGN DVIGLVS\NFSRLIPASPTRLKTKGIRK\FL DGIFCLLEKGLFRQA
295	8346	C	1273	22	282	MSEGPSVRSEEAICLYEEELGGGARQTH VRRPLSECPGDWSHSGVAEGPXCQFL HITSHGAKEALSTWLGLLTSGPATTAAV LP*
296	8347	A	1274	60	1576	GYLGAPVALGLWALCWSLAATPLPPT SAHGNVAEGETKPD\DVTERCS\DGWSF DATTL\DDNGTMLFFKGEFVW\KSHKWG PGV*SSERWEGFSPSPCGMLAFPFKVHN SVLS*SKGGDKVLGY*PSLKKGKRGKLP KVC\SKIDFP\GIPHSPLD\AAVECHRG\EC QAE\GV\FFQGDRE\WFDFA\TGNHGR ERSW\PAVWGTCSS\ALRWAGPLTYWLS RGNQ\FLRFRPCQGEVPPR\YPRDVREY FMPCPGKGHG\TQEWGLGHGNSNHGHP *IYAACSP\HLSLCLALTSDNHGANFCLS VGTHYWR\LDTSRDGW\HSLAPLLIKWP QG\PSAVDAAFSWEEKLYLVQGH\PGYY VFLTKGGY\TLS*GGYPKRLG\EREV\GDP SWG\FIL\DSVDAAFICPGVFLRLHYSWA GRRLWVGW\VP*KSGSPKPTW\TELSFGP HEKVDGALCMEKSPFGPKFMFPNPGP L\YLIHGPNFTL\YSVVEK\LN\AKALPO

						PQNVQTQSPGACTH
297	8348	A	1275	1	3431	MLPHERGLETTTPRGECIPVRIDTKLFEML VPQCHKEIALEHKFIYSFLVTLNTPPGY SHSHPEALLDPEVGDPNGTNAQLIKCFLL PLCPSFPLCPEECMHCSGENYDYGKISKT MSGLECAWDSQSPHAHGYIPSKFPNKN LKKNYCRNPDRELRPWCFTTDPNKRWE LCDIPRCTTPPSSGPTYQCLKGTGENYR GNVAVTVSGHTCQHWSAQTPHTHNRT ENFPCKNLDENYCRNPDGKRAPWCHTT NS
298	8349	A	1276	111	2785	VNNVLGLGHTFWALLASPKMEHKEVVL LLLLFLKSGQGEPLDDYVNTQGASLFSV TKKQLGAGSIECAAKCEEGEFTCRAF QYHSKEQQCVIMAEENRKSSVIRMRDVV LFLKKKVYSLQSAKTGNGKNYRGTM KTKNGITCQKWSSSTSPRRPRFSPATHPS EGLAENYCRNPDNDPQGPWCYTDDPE KRYDYCDILECEECECMHCSGENYDGI SKVTMSWDWECQGLGTFQEPHTVHG
299	8350	A	1277	29	454	
300	8351	A	1278	1	1368	
301	8352	A	1279	1	1269	PPTRPPTRPAPGLVPKPSTTCTPACQGLS GAAMKSLVLLLCLAQLWGCHSAPHGPG LIYRQPNCDDEPETEEAALVAIDYINQNL WGYKHTLNQIDAEVKVWPQQPSGRAVL RFEIRTPWGTTLPCCWDPTLVGQDASLE GSLKEHAVEGDCDFQLKLDGKFASVVY AKCDSSQDSAEDVARKVCQHCPLLAPLA NDTRVVHAAKSCPGPPFNAQNNGFQFFS LEEISRAQLVPLPPSYVVEFTVSGTDL FA*KKATEAAKCNLSGQKSNMGFCKAT LSEKLGSGQRLQLTCTVFQTPVTSQP NPEGANEAVPTPVVDPDAPSPPLGAP GLLP SWLTPKTTMVLLAAAPPGHQLHRA HYDLCHTFMGVVS\LGSPFRRKCSHPRK NT/RTVVEA*WLGAAAGATGFLPLFRGG IRHFKV
302	8353	A	128	1445	1778	NLSRNKEVLLFGKNIPWVGWARWLVPG NPNTLGGQGRADHLKLGVDQPGQHGE IPSLKIQKLTRHGGVCL*SQ\NHLNPGG GGCSELRSHHCTCTPAWAME*DSIPKN K
303	8354	A	1280	1	1254	
304	8355	A	1281	1	921	
305	8356	B	1282	70	572	MGKEKTHINIVVIGHVDSGKSTTTGHLIY KCGGIDKRTIEKFEKEAAEMGKGSFKYA WVLDKLKAERERGITIDISLWKFETSKY YVTIIDAPGHRDFIKNMILNHPGQISAGY APVLDCHTAHIACKFAELKEIDRRSGK KLEDGPKFLKSGDAAIVDMVPGKPI*
306	8357	A	1283	1	1410	
307	8358	A	1284	1	1386	

308	8359	A	1285	70	1538	KPKWERKRLIFNIVVIGHVDSGKSTTTG HLIYKCGGIDKRTIEKFEKEAAEMGKDSF KFAWVLDKLAERERGITIDISLWKFET SKYYVTIIDAPGHRDFVKNMIGDISRL DCAVLDLFAISGVGEF*SLVSPKNGQVTR EHALLAYTLGIVEQLIVGVNKMMDSTPP YSQKRYEEMWLREVSTFAIKKIWLQPPTQ *HFVPISWFGIGDNMLEPSANMPWFKG WKVTRKDGNASGTTLLEALDCILPPTRP TDKPLRLPLQGVHKLGGIGTVSSAPME TIGFSNPGMVVTFAPSPR*QRKVKSCRKC THEALK*SSFLGTNVGLQLSGIVSCQGM FRPWQTVAG*PAKNDPTQWESSWASLV RGDYP*PIPGQNKAPGYAPCIGIAHGLT FACKFAELKEKIDRRISGKKLEDGPKFL KS\GDAAI\VDIVPGRPMCYESFSFYPL GRFAVRDMRQTVAVGVKAVDKKVCW SWARSPKFAQKG
309	8360	A	1286	41	601	APSPRRPWGHFTEEDQGLLSTSLWGKIV KCGKNAGRKKPLGKAPLVV/HPWDPK RSFEQALGNPVPLPSANMGNPPKSRAHG KKVLTSLGEMPIKHPG*SSKGTFQAQA*S ELH\CDK\LVDPENFKLLGNVLT\TVLA AIPFSAKEFTPGGCRASWAERWVTWSW PVPSSRIPLSSLAHDCRAFQG
310	8361	A	129	3	369	PGFPLFSFPEGNGPSKRQTD*IRCLF*DG KVWECSPSSSSSPKKRKKAVIF/CVPVQ TKCIVVEGGEETLVGDV*V*P*IGSFKHV VAMFPEK/DCLCTLYEASFKTESRRVD GFVCVRVGT
311	8362	A	1290	2	217	
312	8363	A	1291	1	2283	
313	8364	A	1292	249	433	KWRCGNWPRRTLMPWLH*NFPVTLGQT ELQLKEFLSICKEENMKFCWQKQHFEEN KKVPAS
314	8365	A	1293	778	1578	PRQVDPSWGFHSRLSGPW/H/WTERDAT SLSKGKVPAGPGHPLWKNDAGRGEIN ELKQVEGEASCSSRKGLIFFYEWNIKL GWKGIVKESGVKHKGLIEIPNLSEENEV DDT/EEFTTGMLPTKAMATQELTVKRK LSGNTLQVQASSPVALGVRIPTVALHMM ELFDPT/S*SSLYSIFTVKEEERVCVLFSLT NKKIIMKWR\WGTWPEEHYAMVALNFV PTLGQTELQLKEFLSIYL*RKVP*NFCWQ KQHFEIIGSLQLTPLNG
315	8366	B	1294	46	386	XIRHESGSRSHSHCSTLSSIGDVAKKLGE MWNNTAADDKQPYEKKAALKKEKYEK DIAAYRAKGKPDAAKKGVVKAESKKK KEEEEDEEDEDEDEEEDXEDDDEEEDD DDE*
316	8367	A	1295	263	484	
317	8368	A	1296	157	886	TWGGKDLKKPRANMSSYAFFVQTCRGG \HKKKHPDASVNFS/ESFSKKCSERWKT MSA*R/EKGKFEDMAKADKARYER\EM KTYIPPQRGRQKRKFKDSQLHPRGPPSG LLSSSCSEYRPKIK\GEHPGL\SIGDVAKK LGRDVG\NTAAD\DKQPY\ERRAAKLKE KYEKDIAAYRAKGKPDAAKKGVVKA KSKKKKEEEEDEEDEDEDEEIEEDEE DEEDEEDDGLMNKLGSGAVFFFSCL
318	8369	A	1297	1	450	CKSRGNSNLRVHFKNTRETAQAIKGMHIR TATKYLKDVTLQKQCVFRRYNGGVGR CAQAKQWGTQGRWPCKSAEFLVIEHI QVNKAPKMRRRTYRAHGRINPYMSSPC HIEMILTEKEQIVPKPEEEVAQKKKISQK KLKKQKLMARE
319	8370	A	1298	1	1725	

320	8371	A	1299	278	879	SVKMMVRYSLDPGGTPRKSC/SQRGSNL RVPFKDHS*KLPQAHQGVCHIRKSPTKY LKDVHLTRNQCVPIPDYNGGICKVCR RPKQWG\WTQGRWPQKGVNLFLHML KNAE\SNAELKGLDVDFLVIEHIQVNKA PKM\RRRTYRAHGRINPYMSSPCHNIEMI LTEKEQIVPKPEEEVAQKKKISQKKLKE TPTLWHGE
321	8372	B	13	7	177	MSVSARSAAAERSVNSSTMVAQQKNL EGYVGFANLPNQVYRKS VKRGFEFTLM VVE*
322	8373	A	130	412	616	VFVCLFVCFETGSCSVTQAGGQWCNHG SLQPOPATSAS*IVGIGVAGVYHHFQVFL LLLFNRDEVLLY
323	8374	A	1300	85	266	
324	8375	A	1301	1	1776	
325	8376	A	1302	207	1645	LSQRALRLSPRARSFSLSPACPLPCLLALS LALSSRIEGLTTACGWGRETEAAAAQG KRGCSGGSRKMSGEDQEQTIVD/DSL VVTKYKMGDIANRVLRLVEASSSGVS VLSLCEKGDAMIMEETGKIFKKEKEMK KGIAFPTSISVNNWCM/CHFSFERSDPG LYSSKEGDLVKIDLGVPCWGMFIANVA SH/SFVVDVAQGTQVTGRK\ADVIKAAH LCAEAA\RLVKPGNQNTQVTEAWNKV AHSFNCTPIEGMLSHSLKQHVIDGEKP*F QNPTDKQKRAHEKADFEV\HEVYAVDV LVKPQERARPKDAGQRTTIYKRDPSKQY GLKMKTSRAFFSEVERRFDAMPFTLRAF EDEKKARMGV\VECAQT*TCWQPFNVL Y*EGRVILFAQFKFTVLAHGPNQPMRINT S\GPFEP\DFYK\SEMEV\QDAELKALLQ\S SAKSEKPQKKKKKASKTAIENATGGIL CSLGNIRRK
326	8377	B	1303	29	200	MSRTRLVCPSLIPFCIYVVDVGFSPGPQS CTSHEPKDIAKCELAFLHHQRFYKNEG X*
327	8378	A	1304	138	1908	ASRTAVARWECVLQNVRRSPSPRAWP SQLRPIASTATKCRE\CGPGYSTPLEAMK GPREENVYLPCILPETQGTGPRLSWAT VDVDPKSPQYCQVIHRLPMPNLKDELH HSGWNTC\GSCFG*LAPSRGTK\LVLP SF HLLFGIYVGGTWGSEPRAPKLAQGSLS RDIHAKC\NWAFLHTSHCLASGEVMISL GDVKGNKGKGGFVLLDGETFEVKGTWER PGGAAPLGYDFWYQPRHNMISTEWAA PNVLRDGFNPADVEAGLYGSHLYVWD WQRIEIVQTL\SLKDGLIPLEIRFLHNPDR CPKAFVG\CALQAPNIQRFLQRTRGGTLF SGRR*FQV\PPRKLKGWLLPKMPGLITTI LASPWNDGFLYFS\NWLAWGP*GKYDIS DPQRPALTGQLFLGGSIVKEGPVQVLED EEL/TSPSPEPLVVKGRVGEQP\QMIQL SLDGKRLNNHHGRCTSALGQSSFP*SQ SGERLLVNAGRVEW*DNSKKGGA*KLN PQLSWVDFGEGAPLPKPLPH*ARYP\GGA DCSS\DIWILNSPPSHPHSLFWALHFPGGP GLSFCISLGRITLGHVPTTAKLRLWQC VES

328	8379	A	1305	1	1000	STRAPSPGPFSSKLAGAYKSWCRRDPR THSAGAQAAAAARSVPIRCAPTASATMS HHWGYGKHNGPEHWHKDFPIAKGERQS PVDIDHTAKYDPSLKPLSVSYDQATSL RILNNIGHAFNVEFDDSDQKAVLKGGP LDGTYRLISVTFHWSGF*WDKVSEAY CGIKKKYAAE\TLGHWNTKYGDFGKA VQEPDGLAVLGIFLKVGSAPGLQKVVD VLDSIKTKGKSADFTNFDPRGLLPESLD YWTYPGSLTTPPLECVTWIVLNFPSV SS\EQVFEIP*TLTFNGGGVNPEELMVDN WRPA\QPLKNR\QIKASFQIRWSHSLYSK
329	8380	C	1306	127	435	MAASXNPEVLDITEETLHSRFLGVRNV ASVCLQIGYPTXASVPHSIINGYKRVLAL SVETDYTFPLAEKVKAFLADPSAFVAAA XLGCCHHSCSXCCCSPS*
330	8381	A	1307	1	689	KCFI\VGADNVASKQMQQIRMSFRGKAV C*WGKNTMMRKPIRGHLENNPALEKLL PHIRGNVGFVFTKEDLTEIRDMLLANKV PAAARAGAIAPCEVTVPAQNTGLGPEKT SFFQALGITTISRGTIELGVRNVASVCL QIGYPTVASVPHSIINGYKRVLALSVETD YTFPLAEKVKAFLADPSAF/VAAAP/VAA ATTAAPRAAAAAPAKVEAKEESESEDED MGFGLFD
331	8382	A	1308	68	1111	RTAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNVGSKQMQQIRIVPWGEA CVLMGQKTMMGQAHPKGT*NNPSLW RKLLPHIRGNLGFCTQGGPSLEIKGHV CLANKGLPSWLPVVGANCPHGESHWWP APEHWSSGPEKTSFFPGL*AITKVISQGA PIENPEVNVPAESRTGDQSGEPSEANAA* TCSNISPF\SFGAGSSQPGVSTNGSHLPPL KGLDIHRRNLCIFWLSWEGVRKCCPVSV CQIGYPTVASVPHSIINGYKRVLA\LSV EPDYTFPLAEKVKAFLADPSAFVVAATC GLLPQLLL\VVVAAPAKVEAKEESESED EDMGFGLFD
332	8383	A	1309	60	569	STDLEELPTLGWF*KQELIILSCFFVSLTY RERLPANFFKFQFRNVEYSSGRNK\FLC YVVEAQGGQVQASRGYLEDEHAAA HAEEAFFNTILPAFDPALRYNVTWYVSS SPCAACADRIKTLSTKNLRLILVGRL FMWEEPEIQAALKKLKEAGCKLRIMNLV
333	8384	A	131	278	464	YTHILRQLPTLRHEQKSRENCLEEMSLD RFQAAKP\SPTPHHTYKPTLAGH*KIHA MGLTRA
334	8385	A	1310	62	858	QLRWDSGARAWPRPACLSPLPQRLLSHS PSMAQKEEA\AVATEAASQNGEDLENLD DPQKLKELIELPPFEIVTGERLPANFFKFQ FRNVEYSS\GRKTL\LCYVV*STGARGG KVQASWGYLEDE\HAACPLQKESFSFNT ILPAFRPKPLAVTNVT/WGYVSSSPCAA CADRUVKTLSTKNLRLILVGRLFMWE EPEIQAALKKLKEA\GCKLRIMKPQDFRI LSWE\NFVEQEEGESKAFQPWEDIQENF LYYEK\LDILK
335	8386	A	1311	1	727	NTEDQRNEEKAQREANKKIEKQLQKDK QVYRATHRLLLLGAGESGKSTIVKQMRI LHVNGFNGDEKATKVQDIKNLKEAIET IVAAMSNLVPPVELANPENQFRVDHILS VMNVPDFDFPPEFYEHAKALWEDEGVR ACYERSNEYQLIDCAQYFLDKIDVIKQA DYVPSDQDLLR\CRVLTSGIF\ETKFQVVD K\NVFHIV*RGVGQDERRKWIQCFNDV TAIFV\VAASSYNMVIREDN

336	8387	A	1312	2	1271	PVRSSAPRRGHSVASAPRSGLRQVAGRR GAALPCSLAPGCGAAAGASPCPGAGRR RAAGGRCLACECTSLTCAGESGKSTIVK QMRILHVNGFNNEGGEEDPQAARSNSD GEKATKVQDIKNNLKEAETIVAAMSNI VPPVELANPENQFRVDYILSVMNVPDFD FPPEFYEHAKALWEDEGVRACYERSNE YQLIDCAQYFLDKIDVIKQADYVPSDQD LLRCRVLTSGIFETKFQVDKVNFMFDV GGQRDERRKWIQCFNDVTAIIFVASSS YNMVIREDNQTNRLQEALNLFKSIWNNR WLRITISVILFNKQDILLAELVLAGKSKI EVDYFPEFARVYTTPEIDATPEPAGEDPR* TRAKYFIRDEFRLISTASGDGGHYCYPH FTCAVDTENIRRVFNDCRDIIQRMHLRQ YELL
337	8388	A	1313	235	1571	GRPRPPPPQGRAPPPPPRMGCLGNSKT EDQRNEEKAQREANKKIEKQLQKDKQV YRATHRLLLLGAGESGKSTIVKQMRILH VNGFNNEGGEEDPQAARSNSDGSEKAT KVQDIKNNLKEAETIVAAMSNI VPPVEL ANPENQFRVDYILSVMNVPDFDFPPEFY EHAKVLWEDEGVRACYERSNE YQLID CAQYFLADKIDVIKQADYVPSDQDLLR/ CARVLTSGIFETKFQVDKVNFMFDV GGQRDERRKWIQCFNDVTAIIFVVGSS SYNMVIREDTGHNGLAGRL*TSPKGIW DNRWAAAPSLVILFLTKQ/EILLA*ESPLA GNSKVKDYFPEFARVYTTPEGCYSRPG EGPHGVYRGQVTPFEDEFLLSSNCPVED GRHYCYPHFTCAVDTENIRRVFNGLAV DIHFSGMHLFSYAGFGKEGEPKFNLK A
338	8389	A	1314	3	784	
339	8390	A	1315	3	2231	PAMNGLSLSELCLFCCPPCPGRIAAKLA FLPPEATYSLVPEPEPGGAGAAPLGT RASSGAPGRWKLHLTERADFQYSQREAR STIEVFPTKSARGNRVSCMYVRCVPGAR YTVLFSGHNAVDLGQMSSFYIGLGSRL HCNIFTYDSSGYGASSGRPSERNLYADID ATWQALRTR*GRPLVGRVRARWRPRLT LLRRRQVRHQPGQHPSTGRSIGHGAPP WDWASRYECAA VILHSPLNLGHARRIPR HPRKTYCFDAFPLHSRKVSKINVSPCSSS HGHEGRGDRLSRTGWALYEALPPRVE PLWVEGAPGTTDIEPLQVPVGAAGVAFIL PGAAQPARLAAAPNRPDLNKAAPGLHP APAPTQGLACGPPGRPRWRPGLGGARH EWAVDDVQATRRTHSFPPGSKKKIRENG QLKI
340	8391	A	1316	1	1347	
341	8392	A	1317	53	1027	NFRVEAGVRGVQQKETCAFKVLESIGKL G\LALSVAGGAENSALYNVDAGHRAVIF DPIPGQK*QDIVGEGTHFLIPWVQKPQ LSNDCRSRPRNCCQSITGSKDLQNVNIT LRHPSSGPVRQPSFPRIFTSIGEDYDERV LAVPSQLENLK\SVWARFDAGELITQRE LVSRQV\SDDLITERA\ATFGLLDDVSLT HLTFGK\DFT*AVEAKQVAQOGKQRRRA RFV/VLEKAEQKKAAIISAEGDSKAAE LIANS\ATAGDGLIELRKLGLQRTFAY QLSTLSGTSPYLPAGQSVLLQLPQLRAH PCLAPPAGLTWGHSPD
342	8393	A	1318	424	598	
343	8394	A	1319	3	371	

344	8395	B	132	639	1718	MDPLGPAKPQWSWRCLTTLFQLLMA VCFFSYLRVSQDDPTVYPNGSRFPDSTG TPAHSIPLILLWTWPFNKPIALPRCSEMV PGTADCNITADRKVYPQADAVIVHHREV MYNPSAQLPRSPRRQQRWIWFSMESPS HCWQLKAMDGYFNLTMSYRSDSDIFTP YGWLEPWSGQPAHPPLNLSAKTELVAW AVSNWGPNSARVRYQSLQAHKVDV YGRSHKPLPQGTMMETLSRYKFYLAFE NSLHPDYITEKLWRNALEAWAVPVVLG PSRSNYERFLPPDAFIHVDDFQSPKDLAR YLQELDKDHARYLSYFRWRETLRPRSFS WALAFCKACWKLQESRYQTRGIAAWF T*
345	8396	A	1320	1	1596	
346	8397	A	1321	2	556	WDMMYVTRFASFLRNVLPSFISDWLYV QKMNTWFKHENYGLMPLNGYLKMEIFF IQKRGALI**IYLSIKPSVKEFTETS AVFED GTMFEAIDSVIFATGYDYSYPFLDETIMK SRNNEVTLFKGIFPPLMEKPTLAVIGLVQ SLGAAIPTADLQAWWAACVFASRWAIL SFIHFINEHLLNTCY
347	8398	A	1322	955	1187	IFFFFKMESCPFAQAGVQWCDLGSLO ALPPGFTPFSCSLSSWDYRRPPPHLAN FLYF**TWVFTVLARMVSIS
348	8399	A	1323	6345	9041	
349	8400	C	1324	182	433	
350	8401	C	1325	72	254	MVSTQLRQASDPRTTIGRERFELLRRV DKLMSPRLPTGTLPNPHFWTSLIPQVGR CNAP*
351	8402	A	1326	225	735	GELRVNSLHVSTHFQIPEETDIGWLVSPO QGPAPFEDIQLWPPGSLMAAEPTDQSL EESH*DRWITTTFFAR\QEGRKD*PQRS NEFKE\VTQQLPHL\KLDVGSLDKRN*G AWDVNQDFGGSRFNEY\WRLIGGAWPK EIRKEEKT\KIQERSKAAWLEDGVGQGR T
352	8403	A	1327	55	391	
353	8404	A	1328	996	1334	WASVGLSGPRSPSSRPQ*ARPRPGAPAS LRQADLGRGWRDRLGAPRPRPRTGGW RSCCRGRGPGSRPRGARAGLPGAPGG WRRSRRSWTRARAATRPAAARGSRTP RG
354	8405	A	1329	1	993	
355	8406	B	133	1154	2233	MDPLGPAKPQWSWRCLTTLFQLLMA VCFFSYLRVSQDDPTVYPNGSRFPDSTG TPAHSIPLILLWTWPFNKPIALPRCSEMV PGTADCNITADRKVYPQADAVIVHHREV MYNPSAQLPRSPRRQQRWIWFSMESPS HCWQLKAMDGYFNLTMSYRSDSDIFTP YGWLEPWSGQPAHPPLNLSAKTELVAW AVSNWGPNSARVRYQSLQAHKVDV YGRSHKPLPQGTMMETLSRYKFYLAFE NSLHPDYITEKLWRNALEAWAVPVVLG PSRSNYERFLPPDAFIHVDDFQSPKDLAR YLQELDKDHARYLSYFRWRETLRPRSFS WALAFCKACWKLQESRYQTRGIAAWF T*
356	8407	A	1330	72	496	PPWARGSARRPPAWRTVRMPSPCHPRMF GAPQKTFLRVSVWSRCRPWGIVMRMM* PMRGQVRHNSCMAPKTEE*NPTVSATF CCCSFVSCSWPPVTRYSSILFTAAM
357	8408	C	1331	202	378	MTPYLTLFLSPLPPKGEIWGLLFLTPLG FLLPSLPLLLPCPAPAGVRRQWDGPTG A*
358	8409	A	1332	1	1541	

359	8410	A	1333	9	345	YLSEVGVSUQVIRPRQWIRPEGDPFHG GRLKMDPLRAQQLAAEELEVMMAIDMY NRMTSACHRKCVPPPFKEAELSKGESV CLDARCYSKYLDIHGA*WGKKFDRVVLL QG
360	8411	A	1334	170	842	EHVYKLPKAKITRPLMLSSARGGAEES ERAEPPLRWAFLLGLGTVVGVDESTAF SWPVCDMCGNGRLEQRPEDRGAFSCGD CSRVTSPVLKRHLQVSLDCRSRPQCRV KVKLLQRSISLLRFAAGEDGLYSQWLIR SLLRIWKEADRRWVPEGPG*RC*LRDTQ YGFCQFSGATK*RSVFGKEVGLLNCFVQ SVTAHPTSCIGLEEIELLSAGGASAEH
361	8412	A	1335	2	2925	FVLRRCQAALPEMPRGRSRRGSKRK RSWNTCPSPFGERPLQGRAGLRTAG AAASLSEAWLRCEGEGFQNTSGNPSLTA EEKTVTEKHLELCPRPKQETTTSTKSTGL TDITWSSSGSDLSDEDKTSLQORDELQF IDWEIDSDRAEASDCDEFEDDEGAVEISD CASCASNQSLTSDEKLSLSEPKPSIEILEY SSDSEKEDDLENVLLIDSESPHKYHVQFA SDARQIMERLIDSRTKSPETILHTP
362	8413	A	1336	1	480	NFALEAKNSARAISSVVQTPMGHFTTED Q/ALTITSLWGKVNVEDAGGETPGKGS LVVYPWTQRFDFSFGNLVLLPSCPSMG NPQKSKATWPRKVLTSLGDAITKHLDD LKGHLLPKPEVNLHLLTSLHVG*GTFKL PGEILLVTRFWAIPFSAKEFHP
363	8414	A	1337	52	454	SQTQREPTMVLSPADKTNVAAA/WGMF LSFPTTKTYFPHFDLSHGSAQVKGHGKK VADALTNAAHVDDMPNALSALSDLHA HKLRVDPVNFKLLSHCLLVTLAAHLPAE FTPAAHASLDKFLASVSTVLTSKYR
364	8415	A	1338	3	616	PTLLVPTDSERTHPWLLSPADKDQRCGP AWG*G*GSHPPSNVAKTLERMVLPFPPT PKPYFPHFDLSHGSAQVKGHGKVA DALTNAAHVDDMPNALSALSDLHAH KLARVDPFNFKLLSHCLLG*PWAHLPR PSFTPCGCKASLADKFPGLFVEAPLLEPSK LPLKLGSLRLAMLLCPFGFPQPLLPFA PVPPWSLK
365	8416	A	1339	2	390	GWDWNCVWEPHHWLCQSLNSVTQAG VQLCNLSSLQPLPLGFKQFSCLSLPSWD YRNPSLKQQLFSYAILGFALSEAMGLFC LMVAFLISLPCEGAVSTSHSSPASGWPR VFLFLYLPRQPGERGWLRY
366	8417	B	134	1029	2108	MDPLGPAKPQWSWRCCLTLLFQLLMA VCFFSYLRVSQDDPTVYPNGSRFPDSTG TPAHSIPLILLWTWPFNKPIALPRCEMV PGTADCNITADRKVYPQADAVIVHREV MYNPSAQLPRSPRRQQRWIWFSMESPS HCWQLKAMDGYFNLTMSYRSDSDIFT YGWLEPWSGQPAHPPLNLSAKTELVAW AVSNWGPNSARVRYYSLSQAHLKVDV YGRSHKPLPQGTMMETLSRYKFYLA NSLHPDYITEKLWRNALEAWAVPVVLG PSRSNYERFLPPDAFIHVDDFQSPKDLAR YLQELDKDHARYLSYFRWRETLRPRSFS WALAFCKACWKLQESRYQTRGIAAWF T*
367	8418	A	1340	13159	14007	VLSPLRLKCSGTISAHCNLCPLGSNDSPA SASQVAGITGAHHHARLIFYFFILFYFIFL R/HESDSVTQAGVQLCNLSSLQPLPLGFK VHSLASASQVAGITGTHRYPLIFVFFFL F/SFLRQSL/DSVAQAGVQWRGLGSLHP LPPGFTPFSCSLSSWDYKRLPTRLANF LYF**RQGVTVLARMVIS*PRDLPTSAS QSAGITDMSHCAQ/LIFVFLVETGFHQVG QAGLE/PPDLKQSTHLGLPKCWDYRREP

						PRLA\NFCIF\VSPCWPGWSPTS\GFK
368	8419	A	1341	1	532	DSGTRD\TVLKLREWYMIISREMFNPMY ALFRTSPGDRV\TYTINPSSH\CNPNHLSYF KFVGRIVAKAVYDNRLLECYFTRS\IFYK HILGKSVRYTDMES\EDYHFYQGLVYLL ENDVSTLGYDLTFSTE\VGQFVCEVRD L\KPNGG\NILVTEENKKEYVHLVCQMR MTGAIRKQFG
369	8420	A	1342	1	530	AEADATIQMVREGQARRQQAATSESS QSEASVRREESPM\DVDQSPSAQDTQSI ASDGT\PGVEKEKEERPP\ELLSEQLAL DELWDM\LGEC\KELEESH\DQHAVLETH RTVLNQILRQSTTHLADGPFAVLVDYIR VLD\FDV\KRKYFRQELERLDEGLRKEDM AVHVRRDHVF
370	8421	A	1343	262	587	PVSKESRVAPLCDFCLPFIOSESSQSEASV RREESPM\DVDQSPSAQDTQSIASDGT QGEKEKEERPP\ELP\LLSEQLSLDELWDM LGEC\KELEESH\DQHAVLV\LQPA
371	8422	A	1344	1	2502	MTPPHLPPRRASDDEFENLRIKGPNAVQ LVKTTPLKPSPLPVIPDTIKEVIYDMLNAL AAYHAPEEVGFTSPMLFDERKYPYHLM LQKFLCSGGHNALFETFNWALSMGGKV PVSEGLEHSDLPDGTGEFLDAWLMLVEK MVNPTTVLESPHSLPAKLPGGVQNFQF SALRFLVV\TQKAFTCIKNLWNRKPLKV YGG\RMASMLAILCHILRGEPVIRERLSK EKEGSRGEEDTGQEEGSRREPQVNQQQ LQQLMDMGFTREHAMEAL\NTSTMEQA TEYLLTHPPIMGGVVRDLSMSEEDQM MRAIAMS\LGQDIPMDQRAESP\EEVACRK EEEEERKAREKQEEEEAKCLEKFQDADPL EQDELHTFTDTMLPGCFHLLDEL\PD\TVY RVCDLIMTAIKRNGADYRDMILKQVVN QVWEAADVLIKAALPLTTSDTKTVSEWI SQMATLPQASNLATRILLTLLFEIEVRS WSYPPFQDKDHCKKEKENFEAIAAALA AERESKPPVRD\TRESQLAHSKDEPPPLSP APLTPATPSSLD\PFSSREPSSMHSSSLPPD TQKFLRFAETHRTVLNQILRQSTTHLAD GPFAVLVDYIRVLD\FDV\KRKYFHQELER LDEGLRKEDMAVHVRRDHVFEDSYHTA SQSLTH\TNDWMYPGFS\AQ\LF\SASAFLCR YIVFEGEEGQDAGLLREWYMIISREMF NPMYALFRTSPGDRV\TYTINPSSH\CNPN HLSY\FKFVGRIVAKAVYDNRLLECYFT RSFYKHILGKSVRYTDMES\EDYHFYQGL VYLL\ENDVSTLGYDLTFSTE\VGQEILITA HPSQSGRSNSQVHLRTSTA

372	8423	A	1345	1	2218	MPQLPGISLPEGVDPSFLAALPDDIRREV LQNQLGIRPPTRTAPSTNSSAPAVVGNPG VTEVSPEFLAALPPAIQEEVLAQQTAEEQ RPELAQNASSDTLMDPVTLIQTLPSDLRR SVLEDMEDSVLAVMPPDIAAEAQALRRE QEARQRQLMHERLFGHSSTSALSAILRSP AFTSRLSGNRGVQYTRLAVQRGGTFQM GGSSSHNRPSGSNVDTLRLRGRLLLDH EALSCLLVLLFVDEPKLNTSRLHRVLRN LCYHAQTRHWVIRSLLSILQRSSESELCIE TPKLTSEEKGKKSSKSCGSSSHENRPLD LLHKMESKSSNQLSWLSVSM DAALGCR TNIFIQIRSGGRKHTEKHASGGSTVHIHP QAAPVVCRHVLDTLIQLAKVFPSHFTQQ RTKETNCESDRERGNKACSPCSSQSSSSG ICTDFWDLVKLDNMNVSRKGKNSVKS VPVSAGENKVSEAQANSQSGASSTTTAT STTSTTTTAASTTPPTAPTPTVTSAPAL VAATAISTIVVAASTTVTPTTATTTVSIS PTTKGSKSPAKVSDGSSSTDFKMVSSG LTENQLQLSVEVLTSHCSEEGLEDAAN VLLQLSRGDSGTRDTVLKLLNGARHLG YTLCKQIGTLAELREYNLEQQRRACE TLSPDGLPEEQPQTTKLKGKMQSRFISGL GSASSIQA AVRQLEAEADAIQMSSESSQS EASVRREESPMDVDQPSQAQDTQISIA
373	8424	A	1346	59	6349	KISQYYMHTPISPRLISPSIAPRKVEW TGLKVKSQDRLFAQQLQVELVALPLVLC LAASALGRSTTSFVSLGQPHAAIQTYSQ KWPTAVSASPFLPLRGSGTGNGSSRIPRE SAPEMATAESLVEELSEDAAGGASPGVE LPALGCSELPAAEVSP TASSKNLETICEY AYCMAMLPETGLDPYPKRGFLDLTQERI WTDIPSPGNIPTHPLMVRHADHSSLTL GSGSTTRLTQGIGRSQRTLRLQLTAN
374	8425	A	1347	1	746	MAAAGAFRLRRAASALLRSPRLPARSC RPRPDSITRSPPDVRLPLEKQLKNAINQR GTKGPYIRYYPEVVDHYENPRNVGSLDK TSKNVGTGLVGAPACGDVMKLOQVVG *KRGRFVGC*GFKTFSAVGSANASSSLSH LNGVKGKTVEEALTIKNTDIAKELCLS FPWKLALAPMLGLKVAFKAALADYKIE TRTQKKGEAEKKWSPPLGEASSRPTAV PQPAVPVTLDVSGSRLPSPTGAL
375	8426	A	1348	2	832	SARGSTVAAIICSPRLTPRTRDAKAACE RLRRVGVEPQLSRGLALFWSRPNPPEE MSGGLAPSKSTVYVSNLPFSLTNNDLYP DIFQSIGKSL*KVTNQ*KSKRY/HRKEVK GVAFILFLDKDSAQK\CARAINNKQLFG RVIKASIA\IDNGRAAEFIRRRNYFDKSK\ CYECG\ESGHL\SYACPKNMLGEQ*/RLP KKKEKKKKKKAPEPEEEIEVEESED EG EDPALDSLQAIAFQQA KIEEQKKWET QFQGVPSNIRMIPRTRIKKSTYFQ
376	8427	B	1349	165	520	XNLKLLDNWDSVTSTFSKLREQLGPTQ EFWDNLEKETEGLRQEMSKDLEEVKAK VQPYLDDFQKKWQEEMELYRQKVEPLR AELQEGARQKLLPVLESFKVSFLSALEE YTKKLNTQ*
377	8428	A	135	885	1173	LSQGPRRHSSAVQPPPHSHRGHHDDCA SPSQVRQNYAINRQINVELYASYIYLSM SYFDFHNDVALKNFAKYFLHQSHEERE HAKKLMKLLHFDC
378	8429	A	1350	3	558	
379	8430	A	1351	3	118	
380	8431	B	1352	28	384	MKAAVLT LAVLFLTGSQARHFWQODEP PQSPWDRVKDLATVYVDVLKDSGKDSV TSTFSKLREQLGPTQEFWDNLEKETEG LRQEMSKDLEEVKAKVQPYLDDFQKKW

						QEEMELYRQK*
381	8432	A	1353	2	1093	GGASCCLPRSLWLPSSRFRPCRPGLWV PEVFSRSVPFSSPGCNEWGSTGLLHAEGT PLSQALLLLQVPHGPFMRKAAVLTAVL FSDG*ARRRHFVQGG*SPRAAWDRVK DLATRVPTVTLKEQRTETYVSQFEGSA LGK\QLNLKAPLTTGDSVDLPFSSKLRE QFVGPC*PRDFLGINLGKRETEGP*GKGR* GKDLWKEVKAKVAALTLDDFQERSWQ EEIGAFTROKV\EPLARKNFQEGVAPESL HELARRSLPLGEEMRDRARAHVDALR TVHLAPYSDELRLQRLGARLGALRENGGA RMGQYHA\QATEHLSTLSEKAKPALEDL RQGLLPVLESFKVSFLSALEEYTKKLNT Q
382	8433	A	1354	119	301	INDKRKKRPARPGAGGLHLQLCLSQQP QPRGHPAPIPTGQAGPRDSGPGASP*/GR DPPSD*WTPADLGSDPWAGPLPTPQEP* GSRWPSSATVSLSASTATGTPCTYSHGT GWTQRLWTRGLPLSRDPPSD
383	8434	A	1355	1451	2495	RGLAGNFEDRKSAAHYVFQTFRGGERSL ELEAHLEGWSLGLRFLGLPKGPPAQG HFHPSLPISWRGAGVPHSR/SPFPTLGIP G*IFPPKPGRRPRGPPRKEDLGPGMVGR PSGPLPQLPSAVLSADPAGPRPHVPFCEP/ SPSHGVRASPGSKWVEEIGGEEGRQ/PK CRQAFQEAWLMQG/GARGQGLPGS/GC WRINKPSKPSKRGKGLTCQTFSTNIC*S PPLMPRSLP\GPSFILHLISSQQP*SGLLFID PIPPEKGRGGLSERWGRAFGDSVACSFQ KTPGPWEVFEQDAWPNPWP/QGPPPEN FPKGNPSHSRNIHKGDEQSPVRTKTEPTP WGGKHSQFASR
384	8435	A	1356	2024	2160	KCLCPPR/RCPQPLTPYPC*GVKCPPSEIK YKP*MCPIGCPKPSIQC
385	8436	A	1357	15717	16041	
386	8437	A	1358	41	544	TKLVMMQKLLKCSRLVLALALILVLESS VQGYPTRKPRHQWVRCPNDSSSAHCLE EKGHMFELLPGESNKIPRL\RTDLFPKTRI QDLNRIFPLSEDYSGSGFGSGSGSGSGS VGSWFLTGNGNRNYQLVDESDAFQ*QP LGSLDRNLP\SDSQDLGQHGLEEDSMV
387	8438	A	1359	60	401	
388	8439	A	136	961	1051	
389	8440	A	1360	59	420	QQHGRDLWGCRGLIGTDKVERINEMV NRAKRKAGVDPLVPLR/MLGGVVLISGT GSNCRLINPDGSESGCGGWGHMMGDEG SAYWIAHQAVKIVFDSIDNLEAAPHDIG YVKQAMFHYFQV
390	8441	A	1361	80	384	KEHNFVTSVFARGTMGSLTHLLGNSLT EKCKLP SWLPITAEGNSLKGL/LALTQG KEIQAQNFSSFILMKLRHSSALGGASLL PMDYSANAIAFYSYTFS
391	8442	A	1362	3	124	
392	8443	A	1363	189	242	
393	8444	A	1364	420	557	
394	8445	A	1365	284	362	
395	8446	A	1366	2087	2226	

396	8447	A	1367	1	2956	MNTSQLLEIANQVFNRAAVSLEENRKE NGHQARRNTDLVVSCSNQRGQESLEKL LGRYFYISHLSALAKTMRQRFVTCRHHN ARQGPVPPGIQAYAAPIEDLQAIRNNI TAGVYTPCDIGGNILCPLAYYQRYQTG VVYTPCDIGSIILSTSGCPSHTEPRNLTG VSEFLLGLSEDPELQPVLPGLSLSMYLL TVLRNLLIILAVSSDSHLHTPMYFFLSNPS WADIAFTSATVPKMIVDMQSGVVVSU
397	8448	A	1368	149	1323	PRNEPNSPERRPPLAMDAGVTESGLNVT LTIRLLMHGKEVGSIIKKKGESVKRIREE SGARINISEGNCPERIITLTGPTNAIFKAF MIIDKLEER/DINSSMTNSTAASRPVTLR LVVPATQCGSLIGKGGCKIKEIRESTGAQ VQGWGICLPNSTERAITIA/GVPKSVTE CVQADFAWVMLETL/SPSFPQGRSSWTI PYQPMASFPSSSCAGGQDRCSDVGG YPHGHP*PGKGPLLDGLDFDKGQHTISPL DLGQA*TRIGKPTSLNVHMMHGGTGF AGIDSASPEVKGYWAKFECIYPKTPHEL TTPNNLNGCIHGRQADSDLMRSAQMSG QDQKLANPVEGSSGRQVTITGLCCPVI SLAQYLINARLSSEKGMGCS
398	8449	A	1369	2	125	
399	8450	A	137	2	804	SSGFPASTVLGRNPALVPHGRPPPIASPPS PLHRTLGLPQGP RRSSAAQPPPPAAASP LVAAMKTAVPPRKVRQNYHQGLKRAA HQPARNPGSSTASYVLPCMSYLLLTRD DGGL*RTFAKYFLAHQFSMKEEGNHAEK T**KLAEPNEGGRNLSFKDIQEPDCSDW GERGLNA\MECALHLAEKNV\NQSLLLEH KTGPLTKMTPHLCDFIETHY\NEQGES HQKNLGDHVTNLRKMGAPESG\CAEY LFDKAHPWGDSDNES
400	8451	A	1370	18	1374	LAEQIVPRGVGIRPPDKADQAPCRSPIRT PAPESWHCDQRFRQDSSRMKMRVLG LVVCLVLWTLHSESGGKLTAVDPETN MNVSEIISYWGFPEEYLVETEDGYILCL NRIPHGRKNHSDKGPKPVVFLQHGLLA DSSNWVTNLGNSRLGFILADAAIDVWM GNTRGNTWSPKHKTLSVSQDEFWAFSY DEMAKYDLPASINFLNKTG\QEYVYV GHSQGTTFGFI\FSQMLELAKGLKMFFA WGPVASVAFCTSPMAKLGRLPDHLIKDL FGDEEFLPQSAFWKVAGVPHLATHVIL KELCGNLCFLLCGFNERNLNMSRVDVY TTHSPAGTFVQNM*HWSQAVKFQKFQA FDWGSSAKNYFHYNQSYPTYNVKDML VPTAV*TGGHDWLEDVYGVNI*LTQIT NLVFHESIPEWEHLDFIWGLDAPWRLYN KIINLMRKYQ
401	8452	B	1371	77	471	ANREKMTQIMFETFNVPAMRACSTPPE DHRHRAGLRRRVTHNVPIYEGYALPHAI MRDLAAGRDLDYLMKILTERGYSFVTT AEREIVRDIKEKLCYVALDFENEMATAP PPPPWKRATSCQTGX*
402	8453	B	1372	101	391	MCDEDETTALVCDNGSGLVKAGFAGDD APRAVVPSIVGRPRHQGVMMVGMGQKDS YVGDEAQSKRGILTLKYLIEHGIITNWDD MEKNGPHLLHEL RV*

403	8454	A	1373	92	1323	LPAQKLDTMCEDETTALVCDNGSGLV KAGFAGDDAPRAVFPSPVGRPRHQGVM VGMGQKDSYVGDEAQSQRGILTALKYPI EHGHTN\WDDMEKI\WHHTF/YTNELRV GFPKEDP/TTLA*PKAPLKFPKANREE/M NEPQIMFETFNVPAMYVAIQAV/LCSLY ASGR\TGIVLDSGDGV\THNVPIYEGYA\ LPHAIHAPWTMAGRD\LDYLMKILTE RGYSFVTTAER\EIVRD\IKEKLCY\VALD FENEMATAAIHPSSLEKSYELPDG\QVITI GNE\RFRCPET\LFQPSF/LSGMEVGGAFH ETT\YNSIMKCYIRHPGRTFYANNVLSG GT\TIVPLGFAD\RMQERDSPALAPQHP* GSRHSPPPERK\YSVW\IGGFHPWPRLST SQQKW/VSPKQEY\DEAGP\SIVHR\KCF
404	8455	B	1374	53	302	MTSALTQGLERIPDQLGYLVSEGAGLA SSGDLENDEHAASAMSELVSTACGLRLH RGMNVHFKRLSVVFGHEHTLLETRVLTEX *
405	8456	B	1375	277	573	TSALTQGLERIPDQLGYLSSGDLENDEQ AASAISELVSTACGFR\LRGMNVFPKRL SVVFGHEHTLLVTVSGQRV*FV*
406	8457	A	1376	209	413	EAGRREAELKPLGSSPPLPVPPPRAGAGA HQTGA*RAHSMPCRSRKPQAVLTSSSEM ALAACSSFSRSPDDASTAPSLSTR*PSTTT KGRGRGSPDRRLKGTFNAAVQPETAGC ADQLRDGTGCLLIILQVPR
407	8458	A	1377	116	1253	NPGPVQVGVEGGQEEGPSSKKQAKTRQ WSPASITEAPGPKIRFSEPLRPPAGCRHQ LASRPRVLP/PSPTPFCPG/PPSPSSVCSP KDHWRDTPDRRLKGTFMPCRSRKTAG CAEQLQRWHWLP\PAHHSPPQMTPALHL HSPVGSRAGLGFAPAPGSAQKSSG*RCK S*EAC*RDGRPDTLHLQTQVSGLT\WPQ VFSFSPQVPSRPPPPYMLN\TDLPEPPSA PTLAPRLPWPSTSHLCYPKGPVLP\WPLP SDP\SSPPFVSARPA\ALPAAPEHPPTDPSP AFSSPSLPPSP\PPRADRR*GWSAGPPG G/EPHRLGSRDAEPPAGPLAHASSLTIAV FGAGGAPYQIGSFRLQAPV\TCLQPLRSSF CLRH\WPLAPPLA
408	8459	A	1378	24	364	PTEY/ENL/FPCIKEAF/VVEEWVKETLAV L/WPAKQYFPVTPIERILMEEGKAFFPSR STAKQKLDGNPVSP\TPVIGLSPTPNKEE KHLNLCPEFTGHLDGARDTAGPSWLH HRF
409	8460	A	1379	24	2858	VAGNKRGFPLDRRTMPLRLDIKRKLTA RSDRVKSVDLHPTWPMLASLYNGSVC VWNHETQTLVKTFEVC\DLPVRAAKFVA RKNWVVTGADDMQIRVFNYNTLERVH MFEAHSYIRCI\AVHPTQP\FILTSSDDMLI KLWDWDKKWSCSQVFEGHTHYVMQIVI NPKDNNQFASASLDRTIKVWQLGSSSPN FTLEGHEKGVCIDYYSGGDKPYLISGA DDRLVKIWDYQNKTCVQTLEGHAQNV CASFHPE
410	8461	A	138	3	402	HGKIFYFILFYFFIFLRRSLALSPQVRT ADCS\GAISAHCKL/RLPGFTF\PS\CLSLPS SWDYRRP\HPRPANFFLYFLVETGVSPC* PGMGLDLLNS/SIPRLGLPKCWDYRREP PRPVETFFLKAENVRVNYI
411	8462	C	1380	110	508	
412	8463	A	1381	93	180	
413	8464	C	1382	128	382	MYLGISRRLSSMLTFLAYLHPRERPPHR APXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXQQAQGTGISIPRTCTST GL*
414	8465	A	1383	3	140	

415	8466	A	1384	1	609	
416	8467	B	1385	1	690	MASWDEKDLTVQPQDTRKGSVLRCLGS SRALRWAGRGHVAAGWRPLAPESAGG WGMAAAMVPGRSESWERGEPRPALY FCGSIRGGREDRTLYERIVSRLRRFGTVL TEHVAAAELGARGEAAAGGDRLIHEQD LEWLQQADVVAEVTQPSLGVGYELGR AVAFNKRLCLFRPQSGRVLSAMIRGAA DGSRFQVWDYEEGEVEALLDRYFEADP PGQVAASPDPTT*
417	8468	B	1386	1	975	MSPPGREQGLLLNLLRPSGLDNAGKTTI LKKFNGEDIDTISPTLGFNIKTLEHRGFKL NIWDVGGQKSLRSYWRNYFESTDGLIW VVDADRQRMQDCQRELQSLVVEEVGS SYPLCTWRFFSYLRIEQMYNLVLYRDIQ FPDFCFNSNTDWSKGLKTHARFGNTSLH VAHTDSTNTTNFVDVWRGRTKSLACLL QLSSLTCIYTAGKMRLQDRIATFFFPKG MMLTTAALMLFFLHLGIFIRDVHNCITY HYDHMSFHYTVVLMFSQVISICWAAMG SLYAEMTENKYVCFSALTILMLNGAMFF NRLSLEFLAIEYREEHH*
418	8469	A	1387	25	353	EVCYYSSEAFFSELIKVILRHLCVAGK GLCSIPQLNTRGSSVLRIRKRGSPLAVEI EEGHCLCLPLGTECLGIKPIVHLLNSEIG EKPPFSPLSPCSSAAFLLLR
419	8470	A	1388	79	467	RPESQRANGVDSGPNLKTVPQPDTRKGS VLKWKSRGKPLAVEIEESHCLCLPLRTE CLGIKPIVHLFSCTRPVIVPSLELHYDIDS IAHMFVADLLIITLLSYIPIFYLGFNAG ITGINHRAWFY
420	8471	A	1389	368	611	LCPSHFAPTTLTQSGSSLKTCVVLNSRFK ACRAVPGPCLVNQMFASSILGKSHHSL VPINQGHNALWKAAGPLPLKAGY
421	8472	A	139	210	1640	DPARAGTGVGASFRGATWQQGQGRGS ACSTQCPPATCLLTGADAPTSRPWSLL SRLLGHCFSVLTVPAAAPPPGSL/PEPPR AGPQCP*TRPPLR*PGCSHLAGPHSGSPR PCSLLGASATLYGFRHFLAGPAAQGGGQ AVGSQGDHPTRAQPP*WSSPQTPNLNSA AQEFEPRGTCPQTRW*SRPDALPWPRPW EPWSG*AEGWEQE*WRLQPQGTAAAPRA TSSGYSGSSRGQRARPGPARCGDGGGA GRC\GHVGRWRQLGHRP/RGSSAPAVC CGTLSAAPPQPQHSLSL*SSAPGPQWCP HWHPPQSGRQG*/SPLPPPPGPRPPCAPC SGSPSA*GGCTPGCPTAP*GRRQGRWR*P RTGRLSPLGHLPGCRSQAASVSHRCWPL LPPPR/PSGPPPLRSGSSPGG/PLPKGC*C QGGERPQQHKEAGQGPAAQTWLHPQ APGRRPSHTGWGGGAPGG*QRRNLA* RPLLP
422	8473	A	1390	441	1178	FVALPQPLCPSHFDPTTLIQSGAHKNMC CIKSRFKRDLGLCRTCLVNKMFTSSILGK SHCHSLVSINQGHNAWKAAGPLPFRA GYC\QGFSPCDSLKYGSWDEKDLTVQPQ DTRKGSVLRWISQRGKPLAVEMEEGHC L\CLPLGTECLGIK/PIVHLFNSEIGENRP MVGG\RHVLQ*CCLG*FL*LPLRCLGGE KHKSGL/HVHIPVIVLSLELNYDIDSFAH MFF/SVDLLIITLLSYIPIFC

423	8474	A	1391	3	1078	TRAAGLRAGVVRSPGPSRRMPARSGA QFCRRMGQKKQRPAPAGQPHSSSDAAQ VAPAEQPHSSSNPAQAPCPRECLGPPTT PGPYR\SIYFSSPKGHLTRLGV\EFFDQPA VPLARAF LGQVLVRRLPNGTELGRPHR WETEA/YTLGPEDIEAAPLQGGWPGKTP R\NRGMFH*KPGD/LWVVYIYGYFCM NISSQGDGA\CVFLARALEAPGKSWRPMR QLRS\TLR\KGTRQARVLKGPPKLCSPS KL\CQALPINKSF*PEGTLAQDEAVWLE RGPLEPSEPAVVGS/APRVGVGHAGEWA RK\PLRFYVRGSPWASVVDRAEQDTQ ACAKGLPRQDFLHCLKTRJNVLFLEKKK KK
424	8475	A	1392	3	452	
425	8476	A	1393	26	493	NSTDSETHPWLLSPARQRPSTRPAWGK VGAHAVRSMCAEALERMFLSFPTTKTY FPHFDLASHGFCPG*RATGKKVDDSDAQ TPWPTWDDMPKRRCP*SDLHAHKL/SR LDPVNFKAPKATCLAG*PLAAHLPAEF QPLAVARLPWGQISWGFC
426	8477	A	1394	1	409	
427	8478	A	1395	9	817	HGSSSEQUEEDEKNNQSATPIHSGPATM NSIG*YPTQP\TYPVQSPGNVYPQTLNL PQAPPYT\DAPPAYSELYRPSFVHPGAAT VPTMSAAFPGLASLYLPMAQISVAVGPL GSTIP\MAYYPVGP\YPTLAPQVLGGKG GYDAG\ARFAGAGANGGNIPSPPGICPP NAAQLAVMQGANVLVTQVRKGNFFMG GSDGGYTHLVRNQGHLCAREKTSHTLQ HFSQCNCFSHINLKLQFRHMLLGCLSGA QTRHFSNLIRNHVMVAVPP
428	8479	A	1396	1	367	
429	8480	A	1397	625	2919	
430	8481	A	1398	2	76	HHYAKLGTRAVRRARRCAGWQSYVDN LMCDGCCQEAAGYCDAKYVWAATA GGVAFQSIPIEIDMIVGKDRKGFFTSGL TLGAKKCSVIRDSLYVDGDCTMDIRDK QS/QGGEPTYNVA\VGRSGRALVIVMG KGKVFHRRHTLTRKAYETPLYT*RQAW HEGSAKSGMKRLAELRG
431	8482	A	1399	149	421	
432	8483	A	14	79	533	SSIMTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPE/RS*VFINSAGQKSADT GWSSSKPQN*HLSSFHQAVVGMIPSHS QFLMKRKAASPRKLEWEH/LQPLHPMTL LYR*DGKPFPR*VLLSTYTYCSSRDRPKSS GKNARRFPAHGSS
433	8484	A	140	885	1173	LSQGPRRHSSAVQPPPHSHRGHHDDCA SPSQVRQNYAINRQINVELYASYIYLSM SYFDFHNDVALKNFAKYFLHQSHEERE HAKKLMKLLHFDC
434	8485	A	1400	1	1107	
435	8486	A	1401	25	1486	GPQQPHSRSTHASGRPQSLSPVLSLSPDS MSFTTRSTFSTNYRSLGSVQAPSYGARP VSSAASVYAGAGGSGSRISASRSTFRGG MGSGGLATGV\AGGLAGMGGIQNEKET MQLNDRLASYLDRVRSLETENRRLES KIREVHLEKKGPQVRDWSHYFKNEDLAR AQIFVANTCGTMPRIR SARIDNARLAAD DFRVKYEDRSWPMCPVLWRTDIHGLPK VH/IDDTNYHTDLQLETEIEALKVEELLFQ *RRNHEEGS*KALRRQISSSGMNAWRL D\APKSQDLAK\IMADIR\AQYDELGSKK NPRGSLDKYWSQQNEESTTGGSPQKSA EVGAVETHAHRSLKRTVPVLGRSTLDS MRNLKGQLWRTSLREG*RPAYALTRLE PAPTGSLLHLESEL\AQTRARGTAARPRE

						YEALLNWKLEAEIATYRRLLEDGED FNLGDALDSSNSMQTIQKTTTRRIVDGK VVSETNDTKVLRH
436	8487	A	1402	36	389	
437	8488	A	1403	204	433	
438	8489	A	1404	3	392	
439	8490	A	1405	1	1314	
440	8491	A	1406	2	279	
441	8492	A	1407	3	1462	TSCSSAAPFAAALARDPNPASPLPEHRPR LHRGPGPPARLAAAMADPKYADLTGIA RNDPDVYETSDLPEDDHAEFDAFAQELE ELTSTSVHEHNVNPNAAAYDKFKDKRVG DKGI*FSQIVLGKTKRTGYESGEYEMLGE GLGVKETPQQKYQRLLEHVQELTTEVEK IKTTVKEASAAEEKLTPVLLAKQLAALK QQ/VWVASHL/EGKLLGPDAAINL/TDPD GRPGRLRLLQLLEATKNSLGSRGKTPG TPPDSSLVTYELHSRPEQDKFSSSLPKS QKLEKRL/TEL/ETAVTLLIQDAQNPLSAG LQGACLMETVELLQAKVSALDLAVLDQ VEARL/QSVLGK/VNEIAKH*SLC*EGAG YTKARLHQLIHETITALGAPLPSTLPGAGC RRLVTHQSSLHEASPCQFGQLLDT/HLDT TQPMIANFLGRNTNPL*PQVADKPLRE NLAHQLKGNFAQQ*RNG*KKLGKSEAH LGKLEPPGG
442	8493	A	1408	1	4629	
443	8494	A	1409	96	721	PGQLSSLTPRPASLLPWRAAYLFLALFLP AGLLAQGGYDLPLPPFDHGQYTHYM DQIDNPDYDYQEGTPRPSEGQFQFQS QQEVQQGVIPSPNPRAQGNALPEPTEPG PLDCREEQYPCVTRLVSIHRPCKIQLNE VCFYSLRRVYVINKEICVARTVCAHEVEL LRA\DLCSGTSFSKCGR*WASSGLACQSV AASCA\RSCGSF
444	8495	A	141	170	737	IVTATCLWGSVLVTHSVFPFQSYFDRD DVALKDFAKYFLHQSHEERGTCRLNLM KLQNPRG\GLIFLQDIKVNKR*GCHTSSS GSRVSEIT*TSNCPYKVMHWAFAFCA FLGLPSKLN*ANSNVFFAKTWWLEMMG LLTSRLVGRDALTYSHSKPDCDDWESG LNAMECALHLGKNVNQSLLELH
445	8496	A	1410	118	256	MFCFFLKPIAEAPFKFDMELDDLPEKYL KELIFEETARFQPGYRS
446	8497	A	1411	457	839	AVGGFWGCPVELHMLVHITPLSHFKC GCFSNHVPCRLRI*QRGTLRL*MRKYTILF PSTACQHLKFIFQPTV*QFVIKPPGAHDV KHCSVLKYSNISDTAESDCQKKLSTNSC LELYPYFTDLFKYL

447	8498	A	1412	310	1784	RRRPRQPTMAAAVVGGRGPEVWSAGTL FDVGPRYTNL SYIRRGRLTTCVC SAYDN VNKVRVVAIKKISPFEHQTYCQRTLREIK\N ILLRFRHENNINGINDIIRAPTIEQMKGCI* *YRDLMETDLYKLLKTQHLSNDHIWYF LYQILRGLKYIHSA NVLHR\DLKP SNLL LNT\TCDLKICDFGLARVADPDHDHTGF LTEYVATRWYRAPEIML\NSKGYTKSND IWSVGCILAEMLS*QGSPFQKGHYLDQ L\NHIFGVFLGSPSQE\DLNCHKF*KLGN Y LLSSHTSKIMVPLEHACPNADSKSSGTL LGQNCLTFNPHKRJEVEQALA/HTPYLE QYY\DPSD\EP\IAEAPIQVRPWKLDLDPKE KLKGTNFKRLARFQPGVQILNFVQTK GSEGLDVLHRCSSSQFLTGPVFPQCLG LSTLTPLNPFGRGRFLGSCGFYGFSGKISFS PGGFLLGQPCCVHPLVTLRAVCTSVHL TAYCCFSH
448	8499	A	1413	2	294	GNKMAAPKGS LWVRTQLGLPPLLLLT MALAGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPKVG PVRSGLRPFPCSPFL GSPHVCRLWQPGC
449	8500	A	1414	366	1412	QRGTRWRRERGS LWVRTQLGLPPLLLLT MALAGSGTASAEAFDSVLGDTASCHR ACQLTYPLHTYPKEELYACQRCRLFS ICQFVDD\GIDLTRTKLECESACTEAYSQ SDEQYALPFLGCQNSACHFAELRQEQL YVPRWPKMAPTFFL*LLGEGSFWELT*W DSAQ\SFITSSWTFYLA\DDGKIVIFPV*S QKSQYAPHFGAREPTNFEENHLLSKMSS DLQMGKFHQAHQGIFLKNEERDGLFKK PSILNSGWILTT\TLVLS\VMVLLWICCAT VATAVEQYVPSGEAGVTMGDLEFMNEQ KLNRYPASFCGLVRSKTEDHEEAGPS YLPKVNLAPFLEI
450	8501	B	1415	76	384	MSGWGVLSGR LNPAAREKDVERFFKGY GRIRDIDLKRGFGFVEFEDPRDADDAVY ELDGKELCSE RVTIEHARARSRGGRG RYSDRFSSRRPRNDRRNAPP*
451	8502	A	1416	3	229	
452	8503	A	1417	152	536	PDIMSGCRVFIGRLNPAAREKDVERFFK GYGRIRDIDLKRGFGFVEFEDPK\ADDA VYELDGKEL\CSERV TIEHARARSRGGR GRGRYSDRFSSRRPRNDRRNAPPVRTEN RLIVENLSSRVSWQVC
453	8504	A	1418	771	1383	ILIEYKCGKCHVCTLSNIFSSSLVFFISCD CLCVFPPLCLTQLSCVKDLKDFMRPAG E\VTFA\DAHRPK\NNEGVEFASYGDLK NAIEKLSEKEINGRKIKLIEGSKRHSR SRSRSRTRSSSRSRSRSRSS\KSYSRSR SRSRSRSDVPVLLSRSPRA*EEPRNRGS SSRSKSPASVDRQSRSRSRSRVDSGN
454	8505	A	1419	236	1377	PDIMSGCRVFIGRLNPAAREKDVERFFK GYGRIRDIDLKRGFGFVEFEDPRDADDA VYELDGKELCSE RVTIEHARARSRGGRG RGRY\SDRFSSRRPRNDR/RVCEGWMAA LNNYW*G*PFKIQESLAVMILGPAV*SVL LFPR*PIVLDESI*VIEHKSIDGSH*NGL*Y LMA*TCPQLNTSAVIAFLPL*IRIFFLRNA PPVRTENRLIVENLSSRVSWQDLKDFMR QAGEVTFADAHRPKLNEGVEFASYGD LKNAIEKLSGKEINGRKIKLIEGSKRHS RSRSRSRTRSSSRSRSRSRSRKSYSRSR SRSRSRSRKSRSVSRSSPCPKS\QKRG S\SR\SKSPSHLWNRPEVPGPRSRSQIQLD QWPIKPVK

455	8506	A	142	1	809	VVGVSFCNSAWTEPGARSPRPAHSQP SVTSSPHRTAPRPPPLQRREATAAGR LSLVAAMTTASHLAGCAKNYHQGLKRP PINRQDQPWKLYGLLRFTLSHVLTNFDP RMMLAFERTFAKYFLHQFSMKEEGNHA EET**KLQNIQRGWPEFFLAQDIKETQCD DWEERGLNA\ME\CALHL\EKNVESH LELHKTGQLDKNDPPFCVTFIETHY\NE Q\VKGHQRIWGDHVTNLARKMGSAFNLA WAKYLFHDHSTSLGDSNES
456	8507	A	1420	568	770	PDIMSGCRVFIGRLNPAAREKDVERFFK GYGRIRDIDLKRGFGFVEFEDPRDADDA VYELDGKELCS\ERVITIEHARARFTRLGR GRGRYSDRFNNSAELRNDRRNAPPVRP\ ENRLIVENLSSRVSWQDLKDFMRQAGE\ VTLPDTRRLNLNEGVEFASMGDLRNAI EKLSGRELNGRKIKLIERPAKRPO*VQQS RSSDPGTQKSPLGPRSRSPVAVANLSR SKK\RRGSREPGSPEPSRSC*VGSSPVP* ERFFKGYGRIRDIDLKRGFGFVEFEDPRD ADDAVYELDGKELCS
457	8508	A	1421	1	1317	
458	8509	A	1422	1	816	
459	8510	A	1423	19	2867	PPDPLPGLPCPPGGPPLPAFGGGWGGAR GSWHWSSRACSRRRRLVHAPRAPLLPR AAAEKAKRPAGARQMGLKARRAAGAA GGGGDGGGGGGAANPAGGDAAGD EERKVGAPGDVEQVTLALGAGADKDG TLLLEGGGRDEGQRRTPOGIGLLAKTPLS RPVKRNNAKYRRIQTLIYDALERPRGWA LLYH\ALVFLIVLG\CLILAVL\TTFKEYET VSGDWLLLLLETFIFIGAFAFALRIWAAG CCCR
460	8511	A	1424	2	508	PDSSGPHRLRENPPMVAVSCPTKTNVKG PPGGKVGAGAG\EY\SEALE\RMFLSFPT TKTYFPHFDLASHGLCPRLKGHG\KKVA DALTN\AVAHVD\DMPNGVVRP*SDLH\ AHKL\RVDPVNFKLLSHCLLVTLA\AHL PAEFTPAVPRPPWDKFPWLSVKHRCLT FKYR
461	8512	C	1425	257	358	MILLVFLPXHQVFLERXQSEILHHLNTL ADVL*
462	8513	A	1426	64	467	PAAWLPILVAARQLTVQMMQNPQILAA LQERLDGLVETPTGYIESLPRVVKRRVN ALKNLQVKCAQIEAKFY\EEVHDLQRKY AVLYQPLFDKRFEIINAIYEPTEECEWK PDEEDEISEELKEKAKIEDEKDD
463	8514	A	1427	1	795	
464	8515	A	1428	1	836	
465	8516	A	1429	1	410	ARAKTYRMRSEPDDSDPFPDGPIMGC TGCQIDWKKGKNVTLKTIK\KKQKHM RGTVRTVT\KTVSNDFFNFAPPEVPES GDL\DDDAEAILAADFEIGHFLRERIIPRS VLYFTGEAIEDDDDDYDEEGEKSG
466	8517	A	143	776	1115	APGVDPKPRQONE/IPVSTKNM*LGVD CLRGLRQEDHLNQEVPGCSEP*CHDQAT ALPAWATQQDPVSKKKKKKWWREARK GKPQ*GDGEKSTTHSWL*RWRSLKSRI TVSL
467	8518	A	1430	502	765	LQKQKQANKQQIT*K*ACQMV/SNSSFP GKQKVDPTTKRCLVNGGLNLKIQL/IQ ANF*KSRFIHLTVVPVTILSQVTLQLTMS PKTQ

468	8519	A	1431	58	1335	VTACAAPAAWLPILVADIWSSYNMADID NKEQSELDQDLDDVEEVEEETGEETKL KAR\QLTVQMMQNPQILAA\LERLDGL VETPTGYIESLP\RVVKRR\VNALKNLQV KCAQKETQFYEEVHDLERKYAVIYQPL FDKRFEIHAIYEPTEECEWKPDEEDEIS EELKEKAKIEDEKKDEEKDPKIP*IWL TVFK\NVDLLSDMVQEHDEPILKHLKDIK VKFSDAGQPMFVLEFHFEFNEVFTNE VLT\TKLRWSSIPD\SDPFFF*MEPEH*G CTGCQIDWKKGKNVTLKTIRKRPKPQG TWGQFRTVN*NQFPNDSFSNFFCPLLKFL ESED\ND\DAEAILAADFEIGHFLARERIP RSVLYFTGEAIEDDDDDYDEEGEEADEE GEEEGDEENDPDYDPKK\DNPAECKQ Q
469	8520	A	1432	1	645	PLKRS\GDCNDGRPTRP\TRPD\TVFTSNL KQTL\LVH\TPVEKSAVTALWGKVN\NDE \VGK\KALGRLLV\LPWDPKRSFQSPLGE SVPTP*MAKEKVLGCPLV\GLASPGTTL KGHLCPHWSELALL\TSLPRGIPEELQGS WGKRAGSCV\AWAQSTFGQKNFNP\NKL QGLPNQENWLA\WCWLNALGPTS\NHLSL AFLAGPISN
470	8521	A	1433	240	461	
471	8522	A	1434	2	206	
472	8523	A	1435	2940	3296	
473	8524	A	1436	189	736	ENKISSVFKADFLPPAPCSLPGLEVS\SP KGKNTSGRESGFGWAIWMEGLVFSRLSP EYYELARPHLRDEEKSCPC\LAQEGPQ GDLLTKTPELGP*ITRT\ALTIVQKT*RK MVDKPTQRSVSNAATRVCRTGRSRWR DVC\RFMRRYQSRVTQGLV\AGELAQQ NLV\TSRLCIPSTGPL
474	8525	A	1437	3	452	
475	8526	A	1438	3	485	PTLLVPTDSERTHPWLLSPADK\TNVKG PGGKVG\AHAVRSMCAEALERMFLSFPT TKTYFPHF\DLSHG\SAQV*GPRARKVAD AL\TNAVAHVGR\TLPNALVPPLSDLHAH KL\RVGPGSTFKLLKATCLAGLTLAAHL PARVQPLAVASLPWDKVS\WASC
476	8527	A	1439	217	474	RTCASLKS\LRPHGSHGHGQRGGFL*VF SSSF\SSDG\WQVCS\PGGQIPPTCPHHCC DPESP\SSSGPPVPWHLPCA\VGQSPGGGL
477	8528	A	144	1	419	
478	8529	A	1440	569	737	REHPVAGLQEH\LGQGGSGQD\LRG*WA YFS\HR*SRKV\PTSW*RRWKM\APWAA RRV
479	8530	A	1441	520	1319	SWPQVPK\TNKIEPRSYSINTSCG\IRRLGP ALNTLIFSK*NASGPAGHS\AKSIEGAPRG KGRGRAVARLAADRPAPKIQ\LPFV\LR STL*YPLLELE\LPRL\ATHLPSNGS\SLK\ DLKWT\HSNYRASKEP\CIVIFVTTSPGR EWWICAPAAFLG\CGSRFSGSPLPE\SNP* FPV\TRGHHGRHGDYHRKLIGQTFEWV VRRHGG\RAIGPRLSRVTKAAGARPPAG AGEG\LDRVGF\DLINA\PSPPAKGVSARR HVLALELPQLSK
480	8531	A	1442	2	239	RKTQ\TTRRG\PLWAGPGG*RGGWWSR RLLLAAGFLGTHPGSTH\PG\QPRFKWD HTRSSQGAFITFFPRGGQEH\SF\TS
481	8532	A	1443	234	491	

482	8533	A	1444	126	890	PRSIGELGPSLLCGSGRARFSSGGMSGP RLVVLSPGSGAIGKSTLLKRLQEHSGNF GFSVSRESRALVEGVTTRNPRPGEGRQK ITYFVTREVMQRDIAAGDFIEHAEFSGN LYGVTSKVAVQAVQAL*PHRVCLDVDL QGVNRNIRPTDLRPNLHLLFSPPTATCW KQPGFRQPQLETEGRAWLKAGLLAQ ADMEEPAKEAPALFDVVHPLNDQPGT QAYIAELKEALSEEKKAQRTGALRLAV CSR
483	8534	A	1445	978	1440	AGVGVRGTTGRLVVRKFLTLIFGNPLFL VAPPKPHSEWSQRLTYRRRPSPYNTAIS NKTRLSPNPDGNRICLPFIPKKVGKAPQS LHVVCAPGRLRGVRAVRPKV/LL*RLSK TKKHVSRAYGWFHCVLKCGRDRIKACF SLIGGSRKIRCGKSV
484	8535	B	1446	43	674	MDWTWSILFLVAATTGVHSQVHLVQSG AEVKKPGASVKVSCASFNSFDTYGFN WVRQAPQGQLEWMGWVSAFNGDTNYI RKLQGRVTMTTDSSTSTAYLELRLKSD DSAIYYCAATNSDKYFWGQGTLVTVSA ASPTSPKVFPLSLCSTQPDGNNVIACLVQ GFFPQPELSVTWSESGQGV TARNFPPSQ DAFGDLYTTSSQLTLPATH*
485	8536	A	1447	3	1637	SPGIFRGFSQVIRTEQRELTMESGLNWLL LVAVLKGVCQEVQILESGGQVQPGGSR TLSCAASGFIFSNYVMTWVRQAPGKGLE WVSSTAASGANTFYAESVKGRFTVSREN SENMMYLQMSSLRDEDTGIYYCAKDGD VPNLGVAWIVAGPGNVPRKWFDAWG QGTTVTVSSASPTSPKVFPLSLCSTQPDG NVVIAISCLVQGFPPQPELSVTWSESGQG VTARNFPPSQMASGDLYTTSSQLTLPAT QCLAWPKSVTCHVKHYTNPHPDVDG\PCP VPSTPPTP/CSLNSTYPISLMLPPPTVTAPT GPSKDLFLGSEANLTCTLTGLENASGCH FQSEGLQVGKSAVQGP\PEA*PSVAAYSV VQLSCRGWREAMEPLVRPFTCTAALPRS PRTRANRPSSKSGKHISGPEGPPCCRPPS EELALNELVTLTCLARVAFSPQGPCWVR WLQGSPKLPPRKST*LG/PPAGA QARAP TTFAVTSILGR/VQPEDWKKGDTF\SCMA GH\EALALAF\TQKTIDRLAGKPTHVNV VMAEVDGTCY
486	8537	B	1448	113	249	XAAMTTASTSQVRQNYHQDSEAAINRQI NLGALRLLRLPVHVLL*
487	8538	A	1449	846	1193	VMGPKPLPGIVPEFLKNWPRPSGLLIEFC PHWDTTDMTSN/CLV*EENYSEQCLELL NPVGMDLILRGDCESYHGKPNRKLGS QHLSDAQALTGRLSSPCLMKRRRSASFR FTQAG
488	8539	A	145	3	1363	HASGITMAAGTLYTF\SVNWRAFKALIA AQYSGAQVRVLSAPPHFHFQGTNARTPE VLRKFPAGKGP\AFEGDDGFCVFESNAIA YYVVSNEELRGSTPEAAAQVVQWVSFAI DSDIVPPASTWVFPTLG\IMHHNKQAT*E CKGRK*GRILGLV\DAYLKTEDFCWGAN VERLSGITVV\CTLLWLYKQVL\EPSFRQ AFPNTN\RWFLT\CI\NQPP\AVLGGSETC VRLAPFGA*KVLQRPQPK\DTPRKEE GFTGKKKQKPAERKEEKAAAAPG\PE EEMDECEQALAAEPKAKDPFAHLPKSTF VLDEFKRKYSNEDTLSVALPYFWEHFDK DGWSLWYSEYRFEELTQTFMSCNLITG MFQRLDKLRKN\AFASVILLG\TNSSSIS GVWVFRGOELAFPLSPDWQVDYESYTW RKLDPGSEETQTLVREYFSWEGAFQHV KAFNQGKIFK

489	8540	A	1450	2	1087	AIEHCQSGDNPESTRRGFLQWLGRNPA LVPHPGRTGHSQPPVTFHRHPSDCQSP AGRFKGGPSHRGQPPPFHKSPMTTARP TSQ\VRQNYHQ\DSEAAINR\QINLELYA SYVYLSMSYFFDRD\DVALKNF\AKYFL HQSHEER\EHC*ENLMKACRTNEGWPNL SFQDIKETKTCDD\WESGAECQWKALH \LEKNVESSHYNLHKL\ATDKN*PPICV DFI*DTFTLNEQ/V*KAIKRIWGDH/V*PK LWRKMGSAPNLGFGYLF*QSTPWETV IMKAKPRANFPNSRGVTFLVTKAVHAC WGFLYLFYKLYQNIHLSSLICTIPSNKEI WYPGVVFEVLDESEIYPGYLPDSL SAVV QF
490	8541	A	1451	24	452	APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFDFS FGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLLDLKGT AQLSELHCDKLHVDPENFKLLGNVLT LAIHFGKEFTPEVQASWQKMVTG VASA LSSRYH
491	8542	A	1452	41	542	APSRRPWGHTFEED\KAT\TSLWGK\VN VEDAGGRKPLGKAPWLSTPWTQRFDFS FGNLSSASAIHGQTPKVKAHGKKVLT LGDA\TKHLLDLKGTFAQA*SELHCDK\ LHVDPENFKLLGNVLT\VLAI PFSAKE FTPEGCRASWAERWVTWSWPVPCSSRY H
492	8543	A	1453	1	1233	
493	8544	A	1454	233	884	ESPGVGCSARRGPRRSPGPPPAAPGTPR PHGIPLYTRAGHQ**GEIRRRPCTFISKFL RPQGGASERQLPDLQARAWQELLGRPF NKHHWFPR*SPCKGIGVTRCIRINP*KW IPLIGPGQHS AIGLSSQELFRLLP\SEL\TL WG*PIEVS YRIGEDGSHLCACMKPSPA\ GGSTQNTQNTNVQMV\DSRISCKEELLG RTEFPKTTNMMTVSG
494	8545	A	146	3	452	AVPGPGFLSPTMVTLAELLVLLAALLA TVSGY\FVSIDAHAECEFFERVTSGTKMG LIFEADGGFLDIDVITLPDR/RKIKPRLL KKKGQ*TYRSFMDVTFKLCYNLRMSW MNPNI RNHNHWLLLT SIKFLITQFRSSLS YLSSCIQSE
495	8546	A	1460	255	2154	LAEPEVATDSGQQADLPAEGGDPRAEAS CSVLHSPHAMADSRDAASDQM QHWK EQRAAQKYLGVDDLGHKKADVLTGGA GNPVGDKLNVITVGRGPLLVQDVVFTD EMAHFDREIRIPERVVHAKGAGAFGYFE VTHDITKYSKAKVFEHIGKKTPIAVRST VAGESGSADTVRDPGRFAVKFYTEDGN WDLVGNNTPIFFIRDPILVSFLFSRGPID GHRHMNGYGSHTFKLVNANGEAVYCK FHYKTDQGIKNLSVEDAARLSQEDPDYG IRDLFNAIATGKYPSWTFYIQVMTFNQA ETFFPNPFDLTKVWPHKDYPLIPVGKLV LNRNPVNYFAEVEQIAFDPSNMPPGIEAS PDKMLQGRLFAYPDTHRHRLGPNYLHIP VNCPYRARVANYQRDGP MCMQDNQGG APNYYPNSFGAPEQQPSALEHSIQYSGEV RRFNTANDDNVTQTSLYLTYRFMENIEK VRAFVYNVLNEEQRKRLCENIAGHLKD AQIFIQKAKVKNFTEVHPDYGSHIQALLD KYNAEKPKRSLAFIRVTRSSLEDSPVLD VQMQASGFKIENPTFY SRLCNNFN AISPG ENEALTIEQMGSTEANCLLRNSVQLVAF VIEITSRKSDIVERHKCAWT
496	8547	B	1461	129	321	XYWMLCSKAEGCCSGAPKAVGVVWST TLIVLHAHRAVTLVVGHSS TGRDSSQVY EDNWVPGRWR*

497	8548	A	1462	70	2954	RMLITGSPALGSAIPGTPGRRGEALQLLG QSGTLPFRLLGISGLQASFGPCSEPIGL PILACLAPSSQSEGSPPGAGRGGGADW LSLKSPRTRGNRQICLLRVETHEPRPPAV FCTANRTLWLTAGIPPATRCSTGRSSGPR RIEMRACTTSIQGNNVQDKWKSNCVVP DVEACTFLESCLKPGWLGQSKQGAQRS GGDECLQSSHLWEFVRDLLLSPEENCIL EWEDREQGIFRVVKSEALAKMWGQRKK
498	8549	A	1463	3	452	
499	8550	A	1464	2	521	PDSSGPHRLRENPPWCLSPADKTNVKA AWGKVGAAHVSRMCAEALERMFLSFPT TKTYFPHFDLSHGFAQV*GPRARKVAD ALD/TNAVANVGRTPNALVRPLASDLHA HKLSSGTRFNFKAPKGHLPLCLGEPWAA HLPRPSFNPWRLQRLPWGQSFLGFLKH RCLNLPNYR
500	8551	A	1465	154	678	PPLHLRDCFSPPGRALSPVGLYPYR\RSV PTWLKLTSDDVKE\QIYKLA\AKKGLTPS \QIG\VLRD\SHG\VAQVRLG\TGHD\TFK\ LKSKGLDPDLPEDLYHLIKK\AVAVRKH LERNRKDKDAKFRLILIE\SRHPFWLRY YK\TKRVLP\PNWEI*NHLTASALGRINL VWCTPSK
501	8552	A	1466	23	636	FSYLPPGPSHGTWGLWELQFKMRFGVC RHLMEDSMDMDVSPLR/PQNYLFSCELK ADKDDHFKVDNDENEHQLSLRTPVSL GVFEITPPVLLWLKCGSGPVHISGQHLV AVEEDAEESEDEEEEDVKLLRISGKTKTF MATNGKEYKHYKISSEKSLDNKYKTRTP GFQAFGFEDLHPWPLGSQAFYLSLRVTP PVFLVLRLLDFD
502	8553	A	1467	3	618	AKD/ELHIVEQGHDIRGRSIKIT/LATLKM S/VQPTFS/LGGFEIQPTVV*GLKCVSGPC HISGQHLVA/VEEDAEESEDEEEENVKLLS ISERRSAPGVVSMVPQKKVKLADEDD DDDDDEEDDDDDDDDDDFDDEEAEEKAP VKKSIRDTPAKNAQKSNQNGKDSKPSST PRSKGQESFKKQEKTPKTPGPSSVEDIK AKMQASIEKAH
503	8554	A	1468	1	1689	
504	8555	A	1469	3	535	DSVLRGCSLEQRSFISVRLLSYLSACRHP MEDSMDMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTVSLGAGA KDELHIVEAEAMNYEGSPIKVLATLKM SVQPTVSLGGFEITPPVLRKCGSGPVH ISGQHLVVYRRKHQELQAMQMDCRAL STS*ASSAPRPS
505	8556	A	147	90	512	VQGLGVERVPLGSHRGWMGPPRPLLSP QERASCLLLLLPLVHVSATTPEPR\ELD DEDFRCVLQLSPEPQPDWPEALHRASAV QA*ISAGGSHLQSSFLIGRLRLKTVTVLL WPLFVLICVYLSVYLPFRLCLDTLSCVV
506	8557	A	1470	1	1025	SVLRGCSLEQRSFIYGRLLSYLSACRHPM EDSMDMDMSPLRPQNYLFGCELKADKD YHFKVDNDENEHQLSLRTVSLGAGAKD ELHIVEAEAMNYEGKSN*T*HLATLKMS \VQPTVSL/GGAFEITPPVLRKCGSGPV HIKWTSTYVAVEGKMQKSRRLKKEGRI. VKLLKVYL GKARSAPWKVGSKVSTEEK VKTLA*WKDDDRMNDEEDDD\EDDD DDDFDDEEAEEKAPVKKSIRDTPAQKC SESQNGKRLQKPSFTPKNQKGQESFQ ETRKKLLKTPKG\PISSVEDIKAKMQASIE KGGSLPKVEAKFINYVKNCSRMTDQEA IQDLWQWRKSL

507	8558	A	1471	3	490	SSGPTRLRENTMVAVSCPTKTNVKA WGKVGHAHVRSMCAEALERMFLSFPT TKTYFPHFDLEPRFLPRFKGHGKKVADA LTNAVAHVDDMPKRAVPLSDLHAHKF RVGPGSTFKLLKPLALLG*TLGRPTSPSE FQPLAVARLPWQSQSFLGLLKQPC
508	8559	A	1472	35	1288	
509	8560	A	1473	1	1641	
510	8561	A	1474	212	369	HPVTYVYLLGYLLFQLPCGSEFSTSETHG HSADRLGAAFAVSRLEQDEYAPG
511	8562	A	1475	63	255	VLMFSSSHG*GYQSSRLQCKLQIVQLIQ DILLFFSF*IPE*LLS*LTPLKIFLHQNGPS DFVS
512	8563	A	1476	169	391	
513	8564	A	1477	85	1534	KSSHCIKMGPQIFHKTSELVLPATSCPSC PDQNEEDVSQTQYKECCG*GGWCSSHSIF AVWHFI*RPDAT*FGLEQRLTGLLASGP VSLREV*LYSSLGTVISGK*KTSNVG*R GLALGSWAFSDKYSWFTMTWACISGP TKALTTGVGLIAFGQCDVIVAGGVEL MSDVPIRHSRKMIMLMLDLNKAQSMGQ RLSLISKFRFNLAPELPAVSEFSTSETMG HSADRLAAAFVSLADQDEYALRSHSL SKKAQDEGLSDVVPFKVPGKDTVTKD NGIRPSSLEQMAKLPFAIKPYGTVTAA NSSF/LLTDGASAMLIMAEKALAMGYK PKAYL/RRDFMYVSQDPKDLLGPTYA TPKVLEKAGLATMNDIDAFEFHEAFSGQI LANFKPMDSDWFAENYMG*KKPRFGL PPLWRRFNWVGSLSLGHPFGTGTGCR LVMTAANRLRKKGGQYGLVAACAPG GQGSATDYVEAYPK
514	8565	A	1478	2	359	
515	8566	A	1479	1	585	PRGVIGHGPLGTSFIGKYGCGDYWVKAF LDRPSQPNQGPKNFEVWDLVDVNTPI DLMAIPVSAKKERKVS CMFIPDGRVSVS ARIDRKGFCGDEISIHADFENTCSRIVVP KAAIVARHTYLANGQTKVLTQKLSSVR GNHISGTCASWRGKSLRVQKIRPSILGC NILRVEYSLLIYVSVPGSKQVFIKAL
516	8567	A	148	98	440	KDDTNTKCW*AWNCSSTRAHWKRTL LLGRLLTMNIPHDSAIPLLGAHPT*MWA YVHQNPQTVMLTETLFMIATNWLHKC PQ**KE*CNGAVTEWSAALKQNKQLQH VTPRV
517	8568	A	1480	218	1677	SEIFCKGVSSIWSFFFLPPSFLTTLKTNVSP SWVMFKIKISFEVVFNDPGKGVTAVG EKVAIGRVNSGRCEVTRVKA VRIPAC RSLGKCLWMPGIPSRCKQTSEYPRYEDT VFLAEDQPTGENEMVIMRPGNQYEYKFG FELPQGPLEHSFKGKYGCVDYWVKAF LDRPSQPTQETKKNFEVVDLVDVNTPD LMAVPS/ALKKEKKVSCMVIPDGRVSVS ARIDRKGFCGDEISIHADFENTCSRIVVP KAAIVARHTYLANGQTKVLTQKLSSVR GNHISGTCASWRGKSLRVQKIRPSILGC NILRVEYSLLIYVSVPGSKKVILDPL/V* LGSRLSSRTS/SMGSR/SLRMSWVD LNIP/DTPEVPS/CILGCSFPEGSTVWESPT TPLLDDMDGQNSP/IFMYAPEFKFMP RTYTEVDP/CIFNHQCAVSMWKKRSSFT LLVSFWPSLPWTVHFFQRLNSLCNGSVG PTLSPLTS
518	8569	B	1481	21	410	MPSKVRXCXSVQVFDAMKTATAVAHCK RGNGLIKLEPVLLGKERFAGVDTRVR VKGGGHVAQIYAIQSIKALVAYYQKY VDEASKKEIKDILIQYDRTLVADPRRCE SKKFGGPGARARYQKSyr*

519	8570	A	1482	1	456	MPS/KGPLQSVQVFGRRKTATAVAH/CK RGNGLIKVNRPLEM/IEPRTLQYKVLGS GTGVSGWRTLGD RDVVALESWGAGISN GMFRSCVGC RQWAAGASSASRQERFAG VDIRVRVKGGGPWPRFMSKKFGGPGAR ARYQKSTDKPIVTQNSLV
520	8571	A	1483	172	661	LLEPVLLLGKERFAGVDIRVRVKGGGHV AQIYGESQELGAWRRWLWEGGLHSAPV PFNCVSFSQLSVSPISKALVAYYQKIWSE HGSFP*GRWVCGDQVKDSV*LSKSSLL FLPDVDEASKKEIKDILNQYDRTLLVADP RRCESKKFGGPGARARYQKSYR
521	8572	A	1484	1	556	GAARVRLSSPRSDAMPSK/GVPLQSVQV FGRRKDSGQLLAHCKRA\NGLIQG*TG GPLEMIEARARLQYK\LEP\VLLGK\IER FAG\VDIPCPV*KGGWSTWPQIYAIRQSV SQKPLVAYYPEM*VSMGPSHE/YVDEAF QRREIKDILHPSY\DRNPAGLAGPFVRCE\ SKKFGGPGAIRARYQKSYR
522	8573	C	1485	127	435	MAASXNPEVLDITEETLHSRFLEGVRNV ASVCLQIGYPTXASVPHSINGYKRVLAL SVETDYTFPLAEKVKAFLADPSAFVAAA XLGCCHHSCSXCCSPS*
523	8574	A	1486	1	689	KCFI/VGADNVASKQMQQIRMSFRGKAV C*WGKNTMMRKPIRGHLENNPALEKLL PHIRGNVGFVFTKEDLTEIRDMLLANKV PAAARAGAIAPCEVTVPAQNTGLGPEKT SFFQALGITT KISRGTIEILGVRNVASVCL QIGYPTVASVPHSINGYKRVLALSVETD YTFPLAEKVKAFLADPSAF/VAAAP/VAA ATTAAPRAAAAPAKVEAKEESESEDED MGFGLFD
524	8575	A	1487	66	1104	RTAVMPREDRATWKSNYFLKIIQLLDDY PKCFIVGADNVGSKQMQQIRIVPWGEAC VLMGQKTMNGPGPSEGHLENNPASEEL LPH*VRHGLGFCFTRED\LTEIRDMLLAQ *GCQAAARCWCQLPPCEVTVPA\QNTGL GPEKTSFFPGL*VSPTKNLPGGTH*KS*S YVQL\IKT\GDKMGSQTKAKAAEKMLKN LPPSPFGAGQPKQGVVRKNGKHPTNPESA *ISTRGKLCHSRFLGGCPANVAKCLCKI GYPTVASSTPIPIITNGYKRVPGPCLWTP DYTFPLAEKVKAFLADPSCLCVLLPPV GAAATTACFALLQPPAKVEAKEESESEED EDMGFGLFD
525	8576	B	1488	98	264	XQVVCKKYRGFTIPEAFRGVHRYLSNAY AREEFASCTPDDEIELAYEQVAKALK*
526	8577	A	1489	155	1217	DPPSPVPAPPSSPRDGHFLVPDATMAEEQ PQVELFVKAGSDGAKIGNCPFSQRLFM VLWLKGVTFNVTTVDTKRRTETVQKLC PGGQLPFLLYGTEVHPD\TTKIEEFLEAVL \CPPRYPKLAALNPEVQHSWGWDIFAK FFLPNIQEFQTPALN*QSGRRGFLESP*KV LDNYLTSPSPPEEVDETSK*KIEGVSQR KFVLDGQRRPHPWLDLQTCCKVTH*VQ VV\CKRK*PGNSPHPPKAFPGKCHRVPS KMPYAPGKNSPSHVPDDEEIELRPMK VAKALQISPSLGLPSTPSIFSTKAPGGFHI ATPMGHTPKLAGSQGILGDIEPAKGVVE EGMRERNNGPGSDF
527	8578	A	149	535	917	LVSPGKPPEQQGQLP*PRCQII*LVSPGKP PE/PTGTAPRSQPRLSVCPSTQDICRICHC EGDEESPLITPCRCTGTLRFVHQSC LHQ WIKSSDTRCCELCKYDFIMETKLKPLRK WEKLQMTPRERRKIFCSVTQRNRGSPV WFGLCMY
528	8579	A	1490	2	746	

529	8580	A	1491	217	1007	LNHNRLAVIMANLGCWMLVLFVATWS DLGLCKKRPKPGGWNTGGSRYPGQGS GGNRYPPQGGGGWGQPHGGGWGQPHG GGWGQPHGGGWGQPHGGGWGQGGGT HSQWNKPSKPKTNMKHMAGAATAGAV *GGLCSYSLGSAMSRPIHFGSDYEDRY YRENMHRYPNQVYYRPMDEYSNQNNF VHDCVNITIKQHTVTTTTKGENFTETDV KMMERVVEQMCITQYERESQAYYQRGS SMGLFSSPPVILLISFLIFLIVG
530	8581	A	1492	32	487	SRRHGSSLWGKVNVEDAGGETLGRLLV VYPWTQRFFDSFGNLSSASAIMGNPKVK AHGKKVLTSLGDAIKHLDDLKGTFAQLS ELHCDKLHVDPENFKLLGNVLVTVLAIH FGKEFTPEVQASW/QEDGDWSGQCPVLQ IPLSSLPMMQSFQG
531	8582	A	1493	41	597	APSPRRPWVISQRTKATITSLWGKVN VEDAGGETLGRLLVYPWTQRFFDS FGNLSSASAIHGQPPKVQGTWSKKVLT LGEMP*KHLDDLKGHLLPKPEVNLHCD KPAMWDPENFKAPGEMLLVTRFWAIPF SAKEFHPWRLAGLPQKDG*LGVGQCP CSFQIPLKPLGP*IQSFQG
532	8583	A	1494	1	478	DTRFLERLRLSISSLVPDAMGHFTEEDK ATITSLWGKVNVEDAGGETLGRLLV VYPMDPRGFFDSFGNLSSASAIHGQTPK VKATRAKKVLTSLGKMPIKHLGLIFKGT FCPSLS*TCTC*QACMWD*GTFKLPG MLLVTRFWAIPFSAKEFHP
533	8584	A	1495	3	370	SVCVRAHESVVKSEDFSLPAYMDRRDH PLPEVAHVKHLASQKALKEKASWSS LSMDEKVELYRIKFESFAEMNRGSNE WKTVVGGAMFFIGFTALVIMWQKHYGL ASKWDYEKNEWKK
534	8585	A	1496	24	305	
535	8586	A	1497	197	745	LASEQFSTSVVCTSSMKVFKSEDFSLPT YMESAVTHPLAGRWPVVKAPCSAQPRR PLKEKEKALLGAAFSMG*GKFELFALK FKEEALLED*TRGLRTELGKTGLFGPVPL FPSIGFSPRLVIHVQKHYVLTAPFPQSF *TKSWVGPSRTKRMLGQ*R*TIQGLAS KWDYEKNEWKK
536	8587	C	1498	78	281	MELSNNHQLSMSLVELSMSLVWDANLL GWGKSCELTGPSWSLVRSTSRHSRKKGS SWHLPAKLCSTC*
537	8588	A	1499	302	687	
538	8589	C	15	354	416	MKESPGGELPQTGKKPVFLF*
539	8590	A	150	116	830	EGFPGRSLSGGLCCRLRRRFPIDGYRPW RRRRWSCCPGVRPVRMSHKSWIESTL TKRECVYIIPSSKDPYRCLPGCQICQLV RCFCGRVLKQHAFTASPAMKYLDVKL GDHFNQAIEEWSVEKHTEQSPTDAYGVI NFQGGSHSYRAKYVRLSYDNQPLVILQ LTVKEWQMEPKLVISVHGGMQKFELH PRIKQLL*KGLIKAAVTTGALITGGRNT GVGKHGGDAPQRTC

540	8591	A	1500	1	1622	MSKPKCLVILVGIQKSSQMPQFPPAGSE RRRGIRQWEMGVVGGEMGVWWPPGVQ GSPPQAHRRRLGSREQLFAPPLKEKSHIPP WGYSRENYPIPEPGPNRPVTEVWGSPG PTVQWGWEGLEALSPALINQAQKDPE VRLGAMVRVSVDTHTPPPLTPRQSGPLSA LEELGVSFPTLSYLTPEPQLLGEHQIKGSF PGRSTALLKEVLLRMHSGICGSDVH YWEYLS/RFGNFIVKKPMVLGHEASGTV RKSGIIGKSTLKPG\DRVAIEPGCSPEEN* WNSCQDG/RRYNLSPSIFFCATPPDDGNL CRFYKHNAAFICYKLPDNTFEEGALIEP LSVGIHACRRGGVTLG\NKVLVCGSWAN RGWVTLLVAKAMGAAQVVVTDLSATR LSKAKEIGADLVLQISKESPEIARKVEG LLGCKPEVTIECTGAEASIQAGIYATRS GTLVLVGLGSEM\TVPLLAHAIREVDIK GVFRYCNTWAPVAISMLASKSV/DMSKPL VTHRVS\WRKVLEAFETFKGLGLKIML KCDPSDQNL
541	8592	A	1501	1	804	
542	8593	A	1502	178	1093	TFLLPACLLAALLPLRHHVRGRAWVQG SILNEGVG*ALKDLINEACWGY*APAG VNLQSMGHRPTVSLVQLTLRV*GASTP YRC\DRNLGHGR*NLTSMSKILKMAAG NED/ISLTLRAEDNAGYLG*YFEGTKPG RKFSYEMKLM\DLVEQLGIPEQEYSC VVKMPSGEYARICRESQPILGDAVVISC AKDGS\ENFSASGELGNETIKLSQTSNVD KEEEA\PIKMNEP\VQPNFCH*GYLNFFT KATPLSSTV\DTPVCSADGTP\LVGRS KIA GYGDHLKYLLGLPKDPRIEESLGHS
543	8594	A	1503	32	487	SRRHGSSLWGKVNVEDAGGETLGRLLV VYPWTQRFFDSFGNLSSASAIMGNPKVK AHGKKVLTSLGDAIKHLDDLKGTFQLS ELHCDKLHVDPENFKLLGNVLVTVLAIH FGKEFTPEVQASW/QEDGDWSGQCPVLQ IPLSSLPMMQSFQG
544	8595	A	1504	1	591	NFALEAKNSARAISLVPDAHGVISQRT KATITSLWGK\VNVEDAGGETLGRLLV VYPWTQRFFDQLLANLSSASAHGQPPK VQGHMAKKVLTFLGEMPIKHLDDLKGH LLPKPEVNCTVDKPAMWDPENFKAPGE MLLV\T/LFWAIPFSGKEFT*RLQASWAE RWVTWS\GQCPCSFQIPLKPLGP*IQ\SFQ G
545	8596	A	1505	49	273	
546	8597	A	1506	81	720	LFKAPEPHVEEDD\DELD\SKLNYKPPQ KSLKELQEMDKDDESLIKYKKTALLGDG PVVTDPKA\PNV\VVTRLTLVCEAPG\PI TMDLTW\KIWKALKKGNHLVLKGRFWNI RSSKFHFPKLN\RG*LLFRA*NYVQHTYR TG\VKVDKATFM\VGSYGPRPEEYEF/LS LPVEEASQRAWLARRHVTTKSPFFTD\DD KQDHL\SW\EWNL\SIKKEWTE
547	8598	A	1507	5	290	FNLTHIESRPSRLKK/DEYE/FFTHLDKRS LPALTNIIKILRHDIGATVHELSDKKKD TVPWF\PRTIQELDRFANQILSYGAELDAD HPVSPWPVG
548	8599	A	1508	68	312	
549	8600	A	1509	317	916	TSSPPSSLCFLS\SDICHELLGHVPLFSDR SFAQFSQEIGLASLGAPDEYIEKLATYIW FTVEFGLCKQGDSIKAYGAGLLSSFEL QYCLSEKPKLLPLELEKTGIQNYTVTEFQ PLYYYVAESINDAKEKVGNSAATIPRPFV RYDPYTQRIEGLDNTQQAHDLG*FHLTV EIGILCSALQKNKVKAMDRMVVCQAVE
550	8601	A	151	770	950	CHSEHRNYKNNHHSIKVPRWRWHFHS NVIS*SLVHISKVFVAYKCNQYFHIRKFR

						SVT
551	8602	A	1510	389	1881	NLQPHVLFANLPVPEALKSQRPHSRGAS MSTAVLENPGLGRKLSDFGQÆTSYNE NCNQKWVPISLDPPHLKERKLGALPKY CALFEENDVNLT/HIES/RPSRLK/KDEY FFPPFGIKRSLPALTNIKILRHDIGATVH ELSRDKKKDTPVPWFPRTIQELDRFANQI LSYGSGNWDADHPGFKDPVYRARRKQ FADIAYNYRHGQPIPRVEYMEEKKTWG TVFKTLKSLYKTHACYEYNHIFPLLEKY CASHEDNIPQLÆDVSQFL/QTCTGFRLRP VAGLLSSRDFLGDLAFRVFHCTQYIRHG SKPMYTPEPDICHELLGHVPLFSDRSFAQ FSQEIGLASLGAPDESIEKLAPIYWFTVEF GLCKQGDSIKAYGAGLLSSFGEFYCLS EKP KLLPL/ESLEKTAIQNYTVTEFQPLY YLAÆSFNDAQGEI*GTFAATIPRPFSVR HDPHTPQRIGGSWDNTQQLKILADSI*Q *IGIPFAVALQNIK
552	8603	A	1511	1	191	MQK*ITAWAPAPMKIKIIASPERKYSVWI GGSIWPQLST/FQQMWISKQEYDESGPSI VHRKCF
553	8604	A	1512	1	360	SGACPAFLVDRNLRHHETTFNLIMKCDV DIRKDLYANTVLSGGTTMYPGIADRMQ KEITAL/APPSTLRFRIAPP/ERRKYSVWI GGASILASLSTFQQ/MCLGKQEYDESGPSI VQRKCF
554	8605	A	1513	13	1277	INPPPLSRRCQLSHSVLPPLRRRVSLPVA MEEIEAALVIDNGSGMCKAGFAGDDAP RAVFPSIVGRPRHQGV MVGHGPRTDSY VGDEA/QRSKRGILTLKYPIEHGIVTNWD DMEKIWHHTFYNELRVAPEKHPVLALT EAPLNPKANREKMTQ/ILCFETFNTPGHV PWPIQAVLSL*SLWAQPIGIVMDSGDGV THTVPILRGATTLLHANRLGPGGLARDL TDYLMKILTÆRGYSFTTHGSPGKTFRNI KGEACATSPDFEQÆMGTAASSSSLEK SYELPDGQVITIGNERFRCPEALFQPSFLG MESCGIHETTFNSIMKCDVDIRKDLYAN TALS GGTTMDPGVIADKIAEGRSTALAAP AP*KIR/IIAPP/ERK\YSVWIGGSILASLST FPAFW\ISKQEYDESGPSIVHRKCF
555	8606	B	1514	93	366	XTSVVRPF AKLVRPPVQVYGIEGRYATA LYSVLNPYVKRSIKVKS LNDITAKERFSP LTTNLINLLAENGRLSNTQGVVSASFST MSVHRGE*
556	8607	A	1515	1	785	FRRQARAPLRVFLFPLGFDLOPPGRRW AAPAV\SGLS\RKVRCFSTSV\RHFAKLV GPSVQVYGIEGRYAT\ALYSAASKQKNL E\QLEKELLRVAQNPEGNPKVAAS\VLNP Y\YVKR\SIKSEKALN\DITSKRRFSPSTT QPWIKFALPE\NGSD*SKYPQGSFPALFP THDEVSHPRAGGYPC TVDLWHLLLEGSQ TPPGI*KLSLKS LP*VKGOVLKLEAKTDP SILGGMIVRIGE\KYVDMSVKTKIQKLG\ RAMREIV
557	8608	A	1516	1	2199	

558	8609	A	1517	9	1618	PALCPTLSSGTSARFRGKNQFSGGLPQIT LSPLAQPCGRLAAMYSNVIGTVTSGKRK VYLLSLLDSFGDCVTCHG\SPVDICTAK PRDIPMNP\MC\IYRSPEKKATEDEGS\EQK IPEATNNR\RVWELSKAN\SRFCLPLSYS APGQNSKD*H*LTF\FCSPLSIFQGFLWT K\VGACNDTLQQLMEVFK\DTIS\EKTF* SRSHFFFAK\N\CR\LYRKANKSSKLVS NRLFGDKSLTFNETYQ\DISELVYGAKLR PL\DFK\ENAEQ\SR\AA\NKW\VS\NKTEG RIHRCSPSPGRPFNELTVLGGGFNTIYFQ GACWK\SKFSPENTRKELFYKADG\ESC\ SASMDVTREGKFRYS\GAWLEGT/QVLV VCPFKGDDIT\MVLILPKP*EGAWAKVEK VELTPEVLAKSGWD*FWREMMMLVVHMP RFR\NEDGLQV*REQL\QRHG\PLSDLFSP* KSPKL/LPGIVAEGRDDLYVSDAF\HKAF LEVNEEGSEAAASTA\VV\IAGRSLNPNRV TFQGGQLFPGFLLREVPLNTIYLHGAEL ANPCV
559	8610	A	1518	2	363	ELDTLCDLYEP*PSPSIIFINTRRK/VDWLT EKM\HARDFTVSAMHGDM\QK\ERDVIM REFRSGSSRVLITTD\LRIGRGGFRGRKG VAINMVTEEDKRTL\DIETFYNTSIEEMP LNVADLI
560	8611	A	1519	201	648	GPCGHGRVFPLPSLAAHMDA*GLLLRDR VSSVHMLKRLSFLT*ARGIDVQQVSLVIN YDLPTNRENYIHR*A*IWNTP\PLHTWPS LGLKLLIFLIPFLVFQ\IGRGGFRGRKGVA INMVTEEDKRTL\DIETFYNTSIEEMPLN VADLI
561	8612	A	152	1	253	SKLAAEMTANRLAESLLALSQQEELADF PKDYLLSQSQD\EGDNDGERKHHKLEA ISSLDGKNRRKLAEMSDVILMM*EFVVA
562	8613	A	1520	49	1720	GSTISSASQDSRSDNGLD\GIEPEGVIESN WNEIVDSFDDMNLS\ESLLRGIYAYGF PSAIQQRAILPCIKGETSQSQKTLWTPD LGRVASGW*CPSHISQGSNLLVHPSLA FDPCPCLVHALDT*VSFKEVVL*PAYICI YSHVSSPAWCAILDELITGPCF*SGSHCV TVLIGKVVC\EP*NAWFIGLLTSLT*DLNI PKGMLFTTFNS*FICLGYDVIAQAQSGTG KTATFAISILQQIQ\KVVMALG\DYMGVAS CHACIRGAPTCVAEVQKLQMEAPHIHR GVPPGRVF*YALPEDTLSPKY\KMFVLD EA\DEM\LSRGFKGQIYGHQKAQAAPPR VVLLSATMPFDVLEVTKKFMRGPFRIL VQKGELTLEGIRQFY\NVEPEEFNLD LCDLYENLDHHPRVIFHQP\GGKVDWP HPRRMHAADF/TLYSAMHWRFWTQKER RT*L*REFRSWLLARIFDTQLDLLGQRA LMCQQV\SLVIQTYDPFP\TRGKLLIHRV GSRVDRFGRKGVPINMLTE/EKTKRNLE DIETFYNTSIEEMPLNVA
563	8614	A	1521	3	607	FCPRGOEFGE\GNKLLSPRRPWVISQRR KATINTSLWGK\VKCGKNAGKEETPGKGS LVVL/HPWTPRG\SFELWQTCPSALCPS MGNPQSQGTMAKKVLTSLGRCP*STLD\ DLKGHLLPKPEVNLHLLTSLHVGS*RTF KLPGEMLLVT/LFWAIPFSAKEFHPLKVA GFPQGKDG*LGVGQCPCSFQIPLKLP* IQSFQG
564	8615	A	1522	23	437	KTPGKGS\LVVL/HPWTQRFFDSFG\NLS\ SASAHGQPPKSAHGK\KVLTS\LGDAI KH\LDLKGTF\AQLSELHCDKLHVDPEN FKLLGNVLVTVLAHF\GKEFTPEVQASW QKMVTCSGQCPVLQIPLSLLPMIQSFQG

565	8616	A	1523	23	249	APSPDAMGHFTEEDKATITSLWGKVNVE DAGGETLGRLLVVYPWTQRFFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAIKH LDDLKGTFAQLE*TCPLPLPSWATPKSR HMARRC
566	8617	A	1524	46	379	SQTPMGHFTTEEDKATITSLWGKGEMW KKCWKEKTPGKGSLLVVL/HPWTPRGSF DSFGKPVPLPSAHPWATPKVKAPWPRRC LTSLGEMPIK\HLGLIFKGTFCPSLK*TCT C
567	8618	A	1525	21	457	NPRVRGALTMELSESQKGFQMLADPR SFDSNAFTLLLRAAFQSLDDAQADEAVL DNKNSLEILLGSIGRSLPHITDVSWRLEY QIKTNQLHRMYRPAYLVTLSVQNTDSPS YPEISSSCSMEQLQDLGGKLDASKSLG KSTQL
568	8619	A	1526	1	455	
569	8620	A	1527	3	468	
570	8621	A	1528	50	895	THASDGALTMELSESQKGFQMLADPR SFDSNAFTLLLRAAFQSLDDAQADEAVL DHPDLKHIDPVVLKHCCHAAA\ATYILE AGKHRA\DKSTLSTYLAEDCKILTEKRIEL FFAREYQ\NNK\NSLEILLGKY*GRSLPS YNRVFSWALWIIQVKDQSTFHRM\YRPA AYLGDLLKVVQNTGIPPSVYPRELVFSCQP WNQL\QDLVGETLKDASKKPWKRAATSV VTLGKVNRSPPSSRRKTQKPLPFSWNH RLCRAGCPFSVEKNFSLLNLYPFIHFGHF KNV
571	8622	A	1529	1404	1586	ENESRFSDRNQASAGLYLSDSL*QWIV GNGHATDLWQNCSTSSSGNVHHCFS SSP
572	8623	A	153	1	759	
573	8624	A	1530	187	701	AELAARMLLLLLSIIVLHVAALVLLFVST IVSQWIVGNGHATDLWQNCSTSSSGNV HHCFS SSPNEWLQSCSRGTMDPVDSSFS ILSLFLFFCQLFTLTKGG\RFYITGIFQILA GLCVMSAAAIYTVRHPewnlnsgy* RFA*ILAWVAFPL\ALLSGVIYVILRKRE
574	8625	A	1531	1	485	
575	8626	A	1532	2	459	
576	8627	B	1533	1	2784	MAAMAVGGAGGSRVSSGRDLNCVPEIA DTLGAVAKQGFDFLCMPVFHPRFKREFI QEPakNRPGPQTRSDLLSGRALEIGAD LPSNHVIDRWLGEPIKAAILPTSIFLTNKK GFPVLSKMHQRLIFRLKLEVQFIITGTN HHSEKEFCSYLQYLEYLSQNRPPPNAYE LFAKGYEDYLQSPQLPLMDNLESQTYEV FEKDPIKYSQYQQAIIYKCLLDRVP EEKDTNVQVLMVLGAGRGPLVNASLRAAKQ AD
577	8628	A	1534	2	607	
578	8629	A	1535	1	207	
579	8630	A	1536	232	755	LSCCADDGVSIPGEYTSFLAPNFSPKLYN KVRACRKKARDLKAQFEMPVIVRLHNS NQLSAPQPCSTFSHPNRDPMIDNNRYCT LEFPVEVNTVLQCFAGYFETVLYQDITL SIRPETHSPGMFSWFPILFPIKQPIVREG QTICVRFWRCSNSKKGSSHQSMKTSGQG VRN

580	8631	A	1537	35	2271	LCDWLLVSRNPVSDSARRKMAAMAVG GAGGSRVSSGRDLNCVPEIADTLGAVAK QGDFDLCMPVFHPRFKREFIQEPAKNRP GPQTRSDLLSGRDWNTLIVGKXSPWD FVPDASKVÆKIRRNSEGGPCLQELNFGA YLGPAFLLPLNQEDNTNLARVLTNQIH TGHDFYMFWRRIHLKKPEDLARDDIEN APTHTEEYSGEEKTWMWWHNFRTLCD YSKRIAVALEIGADLPSNHVIDRWLGEPI KAAAILPTSIFLTNNKGFPVLSKMHQRLIF RLKLEVQFIITGTNNHSEKEFCSYLQYL EYLSQNRPPPNAYELFAKGYEDYLQSPL QPLMDNLESQTYEVFEKDIKYSQYQQA IYKCLLDREVPEEEKDTNVQVLMVLGAG RGPLVNASLRAAKQADRGIKLYAVEKN PNAVVTLENWQFEEWGSQVTVVSSDM REWWAPEKADIIVSELLGLIC*PIELSP*V PWIGAQHFP*KMIGVKHPPGSYTSFLAPI SSSKLYNEVRACREKDRDPEAQFEMPYV VRLHNFRLSAPQPCFTFSHRNRDPMI DNNRYCTLGFPVEVNTVLHGFAGYFET VLYQDITLSIRPETHSPGMFSWFPIPLPY* GSPLTVRERAKPFCVRFWRRCRQFPRKV WVWSGGC*QAPVCSCLIQKPKGPPQYT HWPLLSPCRAPSVPEALGKPAFRFLPPCS NSKVPVTSYGAVIPPWPIQRREHFQSCFP CPYIQGGPRDYN
581	8632	A	1538	137	303	
582	8633	A	1539	122	385	YPALEHILKAQAIQSRGCDSCLPSPAPW DHPGPTTPSPGRRAAADPWHLSPIDGRE HLR*VPVLPVTPPSPTLGHVWTDPSPGV GG
583	8634	A	154	1	921	
584	8635	B	1540	277	480	GTGHFYGRTPSDTNCQEYTHRKLCCQIK SKADLVLMKNSKSLTRVIRNIALAPQDQN HQQNPLNSQFLQ*
585	8636	A	1541	32	1386	VLLGPKAERTNSRRNYQRRDYFSAPRSI TSNQSAKSSSRGVYSAYQAPDIECH FRSASFLLDKMATPAVPVSAPPATPTPVP AAVPASAPASVPAPTAPAAAAPVPAAP ASSSDPAAASATTAAPGQTPASQAQA QTPAPALPGPALPGPFPGGRVVRLHPVI LASIVDSYERRNEGACPS*SGTLFGKLV DKHSVEVTNCFSPHNESEDEVAVDM EFAKNMYETGIKKVSPNKLILGWYAT GHDITEHSVLNHEYYSREAPNPIHLTVAD TSLPGTGRMSIKAIYVSTLMGIPLGRT/L WGVMTPLTVKYAYYDTERIRRLTLM K\TCF*PPTRVIWTSQVDLQQEGGGIQLR NPGMPLSTSVANMPEGCTCLGKVSADN TIRKVGHFLMSLVNQVPENRKPMTFET MLNSNINDLFMVITYLANLTQSRNALNE ELVNL
586	8637	A	1542	1	3399	
587	8638	A	1543	1	3126	
588	8639	A	1544	115	348	
589	8640	A	1545	1	513	FHFTPLFRDGETYVV/MLDSTLPRSQYAY ILPQVSFTAVGYHKHITLIFNPARKLPEQ DIAQGSYIALPLTLLVLLAGYNHDKLIPL LLQLTSRLQGVGALGQAASDNSGPEDA KRQAKKQKTRRTLRLQEEFQLMWCLVP WRGTLGIHLFSSLPFASEILLETATCIHY
590	8641	A	1546	1	888	
591	8642	A	1547	1	4710	

592	8643	A	1548	37	3683	LGLGLSMLVGQAGPLGPAVVTAAVVL LLSGVGPAHGSEDIVVCGGFFVKSDEI NYSLEIKLYTKHGTLYQTDCAPNNGY FMIPLYDKGDFILKIEPPLGWSFEPTTVEL HVDGVSDICTKGGDINFVFTGFSVNGKV LSKGQPLGPAGVQVSLRNTGTEAKIQAT ATQPGGKFAFFKVLPGDYEILATHPTW ALKEASTTVSVTNSNANAASPLIVAGYN VSGSVRSDGEPMKGVKFLFSSLVTKED A
593	8644	A	1549	1	474	
594	8645	A	155	1	424	
595	8646	A	1550	1	1554	
596	8647	A	1551	87	736	FIMDNLSSEEIQRAHQITDESLESTRRIL GLAIESQDAGIKTITMLDEQKEQLNRNE EAWAQIHKDMRNETEKTTELNLCCGLC VCPCNRTKELLSLGGQFIKTTWGRWWE KTSPWQC*YSKQGP/VWTNGQLQPP GAASGGYIKRITNDAREDEMEENLTQVG SILGNLKDMLNIGNEIDAQNPQIKRITD KADTNRRFVLDYCPMPEQK
597	8648	A	1552	99	362	
598	8649	A	1553	184	360	
599	8650	A	1554	3	403	
600	8651	A	1555	1	872	EFGTRWDFSMVAFADLDRAGSDLKAL RGLVETAAHLGYSVVAINHIVDFKEKK QEIEKPVAVSELFTTLPIVQKSRPIKILT RLQIMLSDHSPAKVLKNTLKRAGL*D VGAGFPKAEKAFFILLCTHLDVDLVCIT VTEKLPHYFKRPPINVAIDRGLAFDLALIP LLSKDSTMRRYTISPVLQF*CKSCKGKN VIISACKKRPF*KIRGPILTWANLGLPV WGFSESERQGFPCPNCRALLHGETR KTAFGHISTVKKPRPSEGDEDCLPASKKA KCEG
601	8652	A	1556	46	584	SRRPWVISQRRTRLSTSLWCKVNVED AGGETLGRLLVVPWTQRFDFSGNLS SASAIHGQTPKVKAHGKKVLTFLGEMPL KHLADDLQGAFAQA*SELALVDKPAM WDP*GTSKLPGEILLVTRFGQSLFRQKNF TPGGARVSWGRKMGDLELASALVPSRL PLSSLAHECRAFQG
602	8653	A	1557	1476	1747	GNFNSRLRLSKTQLCAHCLYPHTFGRQR WVDHLRLGVRD*PGQHGETPSLLKNNN NNTKISWAWWHEPVIPAMGEAEAGES LEPGRRLQ
603	8654	A	1558	1	507	
604	8655	B	1559	15	400	MSMLRLQKRLASSVLRCGKKVWLDPN ETNEIANANSRQQIRKLIKDGILIRKPVTV HSRARCCKNTLARRKVRHMGIGKRKGT ANARMPEKVTWMRRMEILRHLLTRYRE CETINRAMHLLNLKVMS*
605	8656	A	156	3	1371	INIVVIGHVDSGKSTTTGHLIYKCGGIDK RTIEKFEKEAAEMGKGSFYAWVLDKL KAERERGITIDISLWKFETSKYYVTIADP GHRDFIKNMITGTSQADCAVLIVAAGVG EFEAGVSKNGQTRIEHALLAYTLGVKQLI VGVTKMDSTEPPYSQKRYEIVKEVSTY IKKIGYNPDTVAFVPISGWNGDNMLEPS ANMPWFKGWKVTRKDGNASGTTLEA LDCILPPTPTDKPLGLPLQDVYKIGGIGT VPVGRVETGVLPKGMVVTFGPVNVITE VKSVEMHHEALGEALPGDNVGFNVKNV SVKDVRGNVAGDSKNDPPMEAGFPA QVILNHPGQISAGYAPVLDCHTAHIACK FAELKEKIDRRSGKKLEDGPKFLKSGDA AIVDMVPGKPMCVESFSDYPLGCFVR DMRQTVAVGVIAVDKKAAGAGKVTK

						SAQKAQKAK
606	8657	A	1560	15	710	INPPPPAFLSLLRPQPCSMRLRLQK\RLAS\SVLR\CGKKKVWLDPNETNEIANANSRQQ\ARKLIKDG\LIIRKPV*RVHSRARCCKNTL\ARRKGTAH\CGIGKREGYSPMPRMP/TRKVTWMKENEGFWRRLASERYR*NLKKIRFATLLSQALYPEG*RGNVVSKTRRVFHGNTFHKLEGRQRPRKKAPWLDQA*G/RRRS*DQGKHGKR\REERLPGQRKEEINQRLYSKEETKK
607	8658	A	1562	2	419	MASGRARCTSNLRNWVVEQVESGQFPVCWDDTAKTMFRIPWKHAGWAIFKGYKEGDTGGPAVWKTRLCALNKSSEFEVPERGRMDVAEPYKVYQLLPPGIVSGQPGTQKVPSKRQHSSVFSEERKEEDAIANCTL
608	8659	A	1563	20	431	
609	8660	A	1564	107	400	
610	8661	A	1565	191	353	PHSSTTCPPAPMLVF*KRDPPSLGPHDALVPPCPVPVEILRSSAKTRCGKKASS
611	8662	A	1566	553	690	SRRRFPMSGTKLV*G*GEMESLEEQAQKKGKGTESCALHPVDLFSSPGPLFNSLCLSKPMAPPTL
612	8663	A	1567	2406	4031	GGRAGDGPLSATCTYAPSLWLDEGSPCLPGPLVTEADRRGTLGTEYPPQAEVAEGKGPDEGPMACSLRNSSSTNKEASYHPGFLVVLLPEFDWYLKSPNMYQVGTVGECRC TGVHSSPEVPGLTPGNWPPWGSHTGTQRMASGRARCTRKLNRNWVVEQVESGQFPGVCWDDTAKTMFRIPWKHAGKQDFREDQDAAFFKAWAIFKGYKEGDTGGPAVWKTSLCCALNKSFDKFEVPERGRMDVAEPYKVYQLLPPGILASGHVPGTQKVPSKRQHSSVSSE\RK\EKDAMQNCTLSPSVLQ\DSLNNEEEGSGGAVH\SD\GSSSSSSSPE TTRKITDTTE\APFQGDQ\RSLEFL\LPPEP D*SLLLTFFNYNGRVVGEAQVQSLDCRLV AEPSSGESSMEQVLFPPKPGPLEPTQRLLS QLRRGILVASTPQGLFRCSAFCPIPIFWGIAPQAPPQ\PGPHLLPSNECVELFRTAYFC RDLVRYFQGLGPPPKF\QVTLNFWEEESH GSSHTPQNLITVKMEQAFARYLLEQTPE QQAAILSLV
613	8664	C	1568	77	325	MSLIQEALHLVLTDPDAPAGDDPKYREWHHFLVVNMKGNDISNGTVLSDYXCAAPPKAPSHVPQFSVACIIDFSSSCPPWHG*
614	8665	A	1569	60	287	
615	8666	A	157	1	92	TSHQSHCSTFLTVSKW**LKTAYCLYHYHS

616	8667	A	1570	3	703	VEFFSSQRAELATPLTPAPGPNNGGIPGW TLWLALPRPGNLRKGPGLSLQEVDEQP QHPLHVITYAGAAV/DDELGKVLTPQTQVK NRPTISISWDGLD/SK GKLYTLVLTDPDA PKQGGDPKYREW HHLGWSTLKGQMT SATGTVLS DYVGLGGLPKGTGLHRYV WL VYEQDRPLK CDEPHPSATRS GDHR GKIQRWASLPVKK**SSRAPGGWAPCYP QPEVGMNQCAPKL
617	8668	A	1571	1749	2411	APSCLVSEHSAPGPQRELPOPLLTQAYE QILGITCIGSCP AQGWGAWSSDAVPQLL ARRPPLPHGLPACGEWGRGELGVKPSGL PSHAGPAWGHQVRTVCATAHPQDCISPE GAVEEEIVGG*GCYTEGQSQRVLQIWPS QGVSSLSALVPLNMFTELLIEYYEKIFST PEAPGEHGLAPWEQGSRAAPLQEA VPR TQATGLTKPTLPPSPLMAARRRL
618	8669	A	1575	1	254	
619	8670	A	1576	3	308	
620	8671	A	1577	1	380	IPTPLIGNFGPRGPRIRHERPQKRDDRREP SSFGKRRQ*DGTL LCRRCGSKA\YHLQ KSTCGKCGYP AKRKRKYNWSAKAKRR NTTGTGRMRHLKIVYRRFRAWDFREGT TPKPK*GSLLQHSSSS
621	8672	A	1578	41	544	APSPRRPWGHFTEEDKATITSLWGK\VN VEDAGGETPGKGS LVVYPWTQRFFDS FGNLSSAF AHHGQTPK VKAHGK\KVL SLGDAIK\HLDDLKGTFQA*VNLHL*QS CNVDPENFQAPGEMLLVTR/VLAIHFG K\EFTPGGCKASWAEDG*LAVGQWPCSS RYH
622	8673	A	1579	1207	1369	
623	8674	A	158	232	552	SLH*PRMATQRKHLVKDFNPYITCYICK GYLIKPTTVTECLHTFCKTCIVQHFEDSN DCPRCGNQVHETNPLEMLRLDNTLEEIIF KLVPGLREQELERESEFWKENKPQGNGQ DDTFKSLTNRK
624	8675	A	1580	1	1716	TCIAAVKMEGPLSVFGDRSTGETIRSQN VMAAASIANIVKSSSLGPVGLDKMLVDDI GDVTITNDGATILKLEVEHPAAKVLC LADLQDKEVGDGTTSVVIAAELLKNAD ELVKQKIHPTSVISGYRLACKEAVRYINE NLIVNTDELGRDCLINA AKTSMSSKIIGIN GDFFANMVVDAVLAIKYTDIRGQPRYPV NSVNILKAHGRSQMESMLISGYALNCVV GSQGM PKRIVNAKIACLD FSLQKTKMKL GVQVVITDPEKLDQIRQRES DITKERIQKI LATGANVILT TGGIDDMCLKYFVEAGA MAVRRVLKRD LKRIAKASGATILSTLAN VEG*ERFEGAMWDQAEV VQERICDDE LILIKSTKA RTSASII SRVPIDSMCDEMER SL\HDALC\VVK\RVLESK\SVVPR\GGAV EAALSIYLENYA\TSMGSREQLAIAEFA RSLSGYSPIPLAVNAAQDSTDLVGKN*/ RLFHNEAPGLTPEARKNLKWIGLDLSNG KPRDNKQAGVFEP/TPIVKV KSLKFATE AAITVLRIDDLIKLHPRK*R*KHGSYEDA VHSGALND
625	8676	A	1581	1	513	PRVRNLSREWLC DRHLREKMFSSVAHL ARANPFDTPHLQLVHDGLDLRSSSPGP TGQPRRPRNLAAA AVEEQYSCDYGSGR FFILCGLGGIISCGTTH TALVPLDLVKCR MKVADPQKYKGIFNGF SVTLKEDGVRG LAKGWAPTFL\GYSMQGLLQVLA FYEVF KVLY

626	8677	A	1582	2	1296	ALCEPQPFQSGCVAILGRKMFSSVAHL ARANPFNTPHLQLVHDGLDRLSSSPGP TGKPRRPSQ/HMAAAPVEEQYSCDYSGS RFFILCGLGGIISCGTTHTALVPLDLVK\C RMQVDPQKYKGIFNGFSVTLKEDGVR GLAKGWAPTFLGYSMQGLCKFGFYEVF KSLVSNMLGE\ENTYL*RTSLYLAASAS\ AEFFADIALAPMEA AKVRIQTQP\GYANT *EGISFPKCIKEEGLTSILQGGLPLWMR QIPYTMN*SSPCLERTVEALYKFVVPK\ PRRE*FKQRSRLVVTIW*QVTIARVFCAN CFSPLPEFLG*PVLD*GKKVSQCFLWVLQ RDLGFK\GV\WKGLFAIRIIMIGTLTALQ WFIYYSVKGYFRALPRP\PPPPEMQESLKK KLGVNSVVRIKANCGLNLLVDPVFEEA KGTFIYLTV
627	8678	A	1583	127	433	RPLESWIGLVRCNICRSPIAEAVFRKLVT DQNISKNNWRVDSAATSGYEIGNPPDYRG QSCMKRHHGIPMSHVARQ\DLNRKSNRV KTCKAKIELLSYDPQKQL
628	8679	A	1584	2	535	
629	8680	A	1585	551	1299	PADPPRPSYRHRTPPQAHWSRLRRSRL RRRGSHTRCPVGVGAGLRRRAGARLAV RLRASACGTPRCLGASARGKMAEQATK SVLFVCLGNICRSPIAEAVFRKLVTQNI SKN\WEGRQRGNFRWVIDSGAVSDWNV GRSPDPRAV\SLRNHGIHTAHKARQIT\ KEVFPTFDYILCMDESNIARDLNRKSNR VKTCKS*KFELPWEL*SPQQLIIED\PIY GE*LWTLETVYQQ\CVRICCRAFLEKAH
630	8681	A	1586	1	1239	
631	8682	A	1587	298	408	
632	8683	C	1588	92	244	MRCEILVLIPYVYFYSNKLLCSRLXXXX XGGAVLKNPWGGQSLPGLAR**
633	8684	A	1589	33	191	RDDPRVRPPPNST*PQQEPGL*LIKCTSP PQAPARTVHGPFYFMRLIKMF
634	8685	A	159	445	673	RECLH*PRMATQRKHLVIDFNAYITCYIC KGYLIKPTTVTECLHT/FCRCMEAFPSLL LA
635	8686	A	1590	3	1285	
636	8687	A	1591	3	3469	QPGHTIYLLPTVVICNLLPCELDIFYVKGM PINGTLKPGKEAALHTADTSQNIELGVSL ENFPLCKELLIPPQTQNYMVRMLYDVN RRQLNLTIRIVCRAEGLKIFISAPYWLIN KTGLPLIFRQDNAKTDAAAGQFEEHELAR SLSPLLFCYADKEQPNLCTMRIGRGIHPE GMPGWCQGFSLDGGSGVRALKVIQQGN RPGLIYNIGIDVKKGRGRYIDTCMVIFAP RYLLDNKSSHKLAF AQREFARGQGT A
637	8688	C	1592	398	655	MMFPLAFSLPLKNAFHISVCRVCPGYTG FAKRALTALNLDTSLSANCCNTPPAEXP NVHNPCYMGLSKPARXSKLGSMCKGSS XH*
638	8689	A	1593	1	930	
639	8690	A	1594	1	134	

640	8691	A	1595	3	2455	HASVCPAVGVQRLCLFPCVSLQALFMGS PLRFDGRFFLVTGAGAGLGRAYALAF ERGA LVVNDLGGDFKGVGKSLAADK VVEIRRRGGKAVANYDSVEEGDKVVK TALDAFGRIDVVVNNAGILR/DINSFARIS DEDWDIIHRVH LRGSFQVTPAAWEHMK KQKYGRSMTSSASGIYGNFGQANYSA KLGLGLANSLAIEGRKSNIHWNTIAPNA GSRMTQTVMPEDLVEALPKYVAPLVL WLCHQSCENGGLFEVGAGRIGKLRWE RTLGAIVRQKNHPMTPEAVKANWKKIC DFENASKPQSIQESTGSIIEVLSKTDSEGG VSANYTSRATSTATSGFAGAIGQKLPPFS YAYTELEAIMYALGVGASIKDPKDLKFI YEGSSDFSLPTFGVHIGQKSMGGGLA EIPGLSINFAKVLHGEQYLELYKPLPRAG KLKCEAVVADVLDKSGSVIIMDVYSY SEKELICHNQFSLFLVSGSGFGGKRTSDK VKVAVAI PNRPDAVLDTTSLNQAALY RLSGDWNPLHIDPNFASLAGFDKPIHGV LCTFGIFCQGVLLQQFCR*MDVVQGFKG N*RARFAKPVYPGANFYQT*ECWKEVG NRNSFFKPKVQGNLETLVISKWHMWDL GTQHSGYFSLRTPSEGPSFRVPLVFEEN GRRLKDIGPEVVVKVNAVFEWHITKG GNI GAKWTIDLK\SGSWEKLYQGGS/KK GAADTTIH/ILSDEDF/LWEVVLGQA*PSR KAFFSGPG*RPQGGTMA*AQKLSDGFL KDYAKLLKGTPTLIKMESIKPPHPQIC LDYSAKS
641	8692	A	1596	2	289	
642	8693	A	1597	1	397	
643	8694	A	1598	1	410	STMISPV LILFSSFLCHVAIAGRTCPKPDD LPFSTVVPLKTFYEPGEEITYSCKPGYVS RGGMRKFICPLTGLWPINTLKCTPRVCP FAGNLRKMGAVRLITDFLNYSPTRFSL LTWGFILEWALDSAKCIEGG
644	8695	A	1599	19	1215	CQCDSS TMIFSRCSLSSFLCHVAIAGRT CPKPDDL PFSTVVPLKTFYEPGEEITYSC KPGYVSRGGIEESLSCPLATGTVGPFNTSG NVTPRVCPFAGIFRKMGGRTLITF*NYP NTDPVFSLLTLGF*FWNGALDFWPSTG GKGKWSPELPGLVAPI\CPP\PSIP/TGFA TLHVLLRPFR LGNNSPPIGDTAVFECLAH NMAMFGNDTITCTTHGKLDLNYPECR GSKMPPFP HQDPDNGIW*TYPCQNPNTL FTRVKAPHLGLPHDGIFSGMGRKE NEC *PQTWGKPGSWPLAPSW*KPSLVKGTPV KKRPTVV/YPQGERVKDSREKFKEWECL HG**KFLSFCKNKEKKCSYTEDAQCIDG TIEVPKCFK\EHSSLAFWKT\ DAS\ DVKPC
645	8696	A	16	3	145	SSSSSDFAGQTL*STQT VQN*FKKVLPKG RLYPVPIATMGIKEPLIS
646	8697	A	160	22	849	WIERDLLNCIKRLK/PTTNNMLNDEIVNIS PKIIRQGYLLSMILFIVQKDLTRKLM QGRETGIEIRKEVKL*KRKRI*ISICRCH E*IW*VPCIKVMQAFYDIPAKNMENEIL KKQCHFKDPSSA*REKMR LICFEELYPEN KITKEERDRI/RTISKLLLFPKFLQP*NP RQVSLMLN*QANF*EFICIFQKSKIVKAI L*NGQRGLKFLNIKT CYKAIEIMKVL IWH KDKKLD*WNSIQVSKVDPRVYHHSFE KGDIEV*WGKGCSFQ
647	8698	A	1600	1	282	

648	8699	A	1601	1	453	EFGSQQLGRKEEWQRQGSVSRRLSARR GPQAPGTRLPRRHPARAFPAATMPKRKV SSAEGAA*LEPNRSARLSAKPPAKGEA KPKKAAAKDKSSDKK\VQTKGKRGAKG KQAEVANQETKEDLPAENGETKTEESP ASDEAGEKEAKSD
649	8700	A	1602	146	824	TWKGKDPKPRGKMSSYAFFVQTCRAEE HKKKHPDASVNFSEFSKKCSERWKT SA*R/EKGKFEDMAKA\DKARYEREMK TYIPPQRGRQKRKFQDSQLHPRGPPSGLL SSSCSEYRPKIK\GEHP\GL\SIGDVAKKLG RDVGINTAAD\DKQPYEKK\AAKLKEY EKDIAAYRAKGKPDAAKKGVVKAES KKKKEEEEEDEEEG\DEEDEEEDEE DEEEDER
650	8701	A	1603	1	223	
651	8702	A	1604	1	400	FADD/PSDK/FFTSNNGMQFSTGHNDND KFEGNCAEQDGSWWMNKCHAGHLNG VYYQGGTYSKASTPNGYDNGIHWATWK TRWYSMKKTTMKIIPFNRLTIGEGQQHH LGGAKQVRPEHPAETEDSLYPEDDL
652	8703	A	1605	18	365	NILIKVYFNSKNDFKIFHELFFKQNYMKN MYKSVINVIDIFMNFQ/SEKYPH/DKGS LNK*MLTILALKSNTTVRLIRDTAFYYVR EHIINVSSKRARYWVCVGF*ASC*QPPL F
653	8704	A	1606	212	1645	HYKARSSGHSIMSWSLHARNLILYFY ALLFLSSTCVAYVATRDNCCILYERFGC YCAPTTCGIADFLSTYQTRVD*DLQSLAED ILHQVENKTSSEVKQLIKAIQLTYNPDVES SKPNMIDAATLKSRLMLEEIMKYEASNL THDSSIRYLQEI*FQIIQKIVNLKEK\VAQ LEAQCQEPCKDTVQIHDITGKDCQDIAN KGAKQSGLYFIKPLKANQQFLVYCEIDG SGNGWTVFQKRLDGSVDFKKNWIPYK EGFGHLSPTGTTEFLAGEMRKIHFD*GTQ SAIPYGI*GVGTGKTWEWARNQYCRSM PLFKVVHEVDKYRFTYAYFAGGDAEDA FDGYDFGDDPSDKFFHIPIMAMQFTYLG TMDNDKV*KANCA*/QQGWDPGWWDG NKCHAGVHSSMGVLFTQGVALYFQKAS YLPNGLWIMGIWATWK\TRWVFR*RK TMKIIPFNRLTIGEGQQHHLGGSQTGLE TF
654	8705	A	1607	2	529	GTVAACGACYWLLGLMAVRASFENNCE IGCFAKLNTYCLVAIGGSENFYSVFEGE LSDTIPVVHASIAGCRIIGRMCVGTEEIL ADVCLKVEVFRQTADQVLVGSYCVFSN QGLLVHPKTSIEDQDELSLLQVPLVAG TVNRGSEVIAAGMVVNDWCAFCGLDTT STELSVVE
655	8706	A	1608	18	889	GVQGTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLNTYCLVAIGGSENFYS VFEGELSDTIPVVHASIAGCRNIGRMCV GNRHHGLL\VPNNTTDQELQHISATGLP RHSGRFRAGWKERFLSLWGNFFNHLAID YVGLGSNQDLDKGRQEEISGQMLFKGW EVFRQTVADQVLVESYCVFSNPGRAW VPSRPFQ*RPRNELSSISFKVPLVAGTC* TKGSEVICLLGMGEMNWCAFCGPGTP NPAQSCQVVEECLQS*NEAPALAPIANR ACGNLSLIDSLT
656	8707	A	1609	1	248	GPLIWEWPASPEPPPLPWGKPRMQ/SG*Y G*TP*IPKIRFPKPPFPFPQALEPQQGP N*AHP*EPTPAKKYSPQRVQKVPK

657	8708	A	161	796	1381	SLTSDKRQWALGSMDFKKHWICH/PIK MLHLGVGPKGLSVTQQFSSQN*FPVCAF QSSQYIPLPAQKLMYSQ*PVQNRCSNQ TIPVAHPMSGHQVSHHR/PANNPGKEEV PGQEGKN*NKDVNNF*TGQPWTKGNLEI STWPERNLILALKVPIKAELKRSWASSN CKQT*LRHPQCDDVFISMKEQSMKCRN F
658	8709	A	1610	290	1414	NKRHPSRVYMSLPQGEKVQAMYIWDG TGEGLRCKTRTLDSEPKCVEELPEWNFD GSSTLQSEGFQTVNMYLVPAAMFRDPFR KIDPNKLVLCÆVFRYNRRPAETNLRHT CKR\IMDMVSNQHPWFGMEQÆYTLMG TDGHPFGWPSKGFPGPQGQYLLGVG\G DRSLGRDIRÆAHYRACFY\AGTRIPGTK AGVSPLQ\WEFQIGPCEGIKQGG/HIFWV ARFILHRVCEDLG\VIATFDP*/RPLLGN WNGA\GCHTNFSTKAMRKENGLKYIEK AI*KLTNR\HKSHIRAYDPKRGDLNARRL TGFHETSNINDFSVGVANRSASIRIPRTV GQEKKG YFEDRRPS\ANCDPFSVTEALI RTCLLNETGDEPFQYKN
659	8710	A	1612	129	1182	
660	8711	A	1613	1	353	FGTRSFDSRSEAEAAKNALNGIRFDPEIP QTLRLEFAKANTKMAKNKLVGTPNPSTP LPNTVPQFIAREPYELTVPALYPSSPEVW APYPLYPALAPALPPAFTYPASLHAQ ETL
661	8712	A	1614	129	1238	APPSPPSSGCSPPQQLSALTPGTRVLAPSF ASFLPSFFLPLAPALPLQVALPGPDCLG SPLPARALPRLSLALPESPAAVADSPRE PQPNPSPTATAPAPAPAPQPAAPARGSPG ARGRLQWASAPSPAPQPCPARRGRGTG KMNNGGKAEKENTPSEANLQEEVRTL FVSGPLDIKPRELYLLFRPFKG YEGSLIK LTSKQPVGVSFDSRSEAEAAKNALNGI RFDPEIPQTLRLEFAKANTKMAKNKLVG TPNPSTPLPNTVPQFIAREPYELTVPALY PS\SPEVWAPYPLLPRRELGACFYLPFG/S FTYPASLAWPRCAGSLPRLLLRAGSPVS SAEYYTLQQWLLEGRTIALWLYG
662	8713	A	1615	129	1143	APPSPPSSGCSPPQQLSALTPGTRVLAPSF ASFLPSFFLPLAPALPLQVALPGPDCLG SPLPARALPRLSLALPESPAAVADSPRE PQPNPSPTATAPAPAPAPQPAAPARGSPG ARGRLQWASAPSPAPQPCPARRGRGTG KMNNGGKAEKENTPSEANLQEEVRTL FVSGPLDIKPRELYLLFRPFKG YEGSL* KLTSKQL*GFVSFDSRSEAEAAKNALNGI RFDPEIPQTLRLEFAKANTKMAKNKLV GTPNP\STPLPNTVPQFIAREPYELTVPAL YPS\SPE\WAPYPL\YPALGPA\LP\PAF T\YPASLRCPGNPVEKEIQDSV
663	8714	A	1616	1	669	
664	8715	A	1617	267	1057	GRTMMFGAKRRQEEWEKVRKPEDPEEC PEEVYDPRSLYERLQEQKDRKQQLRGT VSNCKNMVRGLDEDETTFLDEVSRQQ ELIEKQPKRÆELERT*RNTEITSRRLEFSQ ENKKEVEKKLTCE/VL*KPRTKFSQANVL GOEL*SMKSSSESGHQCEKT*NRTPEPD*Q ESRALILAKSLGNNPLSGPFHPLAPSAA SMYRHPRPFGWPTLGAATPSPASDSEGTI QCHRKDCSPPCFRTNTFLRGPLSFFRSLH REAPPQG

665	8716	A	1618	1	641	DTRFLERLRLSISSYVQTPMGHFTTEEDKA TITSLWCKVNVEDAGGETLGRLLVVYP WTQRFDSFGNLSSASAMGNPKVKAH GKKVLTSGRLP*KHLDDLKG\TFAQA* SEULH\CDKAALLDPENFKLPGEILLVTR FGQFHFRANKNFTPEGCQASWQERWVT WSWPVPCSSRLPLKLNCP*MQSFSRIRLL FLQAITNNKSISAKRSP
666	8717	A	1619	1	194	
667	8718	A	162	3	1116	LNQWQEQTGNPERTHRPSEGSLLLQDP GDFSNTLSAPTAVEKGDPLPKIPLEEL KETHLTHKDSHLKIKGWKKAFLANGH QKQTGEAILIPDKTKFKATAVKRDKEGD YIMVKGLVPQENITILNTYASNTEAPKFI KQLLIDLRNEIDSNIIVGVNFNTPVTAIDR SSKPKVNKETMDLNYTLEQMDLTDIYRT FHPTTAEYTFYSTVHETISKIDHMIGHKM SINTFKKIEIMSSLTLDHSGIKLKINSERNL QNHANTWKLNNLLNEHWVKNEIKMEI IQLFELNNNDTTYQNLWDTAKVVLRG KFIALNAYIKKTERAKKTIYSHTSGI*KQE QTKPKPSRRKEIKIRAELEIETKKT
668	8719	A	1620	98	1136	ASDAFHLSAPGLRLGSRSAARPATMTE QAISFAKDFLAGGIAAAISKTAVAPIERV KLLQVQHASKQIAADKQYKQIVDCIV RIPKGAGGVLSFLEGQPLPTVIRYFP\TQA FNFRPFKD/KSYKQIFPGGAWDKHTQFW R*FGGANWASGVAAGADHPSCFVYPLD FARTGLGKGRWKSQAQASFRGLGDCL VKIHQVQTASRGLYQGLPVSPFTATIIYP AAY\YG\Y\DTAKGHASPTPSNT\HILLS RMNRARTVTARGAVGCPNPLKTVRRR MIDAIRGAKGADIMYTG\TLVDC*RKNLS EDEGGQRPFFKGCVVQTLLRGHGRPSV LVPVRTSSRRVI
669	8720	A	1621	4	101	VQWNDFGSLQNPFGVSPFFWLSLPNNL GFKGSSSRPGPFLKF**KP/EVFRVNPDPF PFPAP*FGPPGPPKSWGFPF*PPPGVSPFF WLSLPNNLGFKG
670	8721	A	1622	3	1728	GDRTDGVWWWLGLSRRYAIPFNSLEPSS LGSCPLSIGTHK\ALHALELT\TTDIQCGK AFNSSSSFRYHERHTHTGEKPYECKQCGK AFRSASLLQTHGRHTHTGEKPYACECKGK PFSNFSFFQIHERMHREEKPYECKGYGK TFSLPSLFHRHERHTHTGGKTYECKQCGR SFNCSSSFRYHGRHTHTGEKPYECKQCGK AFRSASQLQIHGRHTHTGEKPYECKQCGK AFGSASHLQMHGRHTHTGEKPYECKQCG KSFGWASRLQMHGRHTHTGEKPYCKQC GKAFGWPSNLRRHGRHTHTGEKPYKCNQ CGKKWKDQNIYEYQNP RRNFRSLIEGN VNEIKEDSHCGETFTQVPDDRNLNFQEKK ASPEAKSCDNFVCGEVGIGNSSFNMNIR GDIGHKAYEYQDYAPKPYKQCPKKA RYHPSFRTOERNHTGEKPYACECKGKTF ISHSGIRRRMVMHSGDGPYKSSFLRSH KVPGHGRRFAMNPTLLNKEDERGKNV VTREHLDRMKNSCIVCNMGHSNTEIDV NVVMGNYERLERDARMTIRKKRKYSD IRFRIMGRYTVRVEVLTAVNSE
671	8722	A	1623	1637	5763	KPGNGACAGREWCDGGGAAWNWRDP GLPVGDSGVWDRVLELLGPRSPRPLDV GGPAAGTPGVLSRPCPSTAALAPKPFCA APRPQPDAPACAGATGGSCADFDGSGVDF VRRRSSGLWGPQPLSPVKNYTEMFQDP VAFKDVAVNFTQEEWALLDISQKNLYR EVMLDTFWNLTSIGKKWKDQNIYEYQ NPRRNFRSVTEKVNEIKEDSHCGETFT VPDDRNLNFQKKKASLK*NHVTALCVQK

					LA*VTHL
672	8723	A	1624	2	656
					APTPTGQRVVRATPAQSAPVRLRRRSYD VNNPIPSNLKSEAKKAAKILREFTETS NGPDKINPGSTVIKAK\GLANSCLLNQS PGSLVTFQGGPGVLVARLPDGK\WSSP FS\ALGIAGFG\GGFEIGI*GIQTLVILEF/D DPCC*EAFKGGNLTGGNLTVAVGPLG RNLEGNVALRSSAAVFTYCKSRGLFAGV SLEGSCLIERKETNRKFYC
673	8724	A	1625	141	1307
					FHVNNPIPSNLKSEAKKAAKILREFTEITS RNGPDKIIPAHVIAKAKGLAILSVIKAGFL VTARGGSGIVVARLPDGKWSAPSAIGIA GLGGGFEIGI/EDTFTATYSL*ALPWLPSIS VECHSSFLRLPSA*HIFLHPFTVNLMSVD LVIIILNYDRAVEAFKGGNLTGGNLTVA AVGPLGRNLEGNVALRSSAAVFTYCKSR GLFAGVSLEGSCLIERKETNRKFYCQDIR AYDILFGDTPRPAQEDLYENLDSFTEK YENEGQRINARKAAREQRKSSAKELPPK PLSRPQQSSAPVQLNSGSQSNRNEYKLY PGLSSYHERVGNFYQPIDLTALYSFEGQ QPGDLNFQAGDRITVISKTDSHFDWWEQ KLRGQTGIFPANYVTMN
674	8725	A	1626	167	401
675	8726	A	1627	133	312
					VRVGECLKPCFWPPEANPDP*CYLHLWI LDSQTKSKPVLTS*PFPNGILGTSVCFCT FY
676	8727	A	1628	1759	1967
					SGCKPLTFPPP*SDSPVKEDPCR/SPPSH RLPPHSLPALPFPPTPNPPPKIYTAVSRIW EMKDRCNPI
677	8728	A	1629	167	1378
					GNTLVTNMTEFWLISAPGEKTCQQTWE KLHAATSKNNNLAVTSKFNIPDFKGWA RWDVLVGLSDELA\KGCIL*EGSWLKE SRLQLHGLDVLEDSKDKVQENLLANGS GLGLPYITKVPSGDMAKYPIKQSLKNISE IIAKGVTQIDNDLKSRASAYNNLKGNLQ NLERKNAGSLLTRSLAEIVKKDDFVLD EYLVTLVVVPKLNHNDWIKQYETLAE MVVPRSSNVLSQDSYLCNVTLFR/RR AVDDFQDTKPGENKFIVRDFQYNEEEM KADKK\EMDRASTDKKKQFGPLVRWL KVNFEAFIAWIVKALRVFVESVLRYG LPVNLQHMIFHRNNNPFKPLRQVLHESY IHLDSSA\AAIDAPMDIPGLNLSQGEYY PYVYYKIDCNLLKFK
678	8729	A	163	41	1133
					HRTYKTKIHLKKQKQSTQATKSRMNAV VPHISILTLNVGLNVPLKRYRVA*WIRI YQQTICCLQETHLTPNTKDSHKLKVKG WKK\AFHANGHQKQAGVAILSDKTNF KATAVKKDKEGHYIMVKGLDQQENITIL NIYAPNTGAPKFMKQLLIDVRNEIDSNTII AGDFNTPLTALDRSSIQKVNKETMDLNY TLEQMDLKDIYRTLHPTTAETYIYSTVH GTFSKIDYMTGHKTSLNKFKKSEIISSSL DHSGIKLEIDSKRNHQNHNANTWKLNNLL LNEHWVKNKIKMEIKTF/FELNDNNGTA YQNLWDATAVLRGKFTALNAYIKKYE RAQTDNLRSHLKELEKQQTCPKSSRRKK K

679	8730	A	1630	569	1050	PLESRRLARSSGGWAGITGTPMNI FTGPD PGPSERSAQPRVWDSTCCLKSNCWFRK VKATTPPMSSMMRQIPRMYMNA/WEKV QVVTEGRQHTNEGDHEHDDAQEDDDG WSQEGTFKGFIFLPLNLCIDAHQRDQGP NQTCNPSTLGGRGGQITRPGDRDH
680	8731	A	1631	1	595	
681	8732	A	1632	2	1121	ARGCGRSSRSRSHRCLFP PPPSRPA SLGPERRPGSSRAAPAASRLSGLSRASG TASCRPPACPPARSPLPAGPWAARAMG TDSRAAKALLARARTLHLQTGNLLNWG RLRKKCPSTHSEELHDCIQKTLNEWSSQI NPDLVREFPDDLAECTVSHAVEKINPDER EEMKVS AKLFIVESNS\SSSTRKVQLTW ACSVLGS/VAQLGFLWIHWLSPPI*KDGG LIFPWEHLQPYWEGI*KNLVQRQKGLLP* GTSDDLKDTQLEQLYQWAQVKPNSNQVN LASCCVMPPDLTAFKQFDIQLLT HN DP KELAFWKASFQGRLFQKAFDPDISSGTE WGAAVGLLRYSVIVKSRGIKSKGYILQA KRRGS
682	8733	B	1633	63	458	SLENTVSTAISKAQNGAPSWG GYPSIHA AYQLPGTVKPLPAAVQSVQVQPSYAGG VKSLSSAEHNALLHSPGSLTPPPHKS NVS AMEELVEKVTGKVN IKKEERPPEKEKSS LAKAASPIAKENKDFPKTEE*
683	8734	A	1634	3	2303	EMEGKEDAQKVLKCMYCGHSFESLQDL SVHMIKTKHYQKVLPKEPVPAITKL VPS TKKRALQDLAPPCSPEPAGMAAEV ALSE SAKDQKAANPYVTPNNRYGYQNGASYT WQFEARKAQILKCMECGSSHDTLQELTA HMMVTGHFLKVTTASKKGKQLVLDPV VEEKIQSIPLPTTHTRLPASSIKKQPDSP AGSTTSEEKKEPEKEKPPVAGDAEKIKE DSEDSLEKFEPSTLYPYLREEDLDDSPKG GLDILKSLENTVSTVINKAQNGAPSWG G YPSIHAAYQLPGTVKPLPAAVQSVQVQT SYAGGVKSLSSAEHNALLHSPGSLTPPPH KSNVSAMEELVEKVTGKVN IKKEERPPE KEKSSLAKAASPIAKENKDFPKTEEVS G KPQKKGPEAETWEAKKEGLDVHTPNG TEPLKAKVTNGCNNLGIIMDHSPEPSFIN PLSALQSIMNTHLGKVS KPVSPSLDPLA MLYKISNSMLDKPVYPATPVKQADAID RYYYENS DQPIDLTKSKNKPLVSSVADS VASPLRESALMDISDMVKNLTGRLTPKS STPSTVSEKSDADGSSFEELDELSPVHK RKGRQSNWNPOHLLILQAQFASSLA SETT EGKYIMSDLGQERVHISKFTGLSMTTI SHWLANVEVTSLRRTGG\TKFLKEPGTQ GHPVFFCNDCASQFRTASTYISHLETHL GFSLKDL SKLPLNQIQRQQNV*KVL TN KTLGPLGATEEDLGSTFQCKLCNR TFAK QARSQTAP
684	8735	A	1635	133	500	YNTVNYKSHPEGQSMCWSMPVITATFG NPRRVDQPLRSGVQDQPGQHGKIPSLLK IQKLAGHG\GACL*SQLLGRLRKENCLN/ SPGGGGCSEPSSRHC\PAWAIA*DTI*KIK K*KPPKMRN
685	8736	B	1636	1568	1588	MGDQQLYKTNHVAHGSENLFYQQPPLG VHSGLNHNYGNAV TGGGMDAPQASPI S PHFPQDTRDGLGLPVGSKNLGQMDTSR QGGWGS HAGPGNHVQLRGNLANSNMM WGAPAQAEPTDGYQYTYSQASEIRTQKL TSGVLHKLDSFTQVFANQNLRIQVNNM AQVLHTQSAVMDGAPDSALRQLLSQKP MEPPAPAIPSRYQQVPQPPHGF TGGLS KPALQVGQHPTQGHLYDYQQPLAQVP VQGGQPLQAPQ

686	8737	A	1637	2	251	FFFFFLINKTKRLFTP*ALQWGYPSGSCG SVSQSCKCILRGRSRATISIEAEMVDL
687	8738	A	1638	36	530	NKVLPPAASEHSDCQISKHQVQLCP/PNII TLADIVKDPVSRTPALVFEHVNNTDFKQ LYQTLTDYDIRFMYEILKALDYCHSMG IMHRDVKPHNV MIDHEHRKRLIDWGL AEFYHPGQEYNVRVASRYFKGPELLVD YQMYDYSLDTWRMGCM LASMI IQKEP
688	8739	A	1639	1	1833	
689	8740	A	164	265	446	
690	8741	A	1640	3	430	
691	8742	A	1641	137	1368	FHISLFEENRVLKQGS LPPPA AFLNTVTA QISQTSKSQALS RQPCSDHVGDPVPKAG HRVYTDVNTHRPREYWEYASHVVEWG NQDDYQLVRKLRGKYSEVFEAINITN NEKVVVKILKPVKKKKIKREIKLGGIW RGGPNIITLADIVKDPVSRTPALVFEHV NNTDFKQLYQTLTDYDIRFMYEILKAL DYCHSRGIMHRDVKPHNV MIDHEHRKL *LIDWGLAEFYHPGQEYNVRVASRYFKG PELLVDYQMYDYS LDMWSLGCMLASMI FRKEPFFHGHNDYDQF/VCRMALVLTGTE DLDYIDKYNIELDPFRNGYLGHRSRKP MGTA LNS ENQH/LLSSPEALDFLDKLLR YDPPSHGLLAREAMEHPYFLHCCEGPRP RNGFHLAMP GCSTPVQQRPI
692	8743	A	1642	874	1183	TPMLEQLGNRYLQNIACYPFRNMCTYQ LGCSGSRL*SQHFGRPRQVDHLRSGVRD QPGQQGETPSLLKVQKFSWAWWRTPVI SATWEAEAGEVLEPGRRRLK
693	8744	A	1643	2	498	
694	8745	A	1644	49	538	SQTPMGHFTTEDQGLLSKSLWGK/VLNV EKMLGRKKTPLGKGSPLVVP TPWDPKR FL*TSFGKTLSPALLPHQWANPPKVKG HHGKEGCLTFPWEDAHKAPLDDPQRAP FAPA*SELHCDKLHVDPAENFKLLGNVL VTVLAIHFVGKEFTPGGCRASWAEDG
695	8746	A	1645	53	393	
696	8747	C	1646	116	379	
697	8748	A	1647	3	200	
698	8749	A	1648	1	637	MRSAARGPRQSCSAFNRFRAANSSSPGF GAPCGRQCWIWESLGKERAKEGKD GGL QSPRTSLKERPKTRITGALPMDHTEGLPA EPPAHAPSPGKFGERPPPKRLTREAMR NYLKERGDQTVLILHAKVAQKSYGNEK RFFCPPPCVYLMGSGWKKKKEQMERDG CSEQESQPGAFIGIGNSDQEMQQLNTLE GKNYCTAKTLYISDS DKR
699	8750	A	1649	111	748	GKREGAGERDQRRRGESREGWSFGES LWKMAPVVTGKFGERPPPKRLTREAMR NYLKERGDQTVLILHAKVAQKSYGNEK RFFCPPPCVYLMGSGWKKKKEQMERD GCSEQESQPCAFIGIGNSDQEMQQLNLE GKNYCTAKTLYISDS DKRKHFMLS VKM FYGPTSDDIGVFLSKRIKVISKPSKKKQS LKNADLCIASGTKV ALFNR
700	8751	A	165	283	398	NWQEKCTFQIIGGRKRMSFRILINFFHN* DRTVCYVP
701	8752	A	1650	1	519	IISTD/KA EYT/FYEGMGVPVFTPVTPVPVV ESLQLNAGGDVAMLELTGQNFTPNLRV/ WFGDVEAETMYRCEQSMLCVVPDISGF REGWRWVRQPVQVPVTLVRNDGNIYS TSLTFTYTPEPGPRPHCSAAGAILRANS SQVPPNESNTNSEGSYTNASTNSTSVTSS TATVVS

702	8753	A	1651	238	1713	STMAWIKRKFGERRPPPKRLTREAMRNYL KERGDQTVLILHAKVAQKSYGNEKRFFC PPPCVYLMGSGWKKIKLQMKCDGCSEQ GSQPCAFIGIGNSDQEMQQLNLEGKNYC TAKTLYISDLKQKHFMLSVKVFGNSD DIGVFLSKSSKPSKKKQSLKNADLCIASG KERWALFNRLLSQTVASTRYLHV/EKEGN FHASSQWGAFHIHLDDDDGSEGEFTV *DGYIHYGQTVKLVCSVTGMALPRLIRK VDKQTTLLDADDPVSQLHKCAFDELEDTE RKYLCLSQERIIQFQATPCPKEPNKEKIN DGASWAIISTHKAKHTFYRESGPLSLAP/ VSCPPALSVECLKNGGGDEPSLKLNR EFQLPKFYKVWFGDVEAEAMYRCGES MLRVVPDVSAF*EGWRIYSQQPIQVSVT LVRNDGIIYSTSLTFTYTPEAGPRPHCSV AGAILKASSSHVPPNELNTNSDGSYTNA STNSTSVTSSTPTVVS
703	8754	A	1652	1	309	FF*DRA*LACPPGWSARSQHTVVSTFLGS SKFSLHGPPELPGDHRHAPPCPANFFYFS *RWGLPMLLVSNSQAQAILLPSPFQKGW DYRAWGHHTWGSYLNFE
704	8755	A	1655	1	2325	
705	8756	A	1656	3	128	
706	8757	A	1657	203	2698	SANMGKKRTKGKTVPIDDSSETLEPVCR HIRKGLEQGNLKKALVNVEWNICQDC KTDINKVKDKAEETENKPSVWLCLAKC \GPQGFGRNFSR/EQHALKHLYLTPRSEPH CLVLSLDNWSVWCYVCDNEVQYCSSNQ LGQVVDYVRKQASITTPKPAEKDNGNIE LENKKLEKESKNEQEREKKENMAKENP PMNSPCQITVKGLSNLGNCTCFNAVMQN LSQTPVLRELLKEVKMSGTIVKIEPPDLA LTEPLEINLEPPGPLTLAMSQFLNEMQET KKGVVTPKELFSQVCKKAVRFKGYQQQ DSQELLRYLLDGMRAEEHQRVSKGILKA FGNSTEKLDEELKNKVKDYEKKKSMPSP VDRIFGGELTSMIMCDQCRTVSLVHESF LDLSLPVLDDQSGKKSANDTPLTKTVTY AECYSEEKYHTDCCYI*RSDISSGTRKHL QKKATKQAKKQAKNQRRQKISGPALH LNDIRTIDHPEDSEYEAEMSLQGEVNITS NHISQEGVMHKIEYCVNQDLNGQAKM IESVTDNQKSTEEVDMKNINMDNDLEVL TSSPTRNLNGAYLTEGSNGEVDISNGFK NLNLNAALHPDEINIEILNDSHTPGTKVY EVVNEDPETAFACTLANREVFNTGE\COIQ HCLYQFTRNEKLRDANKLLCEVCTRRQ CNGPKANIKGE\RKHVYTNAKKQMLISL APPVLT\HLKRFQAGFNLKRVNKHIF PEILDAPFCTLKCKNVAEENTRVLYSLY GV\VEHSGTMRSGHYTAYAKARTVANS LSNLVLAHGDIPQDFEMESKG\QWFHISD THVQAVPTTKVLNS\QAYLLFYERIL
707	8758	A	1658	992	1863	GIWRNVHRQPQLESCEPTACSGRACAC CPVSCGWSHGQDWMVPVAGRCTRAQR CCTGGASLPTVHKSTLSSCSAPPADSAA CVFIYFIIF*QSLNSVAQ\AGVQWR\NL KLLQPLPPAFKA\FSCLSLCNWDYRRVP PGLANFCIFSRDGGFTMLVVRVLSNS*PC DLPASASQSAGIT\ALSHHAWLLFFETES RSVVQAGVQWCDLGSQAPPPGFTPFSC LSLQSSWDYRRPPRPANF\CVFLVETGF HC*PGWSRSPDLMIPPGLSLPKCWDCRR DTKHPASKF

708	8759	A	1659	318	1681	SPRMHALVLLLCIGALLGHSSCQNPASPP EEGSPDPDSTGALVEEEDPFFKVPVKNL AAAVSQTSAYDLRVRVRIQA*APRPNVLP VSLFKCGPTALSA\LSLGKRSKRKNKNIH RVALYYDLIKQAPDIHGYLIRKLP*HGHE PPQKNLKSASRIVFEKKLRIKSSFVAPLE KSYGTRPRVLTGNPRLDLAQEINN\WVQ A\Q\MKGKLARSTKEIPDEISIVLL/GV*AH FKGQ\WETKFDSRKTSLLEGFLGMKERT REGPP*LSDPKGCIFYAMGLGFRFSACKIC PACPLTG\SMIIFLPLKVTQ\NLTLINEES LTLRS*FMTIDPRT*KTVAGGPSLSPKLK LASYEGEEHPKFLAGR*SLQSLV*FHPDFS KINTGK\PIKLD\FRVEHPRLAFEWNE\DGA GNHPPSPRGLQPAHL\TFPLDYHLNQPFIF LLRDTDTGALLFIGK\LDPRGP
709	8760	A	166	283	397	NWQEKCSFQIIGGRKRM\SFRIILNFFHN* DRTVCYVP
710	8761	A	1660	3	340	
711	8762	A	1661	2	500	GKPD PSTKKQHTIWPSPHQGN\SPDLEVY NVIRKQSDVSLAETRPDLKNISFRVCSGE ATPDDMSCDYDNMAVNPSESGFVTLVS VENEIYGY*DI*KTETDNNGKEMISKILLF SIRKIHRRSMNKLRS\GPVDEHVVP\TTSC WTPTFWLYPLSQPV\IQLDLMRRYL
712	8763	A	1662	3	52	
713	8764	C	1663	92	244	MRCEILVLIPYVYFY\SNKLLCSRLXXXX XGGAVLKNPWGGQSLPGLAR**
714	8765	A	1664	336	413	
715	8766	A	1665	233	400	GGAVLKNPWGGPSLPGLAR**FFPYRGA Y*NLPGNFWKEPLFLGGDILGQPPF\GNL
716	8767	A	1666	194	360	GGAVLKDPWGGQSLPGLARK**FFPYGG PN*NLPGNFWKGPLLWGGDILGQPPYRN
717	8768	A	1667	319	391	
718	8769	A	1668	313	542	ALKQPT/PQTKEERAFDPRVHAE*IPYVF EIHIRST*KTT*NGNPTAPLPVRAPTPARV RTWP\NPGHSCAGSHSSR
719	8770	A	1669	143	1316	ERLEIGKELQLVWDEPHLTPG\NDSLLPSS CCVTAASDLDLRGGQPVCRRGGTQRPCY KVIYFHDTSRRLNFEEV\KFSCRRDGGQL GSIESEDEQKLIKFIENLLPSDGDFWIGL RRREEKQSNSTACQDLYAWTDG\SIQFR NWYVDEPSCGSEVCVVMYHQPSAPAGI GGPYMFQW\NDDRCNMKNNFICKYSDE KPAVPSRRS*\GEETELTPVLPEETQEED AKKTFKESREAALNLAYILIPS\PLLLL VTTS\VCWVWICRKRKREQDPSTKKQH TIWPSPHQGN\SPDLEVYNVSKKTNAKSF LSETRPDLRNISFRVCSEESPPDDMSCDY DNMAVNPSESGFVTLVSVE\SGFVTNDIY EFSPDQMGRSKESGWENEIYGY
720	8771	A	167	2	1012	AEALVESFWKAKQHTKEELKSLQAKDE EKNENEKAKAACSAAAMEEDSEASSST GDSSQGDNNLQKLGPD\DVSDTDSIRRV YTRLLSNEKIEIAFLNALVYLS\PNVECDL MYHKVYSQDPNYLNLFIIVMENRNLHSP EYLEMALPLFCKAMSKLP\LAQGKLIRL WSKYNADQIRRM\METVQQLITYKVISNE FNSQNLVND\DAIVAASKCLKMIYYAN AYAVTKNLGLYYDNRIRMY\SERRITVLY SLVQGQQLNPYLR\LRVCDHIIDALVRL EMITMENPADLKQFY/RGI*RRTRWVAA FWDRASEPKANSIGFGGSQLWMPTPVAS YT

721	8772	A	1670	18	686	SPPPPPPAREMNFVRAANRRPRRVSRRP VQQQQQQPPQPPPPQPPQPPHQQPSS PPQ*QQQHPPASSPPPPPLQERNNVGE RDDDVPADMVAEESGPGAQNSPYQLRR KTLPLKRTACPTKNSLEGASTSTTENFVG HRAKRARVSGKSQDLSAAPAEQYLQEK LAPDEVVLKIFSYLLEQDLCAAACVCKRF SELANDPNLWKRLYMEVFYTRPMMH
722	8773	B	1671	155	310	MAAIRKKLVIVGDGACGKTCLLIVFSKD QFPEVYVPTVFENYVADIEVDGKQ*
723	8774	A	1672	162	877	AMAAIRKKLVIVGDGACGKTCLLIVFSK DQFPEVYVPTVFENYVADIEVDGKAGRS LACGDTAGQEDYDRLRPLS*PDTVDILA MCFSIDSPDSLENIPIKSWTPEVKHFC PNGGPSILVGELERRVLSGIDGATQGRGLR PRLKAGSPVET*RKGRDMGKQGLALFG YIGSCSSQRPKDWEVEEVF*KWATESL LWQA*TLGKKKSGVPLSLVPLLAQPL MRLIFEVLFINLSV
724	8775	A	1673	1	711	
725	8776	A	1674	1	2647	MGVTSAAAGLVGSAPQCVALPSEGWTL AVWPVAACCTCSGVGSSPKLTPGSFVHCP WFLLLTEATRAEIKRPFSKAELKASVRP MEGSHCWGGEARRTSQGHTEQKGELEA RRQAQNEDEDVKEVWVGKTKKEESDKL GCQGAWVPPRVPSWIGRFELWVGYWE QPAVSWQMRVRLRLRAALTLLGEVP RRPASRGVPGSRRTQKSGGARTDSAWR RALTVISTSPGTSRMDPVALVAVGGPRR FPGGHTLQRLPVALRTLIPADQAHQAPN STTWLGSRAGLLALAAGLGGIRDSAAHG PLQVGGMGGYTGMGSEVRWEKEKHED GVKWRQLEHKGPYFAPPYEPLPDGVRFF YEGRPVRLSVAEEVATFYGRMLDHEY TTKEVFRKNFFNDWRKEMAVEEREVIKS LDKCDFTEIHRYFVDKAAARKVLSREEK QKLKEEAELQQEFGYCILDGHQEKIGN FKIEPPGLFRGRGDHPKMGMLKRRITPE DVVINCSRDSKIEPPAGHQWKEVRSDN TVTWLAAWTESVQNSIKYIMLNPCKSL KGETAWQKFETARRLRGFVDEIRSQYRA DWKSREMKTRQRAVALYFIDKLALRAG NEKEDGEAADTVGCCSLRVEHVQLHPE ADGCQHVVFEFDLFGKDCIRYYNKIVPGE KPVY*NLQLFMENKDPRDDLFDRLLTTS LNKHLQELMDGLTAKVFRTYNASITLQE QLRALTRAEDSIAAKILSYNRANRVVAIL CNHQRATPSTFEKSMQNLQTKIAKKEQ VAEARAELRRARAELKAQGDGKSRSVL EKKRRL*KLQEHHLAHLVQATDKEEN KQVALGTSQNLNYLDPRISIAWCKRFRVP VEKIYSKTQRRERFAWALAMAGEDFEF
726	8777	A	1675	2002	2238	KGDFTKLPLC/C*SVPAFY*RSLKICCSIY LV*YMSVSVIESICYKYTVFCSRG
727	8778	A	1676	3	428	
728	8779	A	1677	263	899	ISYQEGTSAIQRK*QEVTLRK*TQESE/SA GNDSASTAPRSTEESESDVFTESELSPIR EELVSSDELQDKSSGASSESQTVNQA EVESLTVKSESTGTPGHLRSDTEHSTNEV GTLCHKTDLNNLEMAIKEDQIADNFQGI SGPKEDSTSIGKNSDQDSFLHENSLEHQQE SQKENMPCGETAEFKQKQSVNKGKQKQK EQNQDFTGQORAG
729	8780	A	1678	1165	1530	VKNNGGNEVIIHFHLLTFGIYLLFFETEFCS CRPRLECNGAILAHCNLRPLPGFKRFSCF SLPCC*DYRHLPPRPVKFFVVLVETGFHY LGQAGLKLTPGDL/PPPLGLPKCVSHCA QPRVSTF

730	8781	A	1679	197	843	RLFSSNQTVDSQKNVDITLKGTPQ*SC KGPRGTLR\RD\NHIKCGTSALLGKEKK RGFRVD\KWWGSRRELGYPFGT\CSHV QDHDPRGVTTGASRYQDEGPVYASPSH PTVGLSQENGSSLLKSRNFFGVKKYIPQG FRMRPGCLLVSVSQGRKE*INPLKGNDI *ALLQIPAA\NPASPTRLKTGIRKFFGW VSMLEKGTVPQGLIE
731	8782	A	168	966	3172	
732	8783	C	1680	27	218	MLMADIRKEERNHLCRSSRRTWTILDRA EYSDHVVLQAGVGWGTSSXSPFLYSFEI PYGAQVA*
733	8784	A	1681	490	773	HPQIFVPGQESFNDRIKQPVEGLVVLRE HERHSPSLRLHLEATQRLRHPGLRLRG ELLWLIIRFIQTLPFAAKGPTRGAGIY PRGKQPVEGLVVLREHERHSPSLRLHLE ATQRLCHPGLRLRGELLWLIIRFIQTLP LPFAAKGPTWGAGIYPRGKQPVEGLVVL REHERHSPSLRLHLEATQRLCHPGLRL RGELLWLIIRFIQTLPFAAKGPTWGA GIYPRGKQPVEGLVVLREHERHSPSLRL HLEATQRLCHPG/LPQAQGRAPSLAHHQI HPNTPSSFCSGTYAGGWDLPQQAAC
734	8785	C	1682	48	80	MGLWLFHEIY*
735	8786	A	1683	858	1055	
736	8787	A	1684	1	103	VFFLFGDGVSLCHPGWSAVA*TQEAEE PFVQII
737	8788	A	1685	451	785	CSQDGLRWDLVRHPQTFVPGQESFND RILKQPVEGLVVLREHERHSPSL/PASS*G HTASPPRSPQAQGRAPSVAPPPTTPQICP TTPSSFSSKRTYAGGWDLPQQAADC
738	8789	A	1686	1	1335	MNDDIRSDLPDWRDRTPCVQKKAMD RTKTRFRKRGQITGKITTSRQHPQNEQS LQRSTSGYPLQEVVDDEVLGPSAPGVDP SPPCRSLGWKRKKEWSEDEEEPEKELA PEPEETWVEMLCGLKMKLKQQRVSPIL PEHHKDFNSQLAPGVDPSPHRSFCWKR KREWWDESEESLEEEPRKVLAPPEEIIW VAEMLCGLKMKLKRRRVSLVLEHHEA FNRLLDPVIKRLAWDKDLRVSDKIPSE PTI/HGSITQNPSSGSDLHPTFEYPSIPQFP NEYSHPNTEGGCQS*ARDSPLPS/VSGKL TSAGGLSWWCP*APT*FLSSATWPMTW RRTTRTPNKTSSSCMRPALAYPWSVT VGSSYAVA*TPCVQKKAMDRTKTRFRK RGQITGKITTSRQHPQNEQSLQRSTSGY PLQEVVDDEVLGPSAPGVDPSPPCRSLG WKRKKEWSEDEEEPEKELAPEPEETWV VEMLCGLKMKLKQQRVSPILPEHHKDF NSQLAPGVDPSPHRSFCWKRKREWW ESESLEEEPRKVLAPPEEIIWVAEMLCG LKMMLKRRRVSLVLEHHEAFNRLLDP VIKRLAWDKDLRVSDKIPSEPTILGASP KTLPLASQICIRPSNTPSRNFQMSTVTPT LRVGASPELGTVPYLPWEADLSRRPLL VVPLSTNLISVLSYLANDMEEDDEDPKQ NIFYFLYGKTRSRIPLVNRNRFQLCRLN PRARKNRSQIALFQKLRFQFFCSMSGRA WVSREELEENTGPRGDVDFQQELYSNA NGRQQERGEEPFVQII
739	8790	A	1687	385	889	LEPTLTEQGYARAVLPIQEVEDVLFVGL VLLHVIGQVESQEEMNALVLPGEAGP AEIRYDHSQEILVRHPQIFVPGQESFNDRI LKQPVEGLVVLREHERHSPSL/PASS*GH TASPPRSPQAQGRAPSVAPPPTTPQIGPT TPSSFSSKRTYAGGWDLPQQAADC

740	8791	C	1688	1	1869	MDSPTPHDPAAPLLVTVLESVQKKTKDR TETSFGGIGQILGKIMTSHQPQEQEQSPQ RSTSGYPLQEVVDDEVSGPSAPGVDPSP RRSLGCKRKRECLDESDDDEPEKELAPEP EETWVAETLCGLKMKAKRRRVSLVLPE YYEAFNRLLAPGVDPSPRRSLGCKRKR ECLDESDDDEPEKELAPEPEETWVAETLC GLKMKAKRRRVSLVLPEYYEAFNRLLA PGVDPSPRRSLGCKRKRECLDESDDDEPE KELAPEPEETWVAETLCGLKMKAKRRR VSLVLPEYYEAFNRLLAPGVDPSPRRSL GCKRKRECLDESDDDEPEKELAPEPEETW VAETLCGLKMKAKRRRVSLVLPEYYEA FNRLAPGVDPSPRRSLGCKRKRECLD ESDDDEPEKELAPEPEETWVAETLCGLKM KAKRRRVSLVLPEYYEAFNRLLDPV RFLAWDKDLRVSDKIPSEPTILGASPKTL PPASRICIRPSNTPPRNFHMTVTPMLSY LANDMEEDDEAPKQKIFYFLYGKTHSHI PLRPKHWFQLCRPMNPRARKNCSQIALF QKRRFQFFCSMRCRAWVSPEELEENTGP RGDVFQQLYSSANGRHQEGGEEP FV QII*
741	8792	A	1689	520	1235	WTDFRSIGLMALAGSVLEFSARSKDATP DPP/LGTGKVPSTAPTGAPPPGLPTAAFD VVLHPFRAGRKKYFPSLLFA*WLCQRSS P*RGADPVIGLYLVHRRGGACQPTLGNR QTPRLGIHARPRRRATTSLLTLLAFGKN AVRCALIGPGSLTSRTRPLTEPLGEKERR EVFFPPRPERVEHNVESRWEPRRRGAC GSRGGNFSPRGGSGVASLERAENSSTEP AKAIPIDRKSVMHQICSGPVVPSLRNAV KELVENS LDAGAH
742	8793	B	169	1	2187	MAGKASESWRKVKDTSCMAVTRENEK DAKAETPDKTIRSRETYHKNMSWETAP MIQISQGVPTTTHENYGSTIQDEIWCLTN FCLDDMLS FVLESCNHCAYCLNVWYR KRAAAKHLIERYYHQLTEGCGNEACTN EFCASCP TFLRMDNNA AIAKALELYKIN AKLCDPHPSKKGASSAYLENSKGAPNNS CSEIKMNKKGARIDFKDVTYLTEEKVYE ILELCREREDYSPLIRVIGRVFSSAEALVQ SFRKVKQHTKEELKSLQAKDEKDEDE KEKAACSAAMEEDSEASSSRIGDSSQG DNNLQKLGPDVSV DIDAIRRVYTRLLS NEKIETAFLNALVYLSPNVECDLTYHNV YSRDPNYLNLFIIVMENRNLHSPEYLEM ALPLFCKAMSKLPLAAQGLRLWSKYN ADQIRMMETFQQLITYKVISNEFNSRNL VNDDDAIVAASKCLKMVYANVVGGE VDTNHNEEDDEEPIPESELTLQELLGEE RRNKKGPRVDPLETELGVKTLDCRKPLI PFEFINEPLNEVLEMDKDYTFK VETEN KFSFMTCPFILNAVTKNLGLYYDNRIRM YSERRITVLYSLVQQQLNPYLRLKVRR DHIIDDALVRLEMIAMENPADLKKQLYV EFEGEQGVDEGGVSKEFFQLVVEEIFNP DIGMFTYDESTKLFWFNPSSFETEGQFTP IGIVLGLAIYNNCILDVHFPGLSTGS*
743	8794	A	1690	2176	2641	RKTIEEKADPKLQGGFFVCLFVLETESCSA SQAGMEWPNLNSLQPPPGFTQFLC/SQP PE*LGLTGVP PHQAHCIFSRD GASPC*P GWSPTPGLKRSTCFSLK CWDYRHEPPR LAYFLALFNRDEGLAMLPRVSN SWPQVI LLLWPPSVLGFQA
744	8795	A	1691	112	410	

745	8796	A	1692	2148	2510	SQHFGKLRQEDHLRSGVREQPGQHGT PYLLKIQKLVAGHGGMCLYSQLLMRLRQ ENGVNPGGGACNEPRLRHCTPAWVTEQ DSVSKKKTVHKKKLNWGSVVRGET*RT SPCVALDTAHL
746	8797	A	1693	178	730	IFFFFFFKMESCSVAQAGVQWRDLGSLQ APPRGFTPFSLSLPSSWDYRRPLRPRAN FFYF**RRGFTVLATMVVIS*PHDLPTLAS QNAGITGVSHHTQPVYALFFSFETEFCS\
747	8798	A	1694	2	780	VAQAGGQWRDLGSPQPPPRFKQFSHLS LPSSWDYRHAPPSLANFFCIFSRRDRVSPS WSGWSRTPDLR
748	8799	A	1695	103	532	CWGLRRQRSQDVTMAWALLILTLTQ GTGSWAQSALTQPPSASGSLGQSVTFSC SGTSSDIGNINYVSWYRQHPGKAPKLM YEVTKRPSGIVPEVRFSGSKSGNTASLTVS GLQSEDEGDYCCSMARHHS/VGWVF
749	8800	A	1696	112	1158	GGGTQVDPQLGQPKRAALGSLCFPPSLG EASSQPRPTLVVISDFLPGKP*TVAKA\
750	8801	A	1697	343	586	DSSPVKAGVETTPTPSKQSNNNYAATS YLTLTPEPLKVPQEATACRVTPEGGTLE KTVAPECS
751	8802	A	1698	217	360	SCGLGHRKTFSFVSLPARNETQPKACRE QNMEGDFSVCRCN*RHVVANFTLHEA YCLRFLVLCPECEEPVPKETMEEHCKLE HQQVVGCTMCQIMHKSSLEFHKANECQ ERPVECKFCKLDMQLSKLELHESYCGSR TELCQCGQGQFIMHRMLAQRRDVCRSEQ AQLGKGERISAPEREIYCHYCNQMIPEN KYFHMGKCCPDSEFKKHPVGNPEILP SSLPSQAAENQTSTMEKDVRPKTRSINRF PLHSESSSKKAPRSKNKTLDPMLMSEPKP RTSSPRGDKAAYDILRRCSQCIGILLPLIL NQHQEKCRWLASSKRKTSEKFQLDLEK ERYKFKRHF
752	8803	A	1699	1	390	KQKQTSFSSLPRRVNCNSHLVLL/RCDFK NCNLAFETKICQFIKST*EYMGFIFLCFF LLYNIPFHICGPRVKSSFCYRH
753	8804	A	17	214	464	WEEIQELNEVARHRPRSTLVMGIQQENR QIRELQENKELRTSLAEHQSALELIMSK YREQMFRLLMASKKDDPGIIMKLEQHS KELQAHVDQITEMAAVMRKPLKLTNSR VARNKNEYFNLNKKTKA
754	8805	A	170	270	497	FCGLLLLHPVSADF*PAELINTQEPQERC QLDTGESSRVQHTLPSCPVCQGGTAELS RNVMI GASELKCLHPSPKLEYILPGN
755	8806	A	1700	386	790	MHFLKAGRGSRL*SQHFGPRPWADHE/ RSGDRDNRG*HGETPSLLKNTKKN*PGT VAGALVASTREAEAGEWREPG
756	8807	A	1701	1089	1295	NSIMEEQELNEVARHRPRSTLVMGIQQ ENRQIRELQENKELRTSLAEHQSGGLGN L**AKYREQMLRLLMASKKDDPGIIMK LKEQHSYD*HWYIVTSPKDSSLMHLDTS LKHLNMDWREGTWKQIRMYTK
757	8808	A	1702	2	367	CPPPLFFETEFRRSCCPGWSNSSLHRPPPG FKQFILNFG*K/PSYPYLAQSCARMCV CVCVCIIFTET
						RDNTSPISVILVSSGSRGNKLLFRYPFQRS QEHPASQT/RFSDVILATILATKSEMCGQ KFELKIDNVRVFGHPTLLQHALGQISKTD PSPKREAPTMILFNVVFALRANADPSVIN CLHNLS

758	8809	A	1703	1	452	RCQYSTREAKLI/LALQD/EVSAMAD/GN E/GPQSPFHHILPKCKLARDLKEAYDSL TSQVVRHLHINSWLEVSFCLPHKIHYAASS LIPPEAIERSLKAIRPYHALLLSDEKSL GELPIDCSPALVRVIKTTSAVKNLQQLAQ DALLPPRLP
759	8810	A	1704	1	468	
760	8811	A	1705	2	118	
761	8812	A	1706	1	671	DADSRFSEVF/LATILATQFEMCGQKFEL KIDNVRVFGHPTLHRHALGQISKTDPSPK REAPTMILFNVGFALRANADPSVINCLH NLSRRIATVLQHEERRCQYL TREAKLILA LQDEVSAMADGNEGPOSPFHHILPKCKL ARD/PQLWLPNQR*HDPHQPHGQLQR RATSQRGLATEPEDDGEPAGQVGA*TR SHPQCTRSPEP*GPPHVCQAPSLPRP
762	8813	A	1707	230	345	
763	8814	A	1708	464	763	
764	8815	A	1709	3	156	GRHHL/EEEIMYNENTRGSQLLMLF*QSF AACWMVTTHEDPVIADVQALLP
765	8816	A	171	2	421	PAWLSRFTCAATYIKMPEE*ETHYQPM EEEADTFY/EAKMAPLML*IINTFYSSKE ISLRELISNSSD/AK*LINPQSDGFRVNL GVLNA*INIFC*QALDKIRYESLTDPIKLD SGKELHINLIPNKQDRTLIVDT
766	8817	A	1710	1	1878	FRGTWAPSAGSVLLRLPPPPAPSSSGPL RPRPRPHGMRDNTSPISVILVSSGSRGN KLLFRYPFQRSQEHASQTSKPRSRYAAS NTGDHADEQDGSFSDVILATILATKS EMCGQKFELKIDNVRVFGHPTLLQHAL GQISKTDPSDEGKAPTMLF*CWLFALA RANADPSVINCLHNLRRRIATVLQHEER RCQYL TREAKLILA LQDEVSAMADGNE DPKPPFHHILPKCKLARDLKEAYDSLCT SGVVRHLHINSWLEVSFCLPHKIHYAASS LIPPEAIERSLKAIRPYHALLLSDEKSL GELPIDCSPALVRVIKTTSACERTCRQLA QDADLA LLQVFQLAAHLVYWGKAIHY PLCENNVMMLSPINASVCLYSPAGPSSSS HQPFPSWTWPSVLAKFSLPVFLCQNFN PLAPRCARRTQLH/IQMVVWMLQRRLL IQLHTYVCLMASPSEVEEPRPRIEDDVPF TARVGGRSLSTPNALSFGSPTSSDDMT LTKPQAWTTPSAELLPSGDSPLNQRMTE NLF/APSLSEHERAAILSVPAQNPEDKN MFA/RGILHYFRGRHLEEMYNENTRRS QLLMLFDKFRSVLVVTTTHEDPVIADVQA LLP
767	8818	A	1711	1	613	PLKRS DGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPVEKSAVTALWGQA*TW MKVGGKALGK/RCWVVLWDPKRSFEV LWGNLSQLPDAVNGANP*R*KASMAKE KVLGCPLSEWPLAHLADNLKGHPLPTE VNLNCDK\LRGSLKNFRLLGQTCLVC VPGPINFWQKNSTPTSCACKLIKSWLA WCWLNALGPTSIT
768	8819	A	1714	97	424	SPALWEAYDGWITLRSGVQDQSGQHGE MPSLLKIQKLAGHDGECL*SQLLRRLRR ENHLNLGGRGCSELRSRYCIPAWAPEIAP LHSSLGDLNKTLSQKKTKTVSFI
769	8820	A	1716	18	367	SPPPPPRTRWWPLRRPRLSLGTRAASLR FSSRKPCQNKPDYGLRSEKFR*SRK/A*G RQRP/PREKFPLFPKPIEPGEAKPGEIV NGSVRPPNMPLYIPTSIAPYFTFLAVLT L

770	8821	A	1717	47	409	NSYIYMCISYINTIYIHIYLESNISLPLNI YISTPT/HIY*RHTV*VHTKAYVHML*HV YIHFCCLCVHKSFKGTIYRDASFLESCSKV NTECHKLRKVVRKYSRIHHTGIHQSSFIM RKMS
771	8822	A	1718	89	1560	IMKHTNPEPGSFSRFYSLKVAPVKVATA APVAGAPPQPDLEFTKLPNGLVIASLEN YSPVSRIGLFIKAGSRYEDFSNLG\TTHLL RLYIQS*RTKGASSFQDNVPVIGRQLGGQ IKC*PQQGENMGLYWWECLRGDVDNL MEFLIVTTAPEFRSLGK*VNLQPQLKV DKAVAFQNPQTHAIGNLHAAA\YTGN ALANPLYCPDYRIGKV\SEELHYFVQN HFTSARMALIGLVSHPVVKQVAEQFL NMRG\GVGLSGWQRANYRGGEIREQNG DSLVAHAFVAKSAVAGSAKPNAFSVLQ HVLGAGATMSRGAATTTSHLHQ\AVSQ ATQQPVFVSAFNARYS\DLGLFGI\YTISQ GHQLAGDCIK\AA\YNQVKPIRSKKPFFP TQGVSA\KNKG*KAGIPLMVQWKSFLK CSPGRKSGSPGLLV/GLVPYMPHTHTVPS SQMDSSGLMLDIIN\ARAKKFVFWARSS MGSKFGKFGDITPFCLMEL
772	8823	A	1719	53	420	
773	8824	A	172	1	267	CSAGGPWRAPQPRRFHRRRRPAQLPPPL PLPPLPASPRIHNRTPRPSQRTPPPAALG CPEPGS/RSQGRGHARPPGSGEGDPTVSS PGY
774	8825	A	1720	1	1260	
775	8826	A	1721	403	1334	DTMALTSDLGKQIKLER/EVEGTLLQPAT VDNWSQIQSFQAKPDDLICTYPKAGTT WIEIVDMIEQNGDVEKQCR\AIQHRRHP FIEWARPPQPSGVEKAKAMPSRILKTSP FHFSWLPPSFWEENCKF/LFMLASEIAK D\CMVS*YHFQRMNHMLPDPVTWKEY F\ETFINGK\VFWSWF\DHVKG\WWEM KDRHQ\NLFYEDIKRDPK\HEIRK\VMQ FMGKKVE*TVLDKIVQETSFEKIKENPM TNRSTVSK\SILD\QSIFPPFMRKGTVGAD WEN\HFTVA\QNERFDEIYRRKMEG\TSI NFCMEL
776	8827	A	1722	2	645	HGIQAHGQIPSYKTIGGRDSDSHTFFSET GAGKHVPRLLL*NWKPTVMDEVRTGTY CQLFHLEQFITARKIAANNYARGHYTIG KEIIDLVLDRIKRLADQCTGLQGFLVFHS FGGGTSGGFTSLLMERLSVDYGGKSKLE FSIYPAPQVSTAVVEPYNSILTTHTTLEHS DCAFMEEGEFSEAREDMAALEKDYEEV GVDSVEGEGEEEGEY
777	8828	A	1723	87	1531	SLATMRECISIHVGQAGVQIGNACWELY CLEHGIQPDGQM/TQVTRPLGGGDDSFN TFFSETGAGKHVPRAVFVDLEPTVIDEV RTGTYRQLFHPEQLITGKEDAANNYARG NYTIGKEIIDLVLDRIKRLADQCTGLQGF LVFHSFGGGTSGGFTSLLMERLSVDYCK KSKLEFSIYPAPQVCTAVVEPYNYILTD HTTLEHSDCAFMDNEAIYDICRRNLDI ERPTYTNLNLISQIVSSITASLRFDGALN FTLTNFGTKLVFPRIPLPFCPIMPPVHFA *ERPPMNSFSVREITQMLCFEPSPTRLVK \CDPRPWVKSWPCCLVATGGDVVPKRC QMLPIAHPSKPKRITIQFVDWCPTGFKV GINYQPPHWVPGGNLAKVTREAVCML SKHHSPFAEAWARPGPTSFDLMLCQACP FVHWYLGVEGMEEGEFSEGRER*GCPFR KDYEKV\GVDSVEGEGEEEGKILIHSLF G

778	8829	A	1724	84	1560	EATTSPRLRLRHQLGSREAATMRECISIHV GQAGVQIGNACWEL YCLEHGIQPDGQM PSD/RKPLGEGDDSFNTFFSETGAGKHVP RAVFVDLEPTVIDEVRTGTyrQLFHPEQ LITGKEDAANNYARGHYTIGKEIIDLVLD RIRKLADQCTGLQGFLVFHSLGGGNWV LVPPPPCLQLGGGGAGKRLSVDYGOEVP SWEFSIYPGAPRFPPVVEPYNFHPTNPT PTLGAL*LCPSWVDNEAIYDICRRNLDIE RPTYTNLNRLLIGQIVSSITASLRFDGALN VDLTFQTNLVYPRIHFPLGHIMPPVIFA EKAYHEPAFL*QRSQMLCFEPANQM/V KCDPRPGKYMLCCLLYP\GDVVPQRISF LPLPTIKTQ/RLTIHFLDWSPTDFKL VINY QPPTVVPGGDLTKVQRAVCMLSNTTAI AEAWARLDHKFDLMYAKRAVHWYVG EGMEEGEFSEAREDMAALEKDYEEVGV DSVEGE GEEEGEEY
779	8830	A	1725	153	380	EYKTQNRFLRSPRLDCSGAISAHCNLC LPGS\SNSHAS\ASK*AGITGMHHHAWDN FCILFSRRWGFCHVGQGW
780	8831	A	1726	14	322	IFSSEPLEGRPGRPGGARAACQEGAGK\ AGAAGD*PSP/PG*GHAAAPKCREFGHN QIDAGWNQRP/GKPLVPMWEPQPCPSC PLELSEFPFGAHSSWTSNSIY
781	8832	A	1727	605	3133	DSRGQEG*RTGAPHMGDGKPGVSGPPG FQASIKFGCGQNFSPITLGP GP/PWGGC GQALSPSGVPGLEGVSPTRAKGWARFPP KAPETLNERQIYPNAPPS*AG\GHADTE GQDRTPHLLGANSSGHLGQLPF*SASIG GAGRD\SQLSRAFSSASKHVPASAGTF *HSFSKG*VSKTTTTNAGNALFPMGSSK TKKPNSHQRGQMGS*GRNPPSLGRAPAP LPEREAPIPAPQLGPSAAGTSRQVGQKSS TSP/PPGRGGNIEP*TQEERRKEKMKKAT GLSKHQAGFIQNE*NLKGAGEF/GP/SGL AGSQNPSSKLQGLGK*EQRL**GAG PDCSPLGKHTP*RSPSPLPRTGDASRG* GFSGKEASFPGQPQSTCLSGIRPSLGS*P LGQ*RTL/PCSNLPAGK/RNCLG/PPGLGR GHGRCSDL SQHGSQT*AGANWRKRQ/PP VPAGLLDPGLTAQQAVTRSPWEGAQG RGGEGPVGLCWG*ACAKCRLQSGRTP AGGRQGSRSVWVGSEVMAPRKRPPAG PPGHKEGTAEAVSSQTVTGGRIPEAVWP HHHQKGKTTEQEPCC*DVTKASAPGVS GDTG/MRGPLQPQASPNI*GAAACPFSSQ AGSSLQQRSLPAPSCPQAA/RGPPGLPG LPSSGSEENIHSGAWALVGQEGPSMDGR GNGMMLRGVWTGVHGGGMDMWRRG DLKGKVPHGMIQVWTP/G/DKQDSSPAR TPAPQWLSITTGS*TPE/GDPGGKLDAAQ RGRAIAAHEQPEVAVLGVA/GHL*SPGS ARSSPRWHPHRSACRPPRS GGSPSPSSA *KSDRTDAGAGVAAAASPGAGAPAHCP QGPPRSCQGPQR
782	8833	A	1728	1096	1748	ELFPPTSTSIALAQLRALTAQAGQPLTQVN QGAFSMPLWVLDPRERGLKIKPSFLL WGWAHLGFQHEALWALGCAFIEERGGE REAFLGPEMFSGWGFHPCP*THQFWPG EPQ/EV*GGRHCGKAPREKWPALPTFQ KEKPVVPVTPEAIPVCQEGAPPGTAKSIH CPPEIHTKEACPVPKGKEENVPGKRKIWS KKRDRQGRAQESRIQGSEEIP

783	8834	A	1729	162	788	QKLFFLAENIIRSFRTVKTLFVLNQMM CFISVFDVFSFFSPGFTSFVISLFCGFAAN LIGLGLAAKALDSGAFFSFVVLSPSFPLPS CPHHFTLLKVIMNTRSEIFLAPSTLGFFE MESHCVTQ/CSGA/ISAHCSLHLP*SNFP VSAS*VAGTTGASHDNWLIFLFLVETGF HHADQGGGLKF*PQIHLPLGLPKWLGLQC EPCGWL
784	8835	A	173	218	430	
785	8836	A	1730	158	468	TGAGHGGLMPVIPSHFGRPWADHLRS GVRDQPGQHG*NPVSTKNTKIGWA*WR APVIPAT*EGLRQGESLEPGRAEGARRC HYIPAGGDRVRLCLKKKKLN
786	8837	A	1731	1	1161	
787	8838	B	1732	1	1380	MDKFLDTYTLPRINQEEESLNRPTASEI VAIINSLSSKKSPGPDGFTAIFYWSVGS GQAIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAPNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLIRDVKDLFKENYKPLLKE IKEDTNKWKNI PCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKNTLKF QKRARIAKSILNQKNKAGGITLPDFKLY YKATVTKTTWYWHQNRDIDQWNRTEPS EITPHIYNLIFDKPEKNKQWGKDSL FNK WCWENWLAICRKLKLDLFTPYTKINSR WIKDLKVRPKTIKTLEENLGITIQHIGMG KDFMSKTPKAMATKAKIDKWDLIKLS FCTAKETTIRVNREPTWEKIFATYSSDK GLISRIYNELKQIYKKKQTPPSKSGRRT*
788	8839	A	1733	1	293	
789	8840	A	1734	1	1183	MKLKRNNEMSGKALDPREGFCDASYEI QTTIREYYKHLYANKLENLEMDTFLDT YTLPRLNQEEVESLNRPTGAEIVAINSL PTKKSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASILIPKPGRDT TKKENFRPISLMNTDAKILNKILANRIQQ HIKKLIHHDQVGFIPGMQGWFNIRKSINV IQHINRAKDKNHLIISIDAEKAFDKIQQP MLKTLNKLIGDGYFKI/Y/RDRHFSKEDI YAAKHKMKCSLSLAIREMQIKTTMRY HLTPVRMAIHKSGNNRCWRGCGEIGTL LHWCWDCKLVQPLWKS VWRFLRDLEL EIPFDPAILLGVYPKDYKSCCYKDTCH/ IMFIVALFTIAKTWNQPKCPTMIDWI
790	8841	A	1735	66	1392	QVLLSFGTPLVLTTKREKNQIDA KNDK GDITTDPTIEIQTISIEYYKHLYANKLENLE EMDKLLDTYTLPRLNQEGVESLNRPTG SEIEAIINSLRPISLMNIHAKILNKILGN*IQ QHIKKLIHHDQVGFIPGMQGWFNIRKSIN VIEHINRTKDKNHMIILIDA EKA FDKIQQP FMLKTLNKLIGDGYLKIIRAIYGKPTVN IILNRQKLEAFPLKTGTRQGCPLSPLLFNI VLEVLAKAIRQEKEIKGIQLGKEEVKLSL FADDMIVYLENPIISAQNLLKLTGNFSKV SGYKINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLVKENY KPLLKEIKEDTNKWKNI PCSWVGRINILK MAILPKVIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRACIAKSILSQKNKAGGITLP DFK
791	8842	A	1736	1	432	
792	8843	A	1737	1	413	
793	8844	A	1738	1	1401	

794	8845	A	1739	1	510	MLEVLAWAVRQEKEIKGIQLGKEEVKLS L*LMSNFSKVSGYKISVQKSHAFVYTN RQSESQIMSELPFTVATKRIKYLGIQLTR DVKDLFKENYKPLLNEIQEDTNKWKNIP CSWVGRINIVKMAILPKVIYRFNAIPKLP MTFFTELEKTK\FIWNQKRAHIAKTIL
795	8846	A	174	9	201	
796	8847	A	1740	1	2052	
797	8848	A	1741	1	762	MNIDAKILNKILAKQIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHINRTEDKN HMIISIDAEKAFDKIQPFMLKPLNKLGI DGTYFKIIRAIYDKSTPNILNGQKLELMS NFSKVSGYKISVQKSHAFVYTNNRQSES QIMSELPFTVATKRIKYLGIQLTRDVKDL FKENYKPLLNEIQEDTNKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPKLPMTFFT ELEKTK\FIWNQKRAHIAKTIL
798	8849	A	1742	1	1057	
799	8850	A	1743	1	1380	
800	8851	A	1744	1	862	MDTFLNTYTLPRLNQEEVESLNRPTGSE IVAINSLPSKKSPGPDGFTAKFYQRYKE ELVPFLLKLFQSIEKEGILPNSFYEGSIILIP KPGRDPPKKENFRPTSLMNIDAKILNKIL ATRIQQHIKKLIHHDQVGIIIPGMQGWFI PKSINVIQHINRAKDKNHMIISIDAEKAFD KIQPFMLKTLNKLGIIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTRQGCPLS PLLFNIVVEVLARAIQEKKIKGIQLRKE EVKLSLFADDMIVYLENPIVSA*RLNQEE VESLNRPTGSEIVAINSLPSKKSPGPDGF TAKFYQRYKEELVPFLLKLFQSIEKEGIL PNSFYEGSIILIPKPGRDPPKKENFRPTSL MNIDAKILNKILATRIQQHIKKLIHHDQV GIIPGMQGWFIIPKSINVIQHINRAKDKN HMIISIDAEKAFDKIQPFMLKTLNKLGI DGTYFKIIRAIYDKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVVEVLARAIQ EKKIKGIQLRKEEVKLSLFADDMIVYLEN PIVSA
801	8852	A	1745	1	1551	
802	8853	A	1746	1	947	
803	8854	A	1747	179	887	
804	8855	A	1748	1	1074	
805	8856	A	1749	1	1060	MDTFLDITYTLQRLNQEEVESLNRPTGSE IVAINSLPTKKSPGPDGFTAIFYQRYME ELVPFLLKLFQSIEKEGILPNSFYEASIIIP KLGRDTTKKENFRPISLMNIDAKILNKIL AKRIQQHIKKLIHHDQVGFIIPGMQGWFI ICKSINVIQHINRAKDKNHMIISIDAEKAF DKIQRFMLKTLNKLGIIDGTYFKWKNIP CSWIGRINIVKMAILHKALYRFNAIPKLP MTFFTELEKTTLKFIWNQKRACIAKSILS QKNKAGGITLPDFKLHYKATVTKTAWG PYDR/DID/SWNQTDLMCAVLPSRYVTL QDSSIL*KMR*VKKLQKKSQADLVQG LRKDVSIT
806	8857	A	175	1453	1936	EVEKHLCCQ*ELLRAQHN*AAACRRPRP PAPGPQCSAGGPMARAPQVPPPPPCS APPPPLPLPLPAS/HAHPQPHFRHGRRSA LLPRPPWAVRSRGALAGPRTRAAAGLR GGAGAAPADARFPASSPAE*PKFPQN SARALTGFPRCTDPTVSSPGY

807	8858	A	1750	1	1401	MSELPTIASRKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSWVGRI NIVKMAIMPKVIYRFNAIPIKLPMPFFTEL EKTTLKFIWNQKRARIAKAILSQKNKAG GITLPDFKLYYKATVTKTAWYWYQNRD IDQWNRTEPSKITPHIYNYLIFDRPEKNK QWGKDSL FNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRSKTIKLEE NLGNTIQDTGMGKDFMSKTPTAMATKD KIDKWDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELQQIYKKK TNNPIKKWARDMNRHFSKEDIYAAKKH MKKCSLSLAIREMQIKTTMRYHLTPVRM AIIKSGNNRCWRGCGEIGTLLHCCWDC KL VQPLWKS VWRFLRDLELEIPDPAIPL LGVYPKDYKSCCYKDTCT/RMFIVALFT IAKTWNQPKCPTMIDWI
808	8859	A	1751	1	1410	
809	8860	A	1752	1	1559	MDTFLD TYTLPRLNQEEVESLNRPTGSE IVAIINSLPTKKSPGPDGFTAIFYQRYKEE LVPFLKLFQSIEKEGILPNSFYEASHILIP KPGRD TTKENFRPISLMNIDAKILNKIL ANQIQQHIKLIHHDQVGFIPGMQGWFN IRKSINVIQHINRAKDKNHMISIDAEKAF DKIQQRFMLKTLIKLGIDGTYFKIIRAIYD KPTANIILNGQKLEAFPLKTGTRQGCPLS PLLFNIVLEVLARAIQEKEIKGIQLGKEE VKLSLFADNMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASRKRIKYLGIQLTRDVKDLF TSVISQVWVGS LDTSLILQLWVGS LDISV ILQLWVGS LDTSVISQLWVRSLDTSVISQ LWDIAFLSHVPGMLS*KSQVSLATLMQR MSSHGLGQLQPCGSAGYSSHGCFHRLAL NACGSSSAQCKLLVDLPFWGLDGGLLLT AARGHSPGALCVRVPTPHFPSMLP
810	8861	A	1753	1	1575	MNTDAKILNKILANRIQQHIKLIHHDQV GFIPGMQGWFNIRKSINVIQHINRTKDKN HMIVSTDAEKTDFDKIQQPFMLKTLNKLGI DGTYLKIIIRAIYDKPTANIILNGQKLEAFP LKTGTRQGCPLSPLHKFLD TYTLPRLNQ EEVESLSSPITGSEIVAISS/FTNEKESRTR WIHSRILPEV*GGT/RIKYLGIQLTRDVKD LFKESYKPLLKEIKEDTNKWKNIPC*WV GRINIVKMAILP/KELEKTTLKFIWNQKR ACIAKSILIQSKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNSTEPSEIMP HIYNYLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLD PFLTPYTKISSRWIK DLNVRPKTIKLEENLGNTIQDIGMGKDF MSKTPKAMATKANIDKWDPIKLKSFCT AKETTIRVNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKK/TNNPIKKWAKDMN RHSSKEDIYAAKKHMKKCSSSLAIREMQ IKTTMRYHLTPV
811	8862	A	1754	468	4080	RVRSGTDSIASGPRVLCSTRTERRRRRSY LVHRRCVPCGPVAVDGVFNLTNIDRWFL HINRAKDKNHMISIDAEKAFDKIQQPFM LKTNLKLGIDGTYFRIIRAIYDKPTANIIL NGQKLEAFPLKTGTRQGCPLSPLLFNIVL EVLARAIQEKEIKGIQLGKEEVKLSLFA DDMIVYLENPIVSAQNLLKLISDFSKVSG YKINVQKSQTFLYTNNRQTESQIMSELPF TIASRRRIKYLGIQLTRDVKDLFK

812	8863	A	1755	1	2882	MDKFLDITYTLPRLNQEEVESLNRISITGSE IVAINSLPTKKSPGPDGFTAIFYQRYKEE LVLLLLKLFQSIEKEATLPNSFYEAHILIP KPGRDTTKKENFRPISLMNIDAKILSKIL ANQIQHIKKFVHHDEVGFIPRMQGWFN IHKSKNVIQYINRTKDKNYMIISIDAEKA FDKIQQLFMLKTLTKLIDGTYLKIRAIY DKPTVKIILNGQKLEEFPLKTGTROGCPL SPLLFNIVLEVLAIRQEK
813	8864	A	1756	1	1746	MIISVDAEKAFDKIQQPFMLKTLNKLID GMYFKIIRAIYDKPTANIILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVLAIRQEK KEIKGIHLGKEEIKLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSQYKINAQKSQA FLYTNNRQTESQIMSELPFTIASKRIKYL GIQLTRDVKDLFKENYNPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKNWKK TTLKFIWNQKRACIAKSILSQKNKAGGIT LPDFKLYYKATVTKTAWYQNRDIDQ WNRTEPSEIMPPYNYLIFDKPEKNQW GKDSL FNKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLNVRPKTIKLEENLG ITIQDIGLGKDFMSKTPKAMATKAKIDK WDLIKLSFCAEKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKTNNPI KKWVKDMNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHFTPVMAIHK SGNNRDMDEIGNHHSQQTAMTKNQTP HVLTHR WELNNENTWTQEGEHTLGPV VGNLKLRLPKISLS
814	8865	A	1757	1	2866	
815	8866	A	1758	1	1285	MLEVLAWAVRQEKEIKGIQLGKEEVKLS LFADNMTVYLENPIVSAQNLLKLISNFSK VSGYKVSGQKSQALLYTNNRQTESQIMS ELPFTIASKRIKYLGIHLTRDVKDLFKEN YKPLLKEIKKDTNKWKNIPCSWVGRINI VKMAILPKDIIQENFPNLRQANIQIEIR KTPQRYSSRRATPRHIVRFTKVEMKEK MLRAAREKASHHTYSKIDPILGSKPLLSK CKRTEIITNYLSDHSAIKLEFRIKNL
816	8867	A	1759	2	231	PPSAS/CVQTGPPCHSLAFPPSAPGQEQE GHQLPSHVIPCHLALGTAFPPQAAMAG WGVSQATYCQELEPPFPVSSS
817	8868	A	176	5	711	FEALRMIGHLFAKSPYHGKINSKIVART NIKLMVKVVMWKNGEIIDLQIVYGDN APKKSVAVYKCITSLRRSKVLDEACSSR PVTICKGKINLVYANISIGSAYTILM/EK LNLSKLSTHWPQ/PVHPDQLKTRAKLS ME/ILNKWDQDPKGFL*KIVTRDRTWLY *YTFEDKAQSKQWLPRGGSGPVKAKAG WSRAKVKA/TTGFWNAQIVLLVDFLEGQ RTITSAYESILLKKK
818	8869	A	1760	1842	2096	CHSQKPQVPPPKPWGSLERPNT*VPAC VLPAPAPAQRPGQIARQ*PWVAPGTSGQ SRVGRTPGVSSGHGQTLTCPMALLQPLL
819	8870	A	1761	37	288	WGNTGSQVMTTVLNTALLPPKPSMPLPI KHYAIPPSY/SPHP*PIPSPTANLESAPP ASAP/PPPLPPAQLGEAHAPPE*YAIPPP SYSHTRSHPSAQQQTLSQRHQPLHLSSS ASTLPSWGKLMHHLNNIPQ
820	8871	A	1762	397	506	SFLEDLTGLSNQPATAGANWITRLCTGS P*NV*PPWHMSSGHPEAVSRVCIFNLVG FGI
821	8872	C	1763	291	491	MGADRQTHPQDRWFSHLHLKLLRRSYRI EQPASHSRGRDLNNTSLHRLSLCPCHPPLF LTLFLGIMF*

822	8873	A	1764	630	1159	SFY S A L M L S D R K N G R E R G R H G L S R R I K R Q R K L V E A E A S Q A C L A G K P G P T P A S H P / P G D G L P C P L S A P T L S P A T / A L P L P / S P * R S P N H S A N / P N P L S P T S S V K H S R C S S P H S A L P L S T P K A T P P S P N H R A G L F S S L P L A P M S T S * L L Q K N C V L V R A P A P T S Y I P V F F M T P A Q C P V F L S A Q
823	8874	B	1765	1	1359	M G I K N S K R G S L P L A A P A L L K P D T L W S C I F G E G D L G E E D M P P D Q A P S P A I L P P N H A F G L W P F R Y T Q T H P Q E A A A D P A A A Y H P E P P P L I L A G V R F R S N P A L P E N G K G A W R G D G V A E G H A A L W V L G L R C E R S V T A A L A A R T R E H D G R W R E G A E K G P R R R W V V R A I Q T P R L G K A L I H C W T T R G S L W V N S S V S A G S E R D Q R A D H A A A Q T S C A A G A V A C G L L L L L V R G Q A W V K K Q N L S P E T R T K E L V V S L M P L P H P G Q G H N L A S R A K A R T Q P V P S G P T H G A G A G E S C P C E G R Q A G V Q T F L G I P F A K P P L V R C D L H P L S P L N L G V V W G W N H P S G H I Y T P A H S H E G S N L P H W R Q A R N R Q L G Y L D Q V A A L R W V Q Q N I P T L E A T L T V S P F L A S L R W H E C V F A C C V P H I P R T F H G A I M E S G V A L L P G L L P A Q L M S S P R F P G P C V F Y E F Q H Q P S W L K N I R P R T *
824	8875	A	1766	2	597	R W L I P K V M R I Y D T Q K K M D R E A S Q A A L Q K M L T L L M L P P T F G D L L R E E Y I G D N G D P Q T L Q A Q F Q E M M A D S M F V I P A L Q V A H F Q C S R A P V Y F Y E F Q H Q P S W L K N I R P P H M K A D H V K F T E E E E Q L S R K M M K Y W A N F A R N G N P N G E G L P H W P L F D Q E E Q Y L Q L N L Q P A V G R A L K A H R L Q L W K K A L P Q K I Q E L E E P E E R H T E L
825	8876	A	1767	3	1867	I H P S A P R L G K A L I H C C S F P G Q P L G E Q Q R V R R Q R T E T S E P T M R L H R L R A R L S A G A C G L L L L L V R G Q G Q D S A S P I R T T H T G Q V L G S L V H V K G A N A G V Q T F L G I P F A K P P L G P L R F A P P * S P L E S W S G V R D G T T H P A M C L Q D L T A V E S E F L S Q F N M T F P S D S M S E D C L Y L S I Y T P A H S H E G S N L P V M V W I H G G A L V F G M A S L Y D G S M L A A A L A E N V V V V I I Q L P P G G V L G F F S T G D K H A T G N W G Y L D Q V A A L R W V Q Q N I A H F G G N P D R V T I F G E S A G G T S V S S L V V S P I S Q G L F H G A I M E S G V A L L P G L I A S S A D V I S T V V A N L S A C D Q V D S E A L V G C L R G K S K E E I L C N * T S L F K M I P G V G M G V F L A Q G T P R E L L A S A D F Q P V P S I V G V N N E F G W L I P K V I E D L I D N P E G K L G Q E R A S Q G V L Q K M L T L L M L P P T F G D L L R E V Y I G D N G D P Q T L P K R K F Q K M M A D S M F V I P A L Q V A H F Q C S R A P V Y L P T S S Q H Q P S W L K N I R P P H M K A D H G D E L P F V F R S F F G G N Y I K F T E E E E Q L S R K M M K Y W A N F A R W G N P N G E G L P H W P L F D Q G G A I T L Q L N L Q P A V G P G L * K A H R L Q F W K K A L P Q K I Q E L E E P E E R H T E L
826	8877	A	1768	2	288	C P N S S P G S A S E V G C A R S G Q S S L L R S L P R C D G W P W A E A G A M C A G R N L T S C S V G R Y Y S S R * Q D E E S * T A R H L L C A P Q T G H Q R R R P C R G Q R N F C H I P C
827	8878	A	1769	1017	1463	P R G P W S Q G E P K W L L A R Q A A G C C P P G A C L W G H S P A G A C S P L C A A K G S R Y S R V P A S S G T P A G K G W Q L L A R E G E Q E A G L C I E A S Q I G V P N S S P R K R P Q R * D V P D R G S P V C * E V F P R C D G W P W A E A G A S V Q G G T S P P V S F N R M T S A S T P N I W
828	8879	A	177	1	152	P G A M A V L L E T T L S D V V I D L Y T E E R P R G E A * A P L T C R R G P R A C L P T F P S L R

829	8880	A	1770	1	1181	MAAYKLVLIQHGESMWNPENRFSSWYN TDLSPAGHKEAKCGRQHSGLIGLNKAE TAAKHGEAQVKIWRHSYDVPPPLMEPD HPFYNISKDRRFANLTEDQLPSCESLKDT IAKALPFWNEEIVPQIKEGKQPKYPFEKR LEVVNHYFTTDDGYRIISARFGVPRTQV RTWVALYEKHGEKGLIPKPKGVSADPEL RIKVVKAIEQHMSLNQAAAHFMLAGS GSVARWLKVYEERGEAGLRALKIGTKR NIAISVDPEKAASALELSKDRRIEDLERQ VRFLETRLMYLKKLKALAHPTKKA AEIP RSTFYHLKALSKPDKYADVKKRISEIY HENRGRYGYRRVTL SLHREGKQINHKA VQRLMGTL SLKAAIKVKRYRSYRGEVG QTAPNVLQDFKATRPNEKWVTDVTEF AVNGRKLYLSPVIDLFNNEVISYLSERP VMNMVENMLDQAFKKLNPHEHPVLHS DQGWQYRMRRYQNILKEHGIKQSMSRK GNCLDNAVVECFGT LKSECFYLDEFSNI SELKDAVTEYIEYYNSRRISLKLKDYAS CLTVQLFGVSTLEGLSEEAIMELNLTGI PVVYELDKNLKPIQFLGDEETMRKAME AVAAQVEDEYNLYGDVTTVSSLTPEKL APEVKENVPERLNILLQVGGRSRTNLNR VRVPIHKHPSIRDPN SQASLNKLT DKMD SLWLKSKNRPKGPWKGE GAVKLFVSLE NAAKPVFLQPSQRRVPGNNGSWEFPS*S RKSGISIGAVKRPTH*GS*KASSIS*NAAY VSKKAESLSSSHEKGCGDTAQYVLLSSK GSQQA*QVCGR*KAY**DLSRE*RPRIPI* GNAVSSSRRETDP*P*SCSAPDGNPLT*SS D*GQAIPLLQRRGRANRP
830	8881	A	1771	362	551	DRLDPHSAAH*GAKSSPLAATSDQWHL ALSRRGSGSLYKCTEVKQMSNS*PASRSA CPPSPPR
831	8882	A	1772	2318	3200	FMPLHLDGGYCSPAEGFSSRYEHGLMK DLSRGSLSPPGERACEGVPSAPQNPQR KKVSLLEYRKRKQEA KENSAGGGGDSA QSKSKSAGAGQGSSNSVSDTGAHGVQG SSARTPSSPHTKFFPSHSSMSHLEAVSPS DSRGTSSSHCRPQENISSRWMGSHISRTT P/SKEGASPRSSEAA*G/SAQKGEPSP TWE SNITEKDSDPADGEGPETLSSALS*RSNSF TALSRYSYQT/PLAPFTGTPGYFSSQPHS GNSTGSNLPRRSCPSAASPTLQGPSDSP TSDSVSQSSTGTL
832	8883	A	1773	53	1025	GTRHLEAVSPSDSRGTFLSHCRPQENISS RWMVPTSVRLREGGSIPKVLRSSVRVA QKGEPSPTWESNITEKDSDPADGEGPETL SSALSKGATVYSPSR\SATSSCSVIVLGQN HKASFSRVPPSPEDIPTQSPGYSYRTTAL RPGNPPSHGSSESSLSTS YSSPAHPVSTD SLAPFTGTPGYFSSQPHSGNSTGSNLPRR SCPSSAASPTLQGPSDSPTS VFSFVPAQE L*ASTS/SSSEI/PRSSLAIRLTD*SVCPVLG QSAGYQGLQGICGFQFTALPHTVG VGFS TQYRIPSPLQGSRSQDSRRGLFLGLLGF GKQN
833	8884	A	1774	1	414	AENTILSLMFSGKSWGSLSSCEGALLPGT PTATRLQSLTRRSSLKRG T*GPQIPAARPR REGSRIGTCTSS*PGLRTEAHRSLRNRQA GVSSPFQLSPALKPRKSPSQATGQRP G*G QWGQKSGSALLPTNTTHVEA
834	8885	A	1775	1	458	ENTILSLMFSGKSWGSLSSCEGALLPGTP TATRLQSLTRRSSLKRG T*GPQIPAARPR EGSRISQNVGDGGKENRYRGFGGPPGT KSDPGHQHG*GGEGLWGSWRSKSGPAI ATGAIASPATQLLRVNPDTGDWDVYFLL TLVSGRLRTGA

835	8886	A	1776	1	1387	HSMGWKEHVDRGGHTKGMVFVSLQPA CWLPRERPFQLRLCLIEDPLRLCGQGR GRGQETTSGLILLSHVGTFLRDRWTLTSL WPCPRALLVFLSHSCEVMGAGAPGVSLP EGQLSPLPWLVGRSSRRAPDSGQGPLG PPGLADVSMRGRAPGTSMCGS/RSTPVPP QSPGG*VSMPATPGIGFLCRLPHKSAPEG P/GGFGFLFFIKHLKQHCSLPSRGLSITA STCVVLVGSKADDPFCPHCPHPGLTSS LRGAFSR/PSEQGRAGRGLESSRLSVSQG SCEASVLRPESRGSTHP/ISPVSGFTLRSW VAGEAIAPVAIAGPAGAGLRIGLRGALRP AHGHPRL*SPGNPISPSSTSPCLMPQGH CLPAGPPNPRCLSSFPPSPTLVLTNPASLS GPGCRDLGSLKSLKSNFCGSDSEAELL VGVPGRAPHSLLKLPQLFPENIKLRIVFS AKKKKK
836	8887	A	1777	46	591	LSPPKPQKQSQEQNPFCQWALGKQLGP PQGGQEG/QGPPDSLVLPGV/PPVPLFVG GNLPHPPPP/PQQRNKGRQTEGSCSPFF KGQHNS/PCGPQPS*AHPLRHGSGDQAQ PTSAP/PPCR/PES*PQADEMPTCCHNTG KALGPPSQEGMEPGGPQPGPSRSTQSSV AHLTSGTAVRPGLGSP
837	8888	A	1778	1412	1673	KRCPINRFPLECLPLPHLMGIPPEGHFHH PLMGE**NPPCSIQDPHCVTYFETPPVNL CPSTRPPEVGWEGGPSSPPAFEAPGLKG
838	8889	A	1779	646	1098	MVELLVTFPPFSQLQLYFQLTASFTELL KVPLMVLFGMPMKKHFLKPTVSDQW ENNRKLKRR/ISR*FSCRKV*VIAHCHKF CLVLREA/HMHWLILCAKKRF/PPLKKLT WLGMSVHTCNPSTLGG*GR*TA*TQEFK TSLDNMVKPHLF
839	8890	A	178	1112	2085	RHSHAVQKKPLSGGGAGAMAVLLETL GDVVIDLYTEERP/RCQLYGDQASFFAE KVPRIKHKKKGTVMVNNGSDQHGSQF LITTGENLDYLDGVHTVFGVTEGMDIHK KINETFVDKDFVPYQDIRINHVTILDDPF DDPPDLLIPDRSPEPTREQLDSGRIGADE EIDDFKGRSAEEVEEIKAEKEAKTQAILL EMVGDLPDADIKPPENVLFVCKLNPVTT DEDLEIIFSRFGPIRSCEVIRDWKTGESLC YAFIEFEKGGGAYGKTPATRPFGSWPF AGLLTCSFLRYPLILWITVLPPLSELPL AAAERPSAASQ
840	8891	A	1780	109	943	WAKLGKGAKR*PQALGASAPSALYPR HVAPARAPGRTKGAGSSCRNSPRQVVRP QPWQWGGGAQSDVSP*GQTPRGGSFER SSSCSGHTGLVGKERRPLSLEGP*/SPEDP PRARHGGPQGCREHPPWFSRPLCPEAGP EPRAPAWTSDSISGERSTGG/PSRPASKGP VPSAQRAQTGPNPEAAGSLSLPCRALP QGREAPQPQPPPYLPLKLERGILVFALSK IFKN
841	8892	B	1781	98	195	GLCLGQEVGQEDLVMQTLPGVGLGLDR DEEVTG*
842	8893	A	1782	2	1556	

843	8894	A	1783	2	1928	ARGAPRLRAAGAPSSSARVLSVSPSSPA MAALTRDPQFQKLQQWYREHRSELNLR RLFDANKDRFNHFSLTNTNHHGHLVDY SKN/LLVTEDVMRMLVGLWPKSRGVEA ARERMFNGEIKINYTEGRAVLHVALRE TGFKTHPILG*NGKDVMPENVKVLDKM KSFACQVRSGNLKGYTGQRPFTDVINI WIGGSDLGPLMVTEALKPYSSGGPRVW YVSNIDGTHIAKTLAQLNPESSLFIASK TFTTQETITNAETAKEWFLQVAAKDPSA VGEDFLFALSTNTTKVKEFGIDPQNMFE FWDWVGGRYSLWSAIGLTSIALHVGF NFEQLLASLAHWMDQLFRTDAPGRKNAP VLLALLGIWYINCFGCETHAMLPYDQYL HALLRTSSRAITWSPMGNTSPNLEPVWT TRQAPLCGGGQGPMAFMLFTSCIHQGT KMIPCADFLIPVQTQHPIRKGLHHKILL NFLAQDRGP**GGKSTEEGPKGASRVAG KSPEDFERLLPHKGL*KGNRPNTNFYVFT KIVTPIQLGAWSPMYEHKILRFRVWID NSF*PSGELELGK/QPGLRKLEPELDGSA QVTFQDVSTNGLINFIKAAARGPRVPINS VLICSLLCDSHFFSSLSFSPKPELIVP
844	8895	C	1784	127	435	MAASXNPEVLDITEETLHRSFLEGVRNV ASVCLQIGYPTXASVPHSINGYKRVLAL SVETDYTFPLAEKVKAFLADPSAFVAAA XLGCCHHSCSXCCSPS*
845	8896	A	1785	112	1161	RTAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNVGSKQMQQIRMSLRGKA VVLGMKNTMHAQAPFEGTL*NNPSLWR KLLPHIRGEFGLLFHPGRTLTEIRDMLL AQ*GCPAAARPGAICPHVKVTVASPRTL GLGPEKTSFFPGL*VSPTKNLQGAPIENP EVNVAESRTGDQSGEPSESHGWLNML NISPFLLWGWVIPARCSTNGQHSTKPLK VLGLFTGGKLLQFSAFLGGVSRKCLPSV CLPELAYPNCCNQYPDSIINGYKRVLAL SCGDGITPFPLAEKVKAFLADPSAFVCC CNLWVAATTACFA/AAAAAPAKVEAKE ESESEDEDMGFGFLFD
846	8897	A	1786	2	355	RSITCKTKEARMLLAWVQAFVLSNMLL AEAYGSGGCFWDNGHLYREDQTSPAPG LR\CLNWLDAAQSGLASAPVSGAGNHSYC RNPDEDPRGPWCYVSGEAGVPEKRPCE DLRCPGGRI
847	8898	A	1787	1	771	MLLAWVQAFVLSNMLLAEAYGSGGCF WDNGHLYREDQTSPAPGLRCLNWLDAAQ SGLASAPVGYCRNPDEDPRGPWCYVSG E/AGVPEKRPCEDLRCPETTSQALPAFTT EIQEASEGPGADEVQVFAPANALPARSE AAAVQPVIGISQVRMNSKEKKDLGTLG YVLGITMMVIIIAGAGIILGYSYKRGKDL KEQHDQKVCEREMQRITLPLSAFTNPTC EIVDEKTVVVHTSQTPVDPQEGTTPLMG QAGTPGA
848	8899	A	1788	48	375	KGLIKPFGHRTPERKK*LAQGRKQATGM ARAQLPDGAQHFTALC*QLSRASNL*C HTQEALAAPSHKASFSEPFHLPMGRRVN GAFYGAIWFGDLNLKWSSCGNDAG
849	8900	A	1789	6	902	LQGWDWEAEPPRGPRLNTRGSITCKTK EARMMLAWVQAFVLSNMLLAEAYGSG GCFWDNGHLYREDQTSPAPGLRCLNWL DA\QAGLASAPVSGAGNHSYCRNPDED RGPWCYVSGEGGVPEKRPCEDLRCP TTSKALPAFTTEIQGNVLKGPSADEWQ VFAPANALPARSEAAAVQPVIGISQVR MNSKEKKDLGTLGYVLGITMMVIIIAG DGIILGYSYKRGKDLKEQHDQKVCERE MQRITLP*SAFTSPTCEIVNEKTVVVHTS

						QTPVDPQEGSTPLMGQAGTPGA
850	8901	A	179	3	492	GGGAGAMAVLLETTLFYVAIFLYTEKR PRACGNFLKLCRIKYYNYCLIHNVQRDFI IQTVDDTTGTGRG*ESIFGQLYGDQASFFE AEKVPRIKHKKKGTVMVNNNGSDQHGS QFLITTGENLDYLDGVHTVFGVEVTEGMD IKNINETFVDKDFVPYQDIRIN
851	8902	A	1790	1	1995	LGRPTRPAPTFWAVAVRTRCLAELRRQE LMGALCYPPQGDRFLQKSWIFRPVMA DKLTRIAIGNHDKCKPKRRQECKKSCP VVRMGKLCIEVTPQSKIAWISETLCIGCG ICIKKCPFGALSIVNLPSNLEKETTHRYC ANAFKLHRLPIPRPGEVLGLVGTNGIGKS TALKILAGKQKPNLGKYDDPPDWQEILT YFRGSELQNYFTKILEDDLEAIKPQYVD QIPKA\AKGTVGSILDRKDETKTQAIVCQ QLDLTHLKERNVEDLSGGELQRFACAV VCIQKADIFMFDEPSSYLDVKQRLKAAIT IRSLINPDRIIIVVEHDLVLDYLSDFICC LYGVPSAYGVVTMPFSVREGINIFLDGY VPTENLRFRDASLVFKVAETANEEVVK KMCMYKYPGMKKKMGEFELAIVAGEF TDSEIMVMMLGENGMGKTTFIRMLA\GS LKPDEGGEVPVLNVSYKPKISPKSTGS VRQLLHEKIRDAYTHPQFVTRL**KPLQI ENIIDQEVQTLSSGELQRTVLAL*LGQN LPDVYL\DEPPA\YLDSEQLMAARVV KRFIPHAKKTA\FVVGWTFIMATY\AD RVIVFD\GVPSTKNTVANSPTLLGWA*I NFWSSAWKFTFQEELQTNYW\PRINKLI SLEDVDQKKSGNYFFLDD
852	8903	A	1796	1217	2829	GARSEAAEFQQSASCRRRLRGGGGPGTGP RGGALLASLLPPCRTPPDPPDGSCRCTRP LLSPLGKLSAPPRPRPLFVVAQAGHAPQ GLLPTSRPAAPATAGSRNMSTLLSAFY DVFDFLCKTEKSLANLNLNMLDKKAVG TP/VAAAPSSGFAPGFLRRHSASNLHALA HPAPSPGSCSPKFGAANGSSCGSAAAG GAVGGRRRTALLNKENKFRDRSFSENG RSQHLLHLQQQQKGGGGSQINSTRYKTE LCRPFEESGTCKYGEKCQFAHGFHELRS LTRHPKYKTELCTFHTIGFCPYGPRCHF IHNADERRPAPSGG/ASGDL/RPTSRTPPP PSCSSASSCSSASSCSSASAASTPSGAPT CCASAPAAAAAALLYGTGGAEDLLAPG APCAACSSASCANNAFAFGPELSSLITPL AIQTHNFAA\AAAA\YRSQQQQQQQGL APPRAP/APPSATLPAGAAAPPSPFQFL PRRLSDSPVFDAPPSPPDSLSDRDSYLSG SLSSGSLSGSESPSLDPGRRLPFISRLSISD D

853	8904	A	1797	731	2553	GARSEAAEFQQSASCRRRLRGGGGPGTGP RGGALLASLLPPCRTPPDPPDGSCRCRTP LLSPLGKLSDDPPRSPVIRGGSSPATPPQG LLPTSRPAAPATAGSRNMWTTLVSAFYD VDFLCKTEKYLANLNLNNMLDKKAVG TPVAAAAPSSGFAPGFLRRHSASNLHAL AHPAPSPGSCSPKFPGAANGSSCGSAAA GGPTS YGTLKEPSGGGGTALLNKENKFR DRSFSENGVDRSQHLLHLQQQQKGGGGS PDQIPTRYKTELCPFEERARAQYGEK CQFAHGFHELRLTRHPEVQDRSCAAP FHTIGFCPYGPRCHFIHNADERRPAPSGG ASGDLRAFGTRDALHLGFPREPRPKLHH SLSFSGFPSGHHQPPGGLESPLLLDSPTS RTPPPSCSSASSCSSASSCSSASAASTP SGAPTCCASAAAAALRLLYGTGGA*DLL APGAPCAACSSASCANNAFAFGPELSSLI TPLAIQTHNFAAVAAAAYYRSQQQQQQ QQQGLAPPAQPPAPPSATLPAGVAAVAPP SPVFSFQLPRRLSDSPVFDAPPSPDLSLSD RDSYLSGSLSSGSLASGESPSFDPGRRLP IFSRLSISDD
854	8905	A	1798	146	403	RKLDVYFEYEEKIMSKTTLDKSLLDIISD PDAGTPEDKMRFVLIYYISTQQAPSEAF TKMASAPASYGSTTTKPMGLLSRVMNT G
855	8906	C	1799	47	235	MXVXCNIQKXLVSYRAINRPDITDTEME TVMDTIVDSLFCFFVTLGAVPIIRCSRGN SSKKW*
856	8907	A	18	246	730	SSIMTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPE/RS*VFINSAGQKSADT GWSSSKPQN*QLSSTGAALPLASLSRER AWVDDGKHRLTTPMTVPQRAVQQL*E TSG**DWRQKVQIFQAVVGMIQPSHSQ FLQREDVIMLRPFGLHLSWEENG
857	8908	A	180	1	451	MGFRHVGOAGLELLTSGDLPASAYQSA GITDVSHCAQPASPLSYFLQALKHEFVV RHLTPGHLDTPDTKKPGHPDTQTLDT QTPSHLTSRHPDTQTADTQTPDTQWLT GPPDT*HPDTWHLTPDTQTPGHPTLRHP DTQIPRHPET
858	8909	A	1800	48	2100	PAPGLPVLPRVEVFLEEPGSGSWEPRWR RRRQRQQQQQPSFRKDSQLLSCVYCLS MCLILKTAQEHYPGRYSLMHRFGQDIFS PLLSVRELDRMGITLHLLHSDRDPIDV PAVYFVMPTAENIDRMCDLRNQLYES YYLNFISAISSKLEDIANASVRGLSAVT QVAKVWDQYLNFILEDDMFVLCNQN KELVSYRAINRPDITDTEMETVMDTIVDS LFCFFVTLGAVPIIRCSRGTAEMVAVKL DKKLLLENLARDARNSLFYRVDTLGAGHF SFQRPLLVLVDRNIDLATPLHHTWTY*A LVHDLVDFHLNRVNLEESSGVENS PAGA RPKRKNKKS YDLTPVDKFWQKHKGSPF PEVAESVQQELAESYRAQENDEVKRLKSI MGLEGEDEGAISMAF/SDNTAKLTS AVS SLPELLEKKRLIDLHTNVATAVLEHIKAR KLDVYFEYEEKIMSKTTLDKSLLDIISDP DAGTPEDKMRLFLIYYISTQQARS EADL QQYKKALTDAGCNLNR SRYIKQ*RAFT KMASA*AGYGSTTTKTMGLLSRVLNT GSQFVMEGVKNLVLKQQLPVT RILDA NLMEK\KSNPRKLM DYRYFDPKNACGG NDSSVPQKLKIPFRGHSFFVGGEENYI EYQNLCDYIKGKQGHILYGCSELFN ATQFIKQLSQLGQK
859	8910	A	1801	1	394	

860	8911	A	1802	3	536	RIYIFRV/PMA/CD/FSIRT/YTNADTPDDF QLHNFSLPEEDTKLKIPLIHRALQLAQR VSLASPWTSPTWLKTNGAVNGKGS LKGQPGDIYHQTWARYFVKFLDAYAEHKL QFWAVTAENEPSAGLLSGYPFQCLGFT PEHQGGSLKAAAGVPRHPDDSYGTSQEK WQLLKEKMFEPKK
861	8912	A	1803	192	2035	GRYLHPCFCLVDPLSFRDSGTPVVFSSN DPEGMEFSSPSREECPKPLSRVSIMAGSL TGLLLLQAVSWASGARPCIPKSGFYSSV VCVCNATYCDSDPPTFPALGTFSTRYGE /STRSGRTGWSLSMGPIQANHTGTGLLL TLQPEQKFQKVKGFGGAMTDAAALNIL ALSPPAQNLLKSYFSEEGIGYNIIRVPM ASCDFSIRTYTYADTPDDFQLHNFSLPEE DTKLQDTPGFHRLALQLAQRVSLASPW TSPTWLKTNGAVNGKGSLLKGQPGDIYH QTWARYFVKFLDAYAEHKLQFWAATA KNEPSAGLLSGYPFQCLGFTPEHQRFIA RDLSPTLANSTHNVRLMLDDQRLLLP HWAKVVLTDPEAAKYVHGIAVHWYLD FLAPAKATLGETHRLFPNTMLFAEACV GSKFWEQSVRLGSWDRGMQYSHSIHQ QTSWYHVVGWWTAGNLALNPEGVGNW VRNFVDSPIIVDITKDTFYKQPMFYHLGH FKQSSIPEGSSQVGLVAISQKNDLDAVA LMHPDGSVAVVVLNRSSKDVPITIKDPA VGLETISPGYSIHTYLWRRQLDGADYS RRHWGSAGAFKGTESAHTLSVTKEGTA GPV
862	8913	A	1804	113	1799	PSAYSYGRYLHPCFCLVDPLSFRDSGTPV LFSSSDPEVMEFSSPSREECPKPSGRVSI MAGSLTGLLLLQAVSWASGG/RPCIPKSF /SYSSVVCVCNATYCD/FPPTFPALGAFS RYKSRSSGHWMELSTG/PIQANCTGTGL LLILOPEFQKVKGFGGAVTDAGALNILA LSPPAQNLLKSYFSEEGIGYNIIRVPM AS*DFSIRTYTYADTPDDFQLHNFSLPEE DTKLKIPLIHRALQLAQRVSLASPWT SPTRLKTRGAGNGKGPLKGQPRDIYHQT WARYIVKFLDAYAEHKLQFWAVTAENE PSAGLLSGYPFQCLGFTPEHQRFIARDL GPTLANGTHHNVRLMLDDQRLLLPHW AKVVLTDPEAAKYVHGIAVHWYLDFLA PAKATLRETHHLPNTMLFAEACVGSK FWEQSVRLGSWDRGMQYSQSIKKLPV PMWVGWEPNW/ITPSL*NITQATRFNKQ PMFLPLANFSKFIPEGSQVGLVAISQ KNDLDAVALMHPDGSVAVVVLNRSSK DVPLTIKDPVGFLETISPGYSIHTYLWR RQ
863	8914	A	1805	22	424	ALGMAHITLFFFLLFCDSLALSPRLQC SGTISAHCNLPVPGFKQFSCSLSGSWDY RCMPPC/RWLTFFVLVETGFHHVQAGL ELLTSGDPPALA/FPKC*DYRRDPRAWA LFVFLT*FFSKLKYHKAKEKWS
864	8915	A	1806	14	253	LIPCGPQLFNCLSL*PGFWAMVKFAWVQ YVRSCLSGCLKESRSSCESGGDHHPL SSTSLPLSLFMLCKEVLELSGR
865	8916	A	1807	318	455	
866	8917	A	1808	1960	2150	CFVTSNLKCSK*GRAWWFIPVISTLWEA KVGGSLERSLRLQCAMIAPLYCSLGD VRPYLLK

867	8918	A	1809	2	1345	GVVPPGLLAGEGVCQLLRHSSPGRCLLK SRARGSVIMSRYGRYGGETKVYVGNLG TGAGKGELERAFSYYGPLRTVWIARNPP GFAFVEFEDPRDAEDALRGLDGKVICGS RVRVELSTGMPRRSRFDRPPARRPFDPN DRCYECGEKGHYAYDCHRYSRRRRSRA ENLRR*SP*Q*IWLTIGAPLRFKRNRTRLT TFPTRKIFLRQSSLTWLIWLSV*SSLD*RK HLDAAIGYRYF*IV*IY*TMGQRGSTCKL ARFMLNTHYSVLYYVMLSCNSAFNKSF FR**KKKYSTTNRPVYFQMRH*I*IVLR FDFSRGTQTLKNELLSLILFFL*LEK*ISRS RSHSRSRGRRYSRSRSRSGRRSRASPR RSRSISLRRSRASLRRSRSGSIKGSRYFQ SPSRSRSRSRSPRSSRSKSRSPSPKRS RSPSGSPRRSASPERMD
868	8919	A	181	143	647	LRSRCVQIQGSPATEPVSGSHCADTGLVI RGGALSAHAIPGQRLSHALHTASAYIN SGRMWDTVHLPQKRCVRPRPQGRVTRP RTRATH/NRVVGARRGTPQRYTG/WGRD *EPSLSQLPQNGDLLAARRREHPACSTG CTSGARVRSRVWRAGQALVPGCAGCAY ILH
869	8920	A	1810	1	840	VVPPGLLAGEGVCQLLRHSSPGRCLLK RARGSVIMSRYGRYGGETKVYVGNLGT GAGNGELYRVIR*YGPLRTVWIARNPPG FAFVEFEDPRDAEDAVRGLDGKVICGSR VRVELSTGMPRRSRFDRPPARRSFDPN GCYECGEKGHYAYDCHRYSRRRRSR FRSHSRSRGRRYSRSRSRSGRRSRAS PRRSR/SPISLRRSRASLRRSRSGSIKGS RYFPIPRRRSRSKIPGLFHGPRSSRSK\SR PSPKRSRSPSGSPRRSASPERMD
870	8921	A	1811	20	701	DHASGQSTASSGPDSVSGQLQPSQPNAD QGKLTMTMRIAIVICFCLLGITCAIPVKQAD SGSSEKQLYNKYPDATWLNPDPSQ KQNLAPQNGCVL*RNQ*L*TRITLPSKS NESHDMDD\DMDD\EGD\DDHVDSDSI DS\NDSD\DD\DD\DDSHQSDSHHS\DES DELVTGFSTDLPATEVFTPVPTVDTYD GRGDSVVYGLRSKSK\KFRRPDIKYPDA TDEDI
871	8922	A	1812	121	1206	LIAGSTHACAHASGRAQHRRDQTRLKAS CSLLSQPTKENSIPRELPIVCFCLLGITC AIPVKQADSGSSEKQLYNKYPDATWLN WLNPDPSQKQNLAPQ\TLPSKSMESH HMDDM\DD\DD\DHVGTARDSIDSND SDDVDDT\DDSHQS*WSLHHS*WNLDAE LVTGFFPTGPCPGNRSFSPVCSPTVDTY DGRGD\SVVYGLRSKSK\KFRRPDIQYP ATDEDITSHMESEELNGAYKAIPVAQDL NAPSDWANRGKDSYGTSLD*QSAETH R\HQQ\SRLYKRKANDESNEHSDCDW*A RTFPKVSRE\FHS\HEFSS\HGDFACL*PPK SKEEDNTPLEFRYSPGIRMWHFWGSI
872	8923	A	1813	171	459	
873	8924	A	1814	1	235	
874	8925	A	1815	292	1396	AQATGPYSRICACAKGAMAAS\CVLLHT GQK\MP\LIWSWGTWK\SEPGQVKA\AVK VLPLALGYRH\DCGVIYGNLEIG\EAL KGRTVGPGKAGCLGRKPGFVTSKLW NTKHHPEGMWSLPLRKDSGLTFQLEYL DLYLMHW\PYAFERGDNPFPKKCDWNI WLDSPHYKET*RALKALVAKGLVQA/V WGLSNFNSRQ\DDILSVASVRPAVLQV EHPITGLKMRLIA\HCQGTWAWR*TAF NPLGLPLNRAW\RD\DEPVPAGGNPVVL GIGLKKYGRSPSESCLRWPGPSGKVICI PKSITPFSNPFR\TFKVDF\TFSPPEEMNQ

						LNA\LNKNWRTVPM\TV\VDGK\RV\PKD AGHPLYPFNDPY
875	8926	A	1816	133	402	LLTSLVNSRILILFINSKKIFAIHIFSTRGGIL RITAVIWN\NNISVTHGNGDMALAQYSMP VPA*AI\GRRILV\MLYPSRTEAFEKFLIRC
876	8927	A	1817	356	463	
877	8928	A	1818	81	728	TRGPPPAEEMDEDGLPLMGSGIDLTK\VP AIQQKRTV\AFLNQFVVHTVQFLNRFS\T VCEEKLADL\SLRIQQ\AETTLNILADAK\LS SIPG\DDVT\VEVSPFKLS\SVTNG\AHP* RPLSE\QPQPEPVPPGLLDLQES*SIQAGN FL*L*PKDPRYARYLKMVQ\VGVPVMA IR\NKMISEGL\DPDLLERPDA\VPDGEIS EKTVEESSDSESSFS
878	8929	A	1819	1214	1565	LKEITDEM\YR\TLLHSHRIKM\VSPIFFS TNTV\FFPCYN\PFMNIQEMTKVTASRLF LFFVDLLQGVQPCFLCCCLCSIWFCNEH LDL**ASDFVMCMCVMHYI\TPIHV*YI HYIYVD\TY\MEVCIHLYII*CV
879	8930	C	182	225	335	MLARLG\SNSWTSSDPPTSASQTAGITGV SHRAGPLT*
880	8931	A	1820	1	1044	MAEKFDCHYCRDPLQGKKYVQKDGHH CCLKCFDKFCANTC\VECRKPIGADSKEV HYKNRF\WHDTC\FRCAKCLHPLANET\FC GQGQDPCNKCTTREDSPKCKGC\FAI VAGDQ\NVEYKGTV\WHKDCFTCSNCKQ VIGTGSFFPKGEDFYCVTCHETKFAKHC VKCNKAITS\GGITYQDQ\PHADCFVCVT CSK\LAGQRFTAVEDQYYCVDCYKNFV AKKCAGCKNPIT\GEKDCVKSEPPSL*S* EAPSVPRETLASHPV\SQRQPPGQASGWR EDLSLVGGGSL*KKSKLSSSSWPGFGK SSV\VAYEGQSWHDYCFHCKKCSVN\LAT KRFVFPQEQVYCPVCAKKL
881	8932	A	1821	235	1119	GPSSYKVG\TMAEKFDCHYCRDPLQGKK YVQKDGHHCCCLKCFDKFCANTC\VECRK PIGADSKEVHYKNRF\WHDTC\FRCAK\CL HPL\ANETFCG\GQQRSCATSCTTREG PPSAKGCFKAIV\AGDQ\NVEYKGTV\WH KD\CF\TCSNCKQVIGTGSFFPKGKDFYC VTCHETKFAKHCVKCNKAIASWGV\TY* DEP\WHAEGFVCVTCSK\KLAVQHFTTVE DQ*YCVDCYKNFVAKKCAGCKNPITGF GKGSSV\VAYEGQSWHDYCFHCKKCSVN LANKRFV\FHQEQVYCPDCAKKL
882	8933	A	1822	222	622	KCSSSKHFTKEDSQITNKHIEKCSS*LLV REM\QIITKS\VAIHQNG*NENTKQTCQ/ DIDNDMQWEFMR*EWANW*N*KTNW Q*LLRLDKCVS\YDPAIPFLDISP\TERHIY AYHKT\CIRMFKATLFK\IAPNI

883	8934	A	1823	75	1402	VRRRTLSSRRWHRLSHGPRWLPQVLTAS PPLQARGAFRSFPHSWGEDFLASLMFKI QLEPLKLRAWTLNGFVKFRNKETSAGPV AVMGKDYYKILGIPSGAINEDLIVCAYRT MALKYHPDKNKEPNAEEKFKEIAEAYD VLSDPK\KRGLYDQYGEGLKTGGGTSG GFRGF\HYTFYGDPHATFASFFGGSNPF DIFFASSR\STARPFSGFDPDDMDVDEDED PF\GALFGRFGFQWG*VGGPR\RAPGTIV TLGRQGC RDPPVVHEL RVSL E E IYHGST KRMKITRRRLNPDGRTVRTEDKILHIVIK RGW\KEGTKITFPKEGDATP\DNIPADIVF VLKDKPHAHFRRDGTNVLYSALNSLKE ALCGCTVNNPLFD\GRGIPLPCNDVIKPG TVKRLRGEGLPFPKVPTQRGDLIVEFKV RFPDRLTPQTRQILKQHLPCS
884	8935	A	1824	245	486	
885	8936	A	1825	63	1820	RVDKGGLAAGLRPLGRGSRACVREER EREGRLRGDFQPASLLSRGAINAPNFPAC LKEEEDLSKAMSQDGASQFQEVIRQELE LS\VKKELEKILTTASSHEFEHTQKKTWM DFRKL\FHR\FLQRKGAF\WNLGEKFQRP P*DSIQPYEKIKARGLPDNISSVLNKL VV VKLNGGLGTSMGCKGPKSLIGVRNENTF LDLTVQQIEHLNKT\YNTDVPLVLMNSFN TDEDTKKILQKYNHCRVKIYTFNQSR Y P\INKES\LYFPVAKDVSYSGEN\TEAW YPP\GHGDIYASFYNSGLLDTFIGEGKE YIFVSNIDNLGATVDLYILNHLMNPPNG KRCEFVMEVTNKT\RADVKGGGDNLSQ YGRANLRTWWEIAQVPK/AHHVDEFKS VSKFKIFNTNNLWISLAAVKRLQEONAI DMEIIVNAKTLDGGLNVIQLETA\VGAAI KSFENSLGINVPRT\RF\LPVKTTSDLLL V MSNLYSLNAGSLTMSEKREFPTVPLVKI RPV\LRKQVQD\YLKGFEEK\QNRLELDHL\ TVSGRCDHLEKNGFIKGEPIHPLQIHGD R\MDIPTWEPVFREPR\VSGNLRILDH
886	8937	A	1826	48	239	GRAETMSDIEEVVE\YEYEEEGQEEAAVE EEEDWREDEDEQEEAAEEDSEAEA*D/T RETRAEEDE*YEDASD\AEDGPMEESELK P\WS*RPNLVLP*VLI*FIVVYVDLHRLC ME*DE
887	8938	A	1827	78	357	
888	8939	A	1828	3	327	
889	8940	A	1829	1	429	RAEVALKKKKALSSMRAHYS\SYLAKA DQKRGKKQTAREMKKKILAERRKPLNID HLGEDKL RDKAKELWETLHQLEIDKF EF GEKLRKLYDITTLRSRWDSTSSSPHNP VRGSLTVLGVERPSRGVPRVCVLA AFIP WGL
890	8941	A	183	1108	1627	PMDQVMCRT*KG*MGQRDVSPTASEQ VSTARPGPRAVIDYSKADAWAVGAIA Y EIFGLVNPFGQGAHLESRSYQEAQLP ALPESVPPDVRQLVRALLQREASKRPSA RVAANGV\HLSLWGEHILALKNLKLDKM VGLAPPKIGRHVFGQTGSQEEVVVLETK NEDALFG
891	8942	A	1830	3	986	HTPATQSLANGLGRSNVTITRGCEPGA SACSRCCPQGAPALLTDPQKPPTFTMS DEEVEQVEEQYEEEEEAQEEAAEVHEEV HEPEEVQEEKPRPKLTAPKIPEGEKVDF DDIQKKRLNKDLMELQALIDSHFEARKK EEEELSALLERIEKRRAE\RAEQRRIRAEK ERERQNRL\AEKARRE\REDATRR AEDD L\KKKKALSSMGANYSSYLGPRLDQKR GKK\QTA\REMKKKILAERRKPLQPSIHL GERQN*GDQGQRSFWETLH\QLEDLTKF EFGEKLR\QKYDITTLQEPECRCWPES

						TSKEGLGPPAKGKV\GGRWK
892	8943	A	1831	7	1382	PPGLEARPAPARLAGSGVCSGGRGRGAG RRSRRQSMRGAAARAAGWGRAGQPWPRP PAPGPPPPPLLLLLLAGLLGGAGAQYS SDRCSWKSGSLTHEAHRKEVEQVYLPC AAGAVEWMYPTGALIVNLRPNTFSPA HLTVCIRSFTDSSGANIYLEKTGELRLV PDGDGRPGRVQCFGLEHGGLFVVEATPQ S/QDIGRRTTGQYELVRRHRASDLHEL GECPARSSSSSSSSSSSPARAANSHLK WRWSQRCLDVTLPDLALLSVRIL*RW WAAFQSLSRPGCFLTLPFFSAPCRPCSDT EVLLAVCTSDF/A*VSPRQLSSSSSSSSSS SSSSPHLLPRTAVRGSIQQVTHEPERQDS AIHLRVSRLYRQKSRVFEPVPEGDGHWO GRVRTLLECGVRPGHGDFTLGHMHFG EPRILRCAPKASRTFQRMV\DA\QERGL NPLVGWQRN
893	8944	A	1832	1	433	NNPDFKAGV\MALPTL\LQIQRHDDYLV MLKAIRILVQERLTQDAVAKANQTEGL PVALDKHILGFDTGDAVLNEAAQILRL HIEELRELQTKINEAIVAVQAIHFVHW KSKCHILGGGSPENWVCSRDLPLLIAFF FNKV
894	8945	A	1833	1	459	
895	8946	A	1834	2	1108	SFRSDSAPARPLAASPVPAPPAPPRFFSPG RPGDQSEKRWTFRRKLTGSSTTYSP FVFNRRDETEFRNFIVWLEDQKIRHYKI EDRGNLRNIHSSDWPKV\AEKYFKDVN CPFKIQDARQEVITIDWLLGLAVRLEYGR* WLKNTKDLVP**FQNLNDNATKNAEPF DPFWDVNNP*F*GLVLLALG*TWLQIRQR HDDFLVMLKANSQFWVQEP*PPGMP VCLRANSNKRGA*PVAFRQTHILGFD\TG DASSLMKLEILRIACT*EELRELTDQKS TKAIVAVQAIYC*SKRQDHRLGKSLEDE HFEDLQLLTYFRYMLGNHTLLACFGKSK CHNSRGEKSPEKLGYSRGRFYHHWLIAS CFFL
896	8947	A	1835	1	891	
897	8948	A	1836	1	984	
898	8949	A	1837	1	1917	
899	8950	A	1838	2	1411	FVGKGPRQAEDSRCGAGRRTGRTLGE QRACVWCVPKGRKVAKGGESEWVEGG EGREEKKVGGGPGGRVAAHSQPTGGS MRRVTLFLNGSPNNGKAGAGYGTLSL LSGGSSKPGIKATNVYNGKGLIDDIALI RDDDVLVCEGEPFIDPQTDSPPEGLLG FHTDWLTLNVGGRYFTTTRSTLVNKEPD SMLAHMFKDKGVWGNKQDHRGAFLID RSPEYFEPILNYLRHGQLIVNDGINLLGV LEEARFFGIDSLIEHLEVAIKNSQPPEDHS PISRKEFVRFLATPTKSELRCQGLNFSG ADLSRLDLRYINFKMAQFKPL*FAHANL C*ANLERTDLYGSVLDANLQGVKMLC SNAEGASLKL CNFEDPSGLKANLEGANL KGVDMEGSQMTGINLRVATLKNALKN CNLRGATLAGTDLENCDSLGC DLQEAN LRGSNVKGAIFEEMLTPLHMSQSVR

900	8951	A	1839	1	320	
901	8952	A	184	56	335	TGFCFFSRVKCNGTILGPCNL*IS/GSKYF SGL/SLPSKWDFRFPAPRPGNLF**TRF SPVYQDGFDFLTICPPLGLPKLLEFRGA PPLPSE
902	8953	A	1840	1	1430	MAAAEAANCIMELPRAFGIRPSGGSYP SHVEEGWGRFRPGPHVAAARPPRPG HTPWGVIDLGPSTMWGVSWEEQCFSAL YQPPSELRGHLLGYRTRFCAFWVSCGQA ESSEKPNADMTSKDYI*LTHTFGIHE EMLKDEVRTLTYRNSMFHNRHLFKDK VVLDV\GSGTGIL\CMFCCQGPWPRKVIG IECSSYSS*LWR*RCVQA\NKLPRRGTSI KGKGGRKVELPVGERWDIIHQRVGWGY CLFLTESMLQHRALMPRDKWLAPDGL IFPD\RAQLYVTAIRGTGRYKDSRSHLLG ENVY\GFDMS\CIK\DVPIKEPLVDVDPK QLVTQRLAFIKEVDIYTVKVEDL\TFNL PRFCPCKLKR*LTCTALVTLSTFEFTH CHKRTGGTGFFHQPPRSPYTHWKQTVF YMED\YLTRERRAEIFGTIGMRPNAK EQPGTLDFTIDLDFKG\QLCELS\CSTDYR MR
903	8954	A	1841	1	45	
904	8955	A	1842	2	580	GRVGGRVGCEPPAWIDIYKAAGRSSF E*ARKMSS*AAFRTSFVLGAIEDGCISTQ GSWGKVMRMHGPPEHPMRELQEMIDE VDEDGSGTVDFDEFLVMVMVRCMKDD SK\GKF*GRSLDLLPACFDQKMLDGYI DL\DELED*LLQATGRDPFTEDDDIEELM KDGDK\NNDGRID\YDEFLAEMKGVGVD A
905	8956	A	1844	2	368	
906	8957	A	1845	28	479	
907	8958	A	1846	4	458	
908	8959	A	1847	90	769	
909	8960	A	1848	231	909	HCSQHLPSSLWISFCFIIPANQFIFRLCTSEA MGKISSLPTQLFKCCFCDFLKVKMHTMS SSHLFYALCLLTFTSSATAGTGDGSAG AEL\VDALQVPCVEDRGFYFNKPTGYG LPAVRRAPQTGVVDECCFRSCDLRRLE MYCAPPAQCPSQLRSVRA\QRHTDMPQD PERKYI*RTQVEGVQETRRTGLLEDPPGG VKSDMPPQDPLLCTSYLLNFGTPTKK
910	8961	A	185	523	817	SQHSVGPRQADRLRSGVRDQPGQHGET PSILKIQKLPGRGGACL*SQLLSLRREN CLNPGGRGCSEPRSHHCSPAWMTE*DSI SKNK*INKNEIKKK
911	8962	A	1850	141	439	
912	8963	B	1851	851	1807	MAIKSIYAALRSIYHSEHRGLFSGLTAT LLRDAPFSGIYLMFYNTKNIVPHDQGP PLGMFLGQAIHKAQRSCKPALPGPEELP TQGNWK*
913	8964	A	1852	913	1375	SIFPGVVIEHLTLTFIYYHFIINRTSQGIDS QILSLFLFFF/CFETESRSVTQAGVQWR HLGSLQPPPPWFKRFCSLSLQSSWGYRH VPPHPG*FLVFLVGDGGFTMLGQGSQ NSCTSRSTRRLAQLFSQFKNCFKNC KSSIGLIPLYYY
914	8965	A	1853	1295	1679	KCINCKVYFTGVFFLIPTCQMQUIHIVCL CLVIISIHISFFYFIYFYDIIS*MCNL*VLLD YFNPLEITIHAFCIQFM**LIYL/CFKCILFC GFLGCFCLFLLKIYRF**S*FSFLKCIYS FYSLV
915	8966	A	1854	2	410	
916	8967	A	1855	3	322	

917	8968	A	1856	1	666	SGRDDQGRRAQCSAARCGRPSGGVMED ERSFSDICGGRLALQRRYYSPSCREFCLS CPRLSLRSLTAVTCTVWLAGYGLFTLCE NSMILSAGIFITLLRPLGVSPSVKNDQETL LUIDSLGIQMTSSYGSGKESTTFIEMGK VK/EIFVNNEAIYMVSI*KHKAIIYYLWNL FEKIPVVEPHGDIPKYVPVFQSAKPRLDC LIEVYRSCQEILAHQKATSTSP
918	8969	A	186	49	1357	RTPERCLREVKGATGWPECILT*QTIIPRP /YPSVGTAAASDTKKKKINNGTNPETTTSG GCHSPEDAQVQTIRILTCQKTELQMALY YSQHAVKQLEGEARDLISRLHDSWKFA GELEQALS AVATQKKKADRYIEELTKER DALSLELYRNTITDEELKEKNAKLQEKL QLVESEKSEIQLNVKELKRKLERAKLLP QQQLQAEADHLGKELQSVSAKLQAQVE ENELWNRLNQQQEEKMWRQEEKIQERE EKIQEQEEKIREQEEKMRRQEEMMWEEK EEKMRRQEEMMWEEKIRELEEKMHHE QEKIREQEEKRQEEKIREQEKREQEQA KMWRQEEKIREQEEKIREQEKKMWRQE EKIHEQEKIREEEKRQEQEEMWRQEEKI REQEEIWRQKEKMHVRTDEISVCSIFQGF ISVGLCKFAYPFDCFTL
919	8970	A	1861	20	465	VACCVRI PGPPRRSGPAMAVTITLKTLLQ QQTFKIRMEPDETVKVLKEKIEAEKGRD AFQNMQRQVIQQNPALLQQLGQENP QLLQQISRHQEQFIQMLNEPPGELADISD VEGEVGAIGKEAPQMNYIQVTPQEKEAI *RLKALG
920	8971	A	1862	6	448	
921	8972	A	1863	391	1610	VAMCVEIPGPAASLGPRHWPVTITLKTLL QQQTFKIRMEPDETVKVLKEKIEAEKGR DAFPVAGQKLIYAGKILSDDVPARDLFA FDGGRNFVVRWVTKTKAGQGYLQAP PGGPSPHSLPQSPLTSFPPCPHLQACSIPP LAGQRRHKSPSEESGPKTFPESVASGSVP SSG/SGSGREEDA\ASTLVNGAFEY*GR WLTEIMSMGYERERVVAALRASYNPN HRA\VEYLLTGIPGSPEPEHGSVQESQVS EQPATEAAGENPLAEFLARDQP/QFQNMRA QVIQEEPLRCCPALLPASWAQENPQLLT AKSARPPRSQFIQMLERSPPGEAWADIS DVEGEVGAIGEEAPQMNYIHGDARRRK EAIER*KALGFPESLVIQPYFACEKNED LAANFSLSQNFDE
922	8973	A	187	1	408	ASDRPESRATHASGKSPVFSDESDLD DISKLEQQSKVQNTGHGKPREKSIIDEKF FQLSEMEAYLENREKEEERKDDNDDDES KSSRNVNNDKDFDPVESDEDIASDHDE LGSN/EDDEIAEEEEAEESISEI
923	8974	C	1870	293	448	MXKTLOELRAHENEITXVRKVTFNGLN QMIVIGLPPSLTELHLGWQQNQQS*
924	8975	A	1871	1	475	SYIRIADTNITSIPQGLPPS/LTELHLDGK ISRVDAASLKGLNNLAKLGLSFNSISAVD NGSLANTPHLRELHLDNNKLTRVPGGLA EHKYIQVVYLHNNNISVVGSSDFCPPGH NTKKASYSVGS/LFKNPQYWEIQPSTFRC VYVRSAILQGNKYKK
925	8976	A	1872	1	636	

926	8977	A	1873	196	1274	IMKATIILLLLAQVSWAGPFQQRGLFDF MLEDEASGIGPEVPDDRDFEPSLGPS/V CPFRQ\QCHLRVV\QCFLILGLADKVTGI FSPLNTLLDLQNNKITEIKDGDGFKNLKN LHALILVNNKISKVSPGAFTPLVKV/EER LYLSKESA*RELPEKMPKTLQELRALED* /EFTKVRKVTFNGLNQMIVIELGTNPLKS SGIENGAFQGMKKLSYIRIADTNITSIPQG LPPSLTELHLDGNKISRVDAAASLKGLNNL AKLGLSFNSISAVDNGSLANTPHLRELHL DNNKLTRVVYLHNNNISV\VGSSDFCPP\ GHTPKRASYSVSLFSNPVP/QYWEUQH PTFRVCVYVRSAILQGNKY
927	8978	A	1874	248	1393	IMKATIILLLLAQVSWAGPFQQRGLFDF ML*DEASGIGPEVPDDRDFEPSLGPMCPF PLQCHLRVGGSDLCLEQMPKDLPPDT VTL\DLQNNKITEIKDGDGFKNLKNLHAL ILVNNKISKVSPGAFTPLVK\LERLYLSK NQLK\ELPEKMPKTLQELGAHEEWDHQ KWRKS*LFNGLNPMIVHRNWAPIPLKSS \GIENGAF\QGMKKLSYIGIAD\TNITSIP QGLAPPSHTKLHL\DGKQKSSRVDA\ASL KGLNNL\AKLGIEFSNSISAG*TNGLSGP TRPHLRELHLGQQQALPRVPWWGWAE H*VHPRLS*PFITNQYL CRLGSSDF\CPPG\ HNTKKASYSVSLFSNPVQYWEIQPST FRCVYVRSAILQGNKY
928	8979	A	1875	81	137	TMAFPAGFGWAAATAAYQVEGGWDAD GKGPCVWDTFTHQGGERVFKNQTDGVA CGSYTLWEEDLKCIKQLGLTHYRFSLSW SRLLPDGTTFINQKIDYNNKIIDDLK NGVTPIVTLYHFDLPQTLEDQGGWLSEA IIESFDKYA\QFCFSTFGDRVKQWITINEA NVLSVMSYDLGMFPHARSHFGTGGYQA AHNLKAHARSWHSYDSLFRKRQKGMV SLSLFPARLEPADPNSVSDQEAAKRAITF HLDLFAKPIFIDGDYPEVVKSQIASMSQK QGYPSRLPEFTEEEKMKIKGTADFFAV QYYTTRLIKYQENKKGELGTLQDAEIEFF PDPSWKNVDWIYVVPWGVCKLLKYIKD TYNNPVIYITEDGFPQE*PSAFWMDTSTL GSIFRQTFQELFKAIQLDKVNLQVYCAW SLLDNFEWNQGYSSRFGLFHVDFEDPAR PRVPYTSK*YAKIIRNNGP*RTRGAWLL WPKGALLAAEDPSRQLLKPWLSLQDL DGRQPLQLIK
929	8980	A	1876	243	1126	FQRLYRAARRFTMVKIAFNTPTAVQKE EARQDV\EALLSRTVRTQILTG\KELRVC HPGKKEGSSGEMLWFTLFRFQFILG\GL YLFGGACIYK/YTFMPKRHHFTVGEMCF FDESDPANFPFGGGE*LSCLVT*/EADI REDDNIAIDVPVPSFSDSDPAANYFMTF EKGMTAYL\DLLGNC\YLMPLQYFYL LWPPKKIWVELFGQTGRVGRYLPQTYV VR\EDLVAVSRKIRDVSNLGIFYQLCNN RKSFRLRRRDL\LGFNKRAIDKCWKIRH FPNEFIVETKICQE
930	8981	A	1877	985	1401	DFA*V*RDRVFKGTCTFLV*WFLKFFF KMEFLLPRLECNGKIHCNLLLMGSSNSP TSASQVAGDYRHVLIWFLIEMEGFPML VRAGLKLLEYLEWIGSAF
931	8982	A	1878	184	481	SPRCNPSPLPQAFQSGDCPLPCTAAGL MCWRSAREPCLLPHCLPRVWHRDP/ CSQPTSQG*TEALPILCK*KPPPWPQEIS PSQWIHQSPADPAL
932	8983	B	1879	148	194	XNILSVIAVRKLFTAAX*

933	8984	B	188	1	1995	MSKETRQSKLAEAEQLTDHHPQTNPSV GTAASDTKKKKINNGTNPETTTSGGCHS PEDEQKASHQHQEALRRELEAQVHTIRIL TCQKTELQMALYYSQHAVKQLEGEARD LISRLHDSWKFAGELEQALSAVATQKKK ADRYIEELTKERDALSLELYRNTITDEEL KEKNAKLQEKQLVESEKSEIQNLVKEL KRKLERAKLLLPQQQLQAEADHLGKEL QSVSAKLQAQVEENELWNRLNQQQEEK MWRQEEKIQEWEEKIQEKEEKIREQEEKI REQEEKMRRQEEMMWEKEEKMRREQEE MMWEKEEKMRRLLEEMMWEKEEKIREL EEKMHEQEKIREQEEKRQEEKIREQEK RQEQEAKMWRQEEKIREQEEKIREQEKK MWRQEEKIHEQEKIREEEKRQEQEEMW RQEEKIREQEEIWRQKEKMHEQEKIRKQ EEKVWRQEEKMHDQEEKIREQEEKMW RQEEKIREQEEKIREQEEKIREQEEKIREQ EEMMQEKEEKMGEEQEEKMQEKEKMRR QEEKIREQEEKIREQKEKIREQEEKIWEQ EEKIREQEEMMQEKEEKMWEEQEEKMCS RKRRCKNRRRKVVFARIIQRYLLNHIIR NRKSVQILVLSCSDFLNSKNSHLLPDTL MLEDKAYLQIESCLIPNEEEYQYLAE*
934	8985	A	1880	2	1508	PESVGGGKTLQEEKQLQPCMQMDNRL PPKKVPGFCSFRYGLSFLVHCNVIITAQ RACLNLTVMVMVNSVDPHGLPNTSTKK LALDNINPMYNWSPDIQGIILSSVTSYG VIIIQVP/VLGYFSGIYSTKKMIGFALCLSS VLSLLIPPAAGIGVAWVVVCRAVQGAA QGIVATAQFEIYVKWAPPLERGRLTSM TSGFLLGPFIVLLVTGVICESLGWPMV IFYGACGCAVCLLWVFLFYDDPKDHP CISI SEKEYITSSLVQQVSSSRQSLPIKAILKSL PVW AISIGSFTFFWSHNIMTL YTPMFINS MLHVN KENGFLSSLPYLFAWDL/CGNL AGQLSDFFLTRNILSVIAVRKLFTAAGFL LPAIFGVCLPYLSSTFYSIVIFLILAGATGS FCLGGVFINGLGYCSPDILGFIKACSTLT GN**GGLIAS/TLTGLILKQ/DPESAWF*N LQSLMASPLMVTGP*FHPYRLPTARNS RDWAKEKQHHTSPEV
935	8986	A	1881	90	458	HFSRGYLEAFSEISNIRFVPPHSVTVVVV FGACFLCILGIWPPWACLPGPGGEGSGGF GEGRGSEAGRLGSVELTPATLPLQAPEA YPVFEPVPPVPEAAQGDTEDEGAPPLK RICPNAPDP
936	8987	A	1882	15	796	PGSTISWRPGLARSLSPDGRPRRGLGP GPSASMAGRTVRAETRSRAKDDIKKV MATIEKVRKWKRWVTVAAATPFRILNW VAIVVDPQEEER/RREAGGAERSRGRE RRGRGASPRGGGP/LILDLNDENSNQN FHSEG/SLQRGTEVSPGGTPK/PNRP CVTL PDPPEGGP*EGLSPPR/LGQEERS SPGGITV GSTYEPP/MLTKEEPVPELLE AEAPEA/YP VFETVPPVHETAQGDTE DEGAPPLKRICPNAPDP
937	8988	A	1883	566	831	ARSFLLITILIQRTDWRKNKFFPSNFP SNL RTNFDQFLKETILRKH/RVGLGVLAHT CNPSTLGGRGGWSP*GQEFENSLTNMVN HFS
938	8989	A	1884	534	1835	GSSYMHFQGEVWIAQCFKKLHRGVCVC VCL/CLYTHICIF*YITKAILMNY/ACI*KN SCHLAHRFVCMCIYICMYVWCGYIVLKI TQ*CMY
939	8990	A	1885	60	395	
940	8991	A	1886	1	193	FRLARGENLEHLRNKTEDLEATSEHFKT TSQKVARKFWWKNAMIVL/VFIILFIV LFATGAFS

941	8992	A	1887	1	280	
942	8993	A	1888	1	396	
943	8994	A	1889	85	410	DMEEASEGGGNDVRNLOQSEVEGVKNI MTQNVVERILARGENLEHLRNKTEDLEK PTS\EHFKT\TSQKGGSEKFW\WV\KDD CPLICRDCF*SSLLQLWLFAITGAFS
944	8995	A	189	386	1321	RTLERCLTEVGKATGWPCILTYARRSL APVLLGSH/HGRGLQTPGKLWSWGKSEE QECEEDGSETETGGQEDLEDLQEEEEVS DMGGDNPEVGKKARNSSKFELRKSPVF SDESDLDLFDISKLEQQSKVQNKGGQKP REKSIVDDKFFKLSEMDLYLENIHKR*E ERKDDNDDEL RDSPPQTSPSVGTGATDT KKKKINNGTNPETTTSGGCHSPEDAQVH TIRILTCQKTELQTALYYSQHAARQLEGE SRDLVSLHDSWKFAGELERALS AVTTQ KKKADRRQTGAESAAVGELGDTGDTV SEHWT
945	8996	A	1890	122	975	AARPTRHLCCGQQGQVLVCGPSAVGRL PLQWGLGLGPTMSSLGGGSQDAGSSSS STNGSGSGSGSPKAGAADKS AVVAAA APASVADDTPPP\GVGTRAVSSVSPSTRA CA/GSRPLSHYSSFGSSGGSGGSMGG ESA*QGHCGCSRGLPVGQWA*PGGGHG GGQKQPYLKAQKWCCGQPAEQGRAGH GAGSRGTADAAAVFAVHRDAEARGAG ASPADERGGLLACLDMEAVAGAEALNG QSDFPYLGRFPHSTQGLLSLLTPAGVVS WAEKRAAHGRAWA
946	8997	B	1891	1	8736	MPGQILVKAQQLFQQKAKSFHRMVLEQ LGIYWETNKPFPHPITHENEFEMNHRG ECKTKNYKTSRRKYRRTSLTPRGQQSFL RIQKIGQRYLQYIYQAKASNPECTKNSC KPKDKQPDNMGKKTLES DKEGLRPKA PIPADPVAGRTLIGKEHVPILWGGVLAS GTSCSLSPAGSPVHPTTLRDHQLGPPQPL WSCLELQPHQTHNKFVGRGGAKERDRN LARACPPLSQGQWQRPGLNTTINIPAGE NLNL
947	8998	C	1892	377	463	
948	8999	A	1893	753	3000	KLEPCGGTPGPRAGSGPCQDPHIPPEGVG GSPDGP GAWPAPNTHSASWSWGPHEC PPPA*AADCRGTDRESVPASPVCPLSPNS QRPPHLEAPGYLPGGSSRTQPAV/PTCSP PGIP/AVPALCP*PG*KTT/PIYTEAGKLAT SAPGT/PPRQLSPGNAVYCLPPDHTHTQPG RAGLAESAPYPEAQPAVGQEGDAGTE/ PGPSCQTQH*PPQEPLLGPFPQL/PPTSQQ PEGGALHSWPQRWPRKFPDP/PL/PVRP VWSAKPWNT*RRSPPGAPSPTRTAMGT TTPCPRSPDSKHVPLALPGAP/VPAQILD LLPRQALRTEPSAPEPLAGYGDSPWLCG MAVSTGPVLPWLRNGPRTNHSC/CRSRN FASALHGAAIPSKSFIRR*WGRTP*PAGC PF/PGLGIVPRSTSSAPTQLGSGNVA VVG HVRVLPSFSDGFLQPMSSSGSLAQQSV WASLGSEQQVPMPLPPASPGTPAARAGP VQFEQCLLQSPTWKPYP/PARAFQAVP*S RMVCPEAGPRSQQ/PA*QPPGLPPPPAT RVG/PPDVKGRGRLGSPGRPA/PPACMSP EQLPIGPLLAWGLQDARPAGAGGRAFE* PPGGSSQRFPSPGT*EAE**QF/VNGDGPA PTFSCPMGKPASPCPVRAVPPALPDVLT GNTAALGGSCLKAFGNLQPSLDNS\VP*\n LLEGPTQPPTTSAPKECSSPTMPGV GPWVTGTSGRPTFLSPFFSYEEHFKVLLF KEITVQQAEDGFHHRFPFRNKQ

949	9000	A	1894	3	576	LTRIPFLGAKYAPVIFA/EGA/YQ*QRS*T EIQMACFKQATRWWKC/DPRHGKYMAI CCLLYRGD\VF PKDVNAAIATIKTKRSIQ FVDWCPTGFKVGINYSPPTVVPGGDLA KVQRAVCMLSNTTAAIAEAWARLDHKFD LMYAKRAFVHWYVGEEMEEGEFSEARE DMAALEKDYEEVGVDSEGEEGEEEGEE Y
950	9001	A	1895	58	1636	LVGDGNPGPGVCSCRLRLIPYPLCGECI SIHVQQAGVQIGNACWELSCL*HGIQPD GQMPK*PKPLGEGDDSFNTFFSETGAGK HVPRAVFVDLEPTVIDEVRTGTYRQLF HPEQVITGKEDAANNYARGNYTIGKEII DLVLDRIARKLADQCTGLQG\FLVFHSF GGGTG\SGFTSLLE\RLSVDYWQESPSL EFSIYPGAPRFPQPVVEPYNSILTTHT\TL EHSGLCPSWVENEAIYDICRRNLDIERPT YTNLNRLIASQIVSSITASLRFDGALNVDL TEFQTNLVPLRHSTSLRPTYAPVNPPS* EKPTHEQAFCRRSPKCFEFPSQPRWL KCDPSPMGKY\MAC\CLLYR\GDVVPKID V\NAAIAHPSKPKRSIQFVDWCPTGFKI VAINYQPPVTVVPVGDIAKVQKTV\CM SNTTAAIAEAWARLDHKFDLMYAKRAF VHWYLG\EGMEEGEFKAREDMAALR KDYEEVG\VD SVKG\EGEEEGKILIIHSL FGPCSMSCSQNFSLTDRR
951	9002	A	1897	2	350	SQVDR*QSEPEIRICREDHMERLQAFDA NSRKQEAWEKEAIKELEEWYARQDEQ LQKTKANNRVAEKLSTNNPSLT*LVMS EEAFVNDIDESSPGTEWERVARLCDFN KSLD
952	9003	A	1898	2240	2492	
953	9004	A	1899	1	906	ATAVVS VGR LVFVSTGCVRAVQLPAMA ELDPFGAPVAGAPGGPALGNGVAGAGE EDPAAFLAQQESEIAGIENDEAFAILDG GAPGPQPHGEPGGPDV DGV MNGEYY QESNGPTDSYAAISQVDRLQSEPEIRK WREEQMERLE\SLDANSPEKKQSWKEK IAKGA*KEWYARQDE\QLQKTKANNR VADESFLQTTLR*RDWLCHKHKPSLLQP RTGQPEEALFKIDLEGLSPSNEWERVAR LCGL*PPSLSKQA\KDVS PHGASVLI\SLK AGPRWGHLKSHPVETLHLQYLNPTQ
954	9005	A	19	12	288	FGGGYIPTWGKGEGILELNDHISREFC SAPALASRPPTPPPLLPPT/PPLPAPRSPA DATPRRVGGPLR*ALKPRAPGPGWSRRR CRSWW
955	9006	A	190	792	1061	GSGV*DQPGQHGKTPSLLKIQLAERGG GHL*SQLRRLRQENHLNPGGRCC\SEPR LLHCTPAW/VNESKTSSQTNNKISQEW CVPIVL
956	9007	A	1900	29	852	PSRSLVRVVEFAPQRWLPGVVSVGR LVF VSPVGVRAVQLPAMAE LDPFGAPAGAP GGPALGNGVAGAGEENPAAFLAQQES EAGIENDRAFAILDGGAPGPQPHGEPA GGPDV DGV MNGEYYQESNGPTDSY AISQVDRLQ\SQPESIRKWREEQMERFG KPF DANSRKQEAWEKEAIKELEEWYA R\QDEQLPENQKANNR/AQTEARPL*NDI DESSPRPLKWNGWPRAV*TLNPPKS*A KQAQKMSPPHDASVLILPLKAGPRWCH
957	9008	A	1901	1	585	

958	9009	A	902	2	537	GTLRRDFNH ELSLLVKKKKRLRVDT MLGQQKRNWPTRSGLFGSHVQDHDQG VLPLGFFPLPRMRVLCMPHFQSTVVIPGR MGSSLLKTRNFLGVKNTARRVRMRPGC CLVQYPQAQKDELILEGNDIELVSNAG LIQQATTV*KQGISGNFLDGIYVSEKGT SCRLMNKI
959	9010	A	1903	560	898	KCNTECFGSLMHFVVVLFIIIFLRQQGR SVTRLECSGAILAHCNLRPLGSLNSPAS ASRVAGTTGTCYRIQLIFVFLVETGFHYV GQAGHKLLT*VIHPPQPPKVLGLQV
960	9011	C	1904	224	379	
961	9012	A	1905	1249	1642	LGCYPGPFHPVKWMIFPDPCEISVTGVC VC/G/GVCSGCVCG/CG/CGCLPGGKGICK YI*ICSQIL
962	9013	A	1906	415	656	SLPRSPLGRGTPSPQHLSSNLNLASLYHP HEITPWIFSSSGSSI*TP/TPSFYPSPTNCD PQIFDPQTPVSGCRLASSQGPSLSNPTS SGPQIPFASYPCLLLAPHPSLPASRPQSCP SPKTWAPPS
963	9014	A	1907	1	417	TISWNTGPRARSRARGSSSTGLDGCVGGG SGGNSGLPCPDLEPLGGLQSKCRLCAPT EARGLWS/KVPLFRQVRHLALHACGCRE AWPPPGPPPLLVALCFHLKALPSRGSRA GREAVSKHLKFAMLAGGRVCGSRRVLS M
964	9015	A	1908	1	438	QCTPSSAADCELTACYGFSS*PS*GPSPL PWRPRMCESWVLHLPPTPQCFSWDIGPS EVMVRPLGWDTLRGSMPLW*GAGERA GKPLPAPADASPHRSGTGFDRAAGGRGR RRCNRSEEGVIPFAAPRLPPHAFWRVFP HWETT
965	9016	A	1909	113	704	
966	9017	A	191	2	343	LLFFFFFFEMESCSVTRLECSGVISAHCKL C/LPGFKRFSCSLPSSWDYRRM/PPRLA NFLYFVEMGFHRVAQAGLKLLSSGNLP ASA/F/PKY*NYRRDDASLAACSTFLGLG LLWV
967	9018	A	1910	317	470	NYPMSVVPQD\MWRKSHAA/HILREMSS KITAACL*WNNAYFGSSKGLSCVWP
968	9019	A	1911	147	850	MAASGAGAEVSGR*GREPPALPPAP/CG P\RRRRSP*LPKTYRFFSLWQGRPDRSS AP\GNSGLPCPDLEPLGRAARSKCRLCA P\TEATKACWK*GPSCFRQVRHLALHA CGCR/EG/LGLPQGPPTSAGLLCAFTLKA LPSRGSPCKEELASSTNSHAGCGRVC GSRRVLSML*FSGLKLPLSVVPQDM*RK SHAHLR\EMSSKACRSFADGNNALFLE VSKGLSCVWP
969	9020	A	1912	119	1001	GSRTKGRAVPECACAPVGAGEGRPAGV AVSDGVIVFNDMKVRKSSTPEEVKKR KKA\VLFLP*VRTKNNILVEEGKEILVGD VGQTVDDPYATF/VSKMLPDKDCRY\AL YDATY\ETKE\SKEDL\VFIFLGPPEAP PLEQNGFMPSSQGRPSKKGSWTGDSSE FAKPNCLPKEGQGTACTLAREAGGQVP VYSPGRAKPFVSPFWPPCLGASGSPQHL APWGFAGCPPFLQRPRAWGGSPAGGG EIPLNPSCPQTPPNPPGNFSPSNPLDGF WPFPKLLFESFDSSWG

970	9021	A	1913	361	1785	LPLPRWKVLLPRDILGPRKINEVSSDDK DAFLCEQTSQDILKKTSEVVKSSPLGVTP LFMQSNVINSTAIVKTLAATGTGFDCA KTDIQLCAESRGVPPERIIYGKSFVKQVS QIKYAANNGVQMMTFADSEVELMKVVA RGTFPKAKVWVLRIATDDSKAVCRLSV KFGATLRTSRLLLERAKELNIDVVGVSF HVRSGCTDPETFVQAISDARCVFDMGAE VGFSMYLLDIGGGFPGSEVDVKLKFEET RP*STQPLDKYFPASN*KS*LEPGRY YVASTFDALQLISFAKKICIKRNQTGS**P KIESELSRPLMYVYVNDGVYGSFNCILY DHAHVKPLLQKRPKPR*RRYSSSIWGP TCDGLDRIVERCDLPEMHVGDWMLFE NMGAAYTVAAASNVPMLPRGPTIYYVM SGPAWQLIQFQNP\GFPPGSRROPGCP APCPVFCAWESGMKRTRASPVPSPG
971	9022	A	1914	501	746	ARSSLVLLFIYIFRDRVLLCHSGWSAVVQ SWFTAALISQA*VILK*FSHLSLPSSWDY RQVSPHPANF/SYILFCRDR/SFTMLPRVG WNSWAQVLLLIQPPKVLQL*AGCHGSCL
972	9023	A	1915	156	166	VLFLKRPYLVDQAVLWLFTVAISHSTLEL LGSSYPTTSAS*VKHSNSNIMKFKVPVLN ECTMQLGKTMIKVLVKSYP
973	9024	A	1916	452	1017	SLHGISRPHLPTGRLLGPETCAGFSRFGQ NESLTPFVTSDRISKNR\KRHFKAFFPHFE GKIMSSPLSKELRQDVQLCGSDARS*KD DEVQVVRGHL*GSAKLAKVVQ\YVRK KYVIYIER\QREKAINGTTVHVGHFTPS KQVVIT*G*NWDQRPKRSLRTGKPKSR QVKGKGRGKYKERTIEKMQE
974	9025	A	1917	3	474	
975	9026	A	1918	1	246	
976	9027	A	1919	373	560	SQLKNAKFNLRLPPNVY*DKGQYVTS QLYQNAAQPIFKQAFETCAHHTNTIQD QAPRRI
977	9028	A	192	2	447	KEEIIPIL*NLFQNIKAEGILRISFNARITL I/PKPN/RAITRKINPIDQSLMDRHAELNK ISAN*IR*RMKRIIPHGQVRFS*GMWGW NIRKQINVIHHTSLKKNHMIISINAEKE FDKIRKLLKLRLNIYKRG*LT**VMVRNS
978	9029	A	1920	837	1441	IFFFHLSPSHSHARSHFLFAIMNRPAPVEI SYEDMRFLITHNPTNATLNKFTEGT*GS MGVTDGFGVCGWLHMDKAPVWKKE GFHVL\DWPFDDGSSTPLIQVIGWIGFK PV*KTKFSCKSHGCCVAVHCVGRVGE APVL/VLALALDWNVGMK\YEDAVQFIR QKRRGAFNSKQLLYLEKYRPMRLRFR DTNGHCCVQ
979	9030	A	1921	2	1059	GRVGFFAGNPGSDSFGGLLGLTPVLR WVADGGTIPKRHELVKGPKKVEKVDK\ ETELVAQWNYCTLSQEILRRPIVACELG RLYNK\EPVIEFLDKSAEKALGKGSISH* NALTNC*QS*KLSDNCPGKGIGKNTKG DK\HDDLQAGASFI/CP/LVGGPGRWNGR HRFLLPSGGCGLCCFS*AEPWKEIKAFC HTCGAGLSRMMIIVLNGTKEDVDVLKT RME/AEKAVERSFKRISKPKAAESVSKT QMSVEGSPRAHQKLPGKP*RSPALDSR EKKTNLAPKSTAMNESSGKAGKASVW SHKEVHR*PVKNRKPNSLFTTHSFRQS APKEGVCPTGVHPTRPTCF
980	9031	A	1922	272	467	
981	9032	B	1923	131	268	XFVTCPNEKVAKIARAVVEKRLAACV NLIPQITSYEWKGKIEEDX*

982	9033	A	1924	2	353	GSPPTQPSPASDSGSGYVPGSVSAAFVT CPNEKVAKEIARAVVEKRLAACVNLIPOI TSIYEWKKGIEEDSEVLMSVHPYEVAEV IALPVEHGNFPYLQWVRQVTESVSDSIT VLP
983	9034	A	1925	70	357	
984	9035	B	1926	120	839	MSGGRAPAVLLGGVVSDRPRPAPSGPRS LDRYPHPKSQRRFAKEIARAVVEKRLAA CVNLIPOITSIYEWKKGIEEDSEVLMMIK TQSSLVPALTDFFVRSVHPYEVAE*
985	9036	A	1927	259	935	GASLLLSFVWMPALLPVGLPAFLFANPE SLLTMG/SLGSPSPSPRSPASDSGSGYVP GSVSAIAFVTCPNEKGSPEIARAVGGR RRLAAACVQPSSPQITIPSMKWKGKDSR EDS*GCWMDGFKTQKFPWVPSFWTDFV VRSVAPYEVAEVIALPVEQGNFPYLQW VRQVTESVSDSITILAMMSPVPAHEDP RDTSKAFLTQVMTWAPNKSRLWVKKK KKS
986	9037	A	1928	285	476	LLKHLINMMVSKTTWLGVLHTCNPS/ TNFLGGRGRIS*QEFESLGNMGRPC LYKNRQKTN
987	9038	A	1929	218	602	NGGQAVAHACNPSTLGGQWRVDHLRS GVRDQPGQRGETPSLLKIQKLAGRGGAR LWSQLLRRLRQENRLNLGGGGCSEPRW HHCIPAWGNKKE*NGNYAQRMGERWL TGLKHQRNGEDRTVRELSGR
988	9039	A	193	128	363	VHTWMLSSP*GPQPGVFHAQIRGCPFLSP *RICQFQVFSLFYFDLLWVFTILFFLEAE YHFVARLECSGLISAHCNLC
989	9040	A	1933	2	355	TSMLGCTVFLR/YCVYSVCNVLATVW SSLV*RSRLICLHLVS/WSFVTDCKACYN TGMLFYSDY**FVYYF*YYCFFLCSLFFSI CLLMYFNIFFF/CNFMFDCYILLLSFYFIIL YHYF
990	9041	A	1936	139	782	GLHHGCSLGMEEAAGRGDRSRSRCRAP QHHRPPPLSCQPRLGEAGRGVVRGK HGSL*KQAPPPRGAETPGLANHTLPPR VPP/SEGQHPREGQGLHGGPGEKGKPH RRKLKASVPCVSAERVNGPKGSSLQTAR IHPTGGHRKPTGAVCVCACAAHTSAAR GPLRPHHTACPAHVCTRRCRREHTPPSL CTRVPLSGPGGSSLLHVLSRA
991	9042	A	1937	1	1878	
992	9043	A	1938	345	557	LYMLIRMRLKEGRAKMVESIFR**FILE* SVLS/RIMKPGMYPVLNRWVKCGNSSSV SYPEEKVVGWLLKFI
993	9044	A	1939	345	511	ARDATFVNGLDYLTLPYCGWKDCKKK CPLRQFP*PFNCCFFLVVFVRV*KHSLP
994	9045	A	194	233	598	
995	9046	A	1940	827	2660	
996	9047	A	1941	478	1150	SMPWQIGRSSVSAPPTITPTSSTASWTIVS STIWSPHVPATTKVSTLHWTVVRLLVII SKIIIVISTSISSSIVVITTSVAPTLVAJSRSS TTISSSSSITGATSKIATSRSSSAGSRAE VLLAELFLEQRQFSLQRQDESGSCSSAEI SLISLGCCKSG*SD*VRDGERKRNSSVSS LLVA*ALKPQKKV*GTTNNGESLQTVW **GILQAKDQEDLV
997	9048	A	1942	123	734	LFKSAIKNGLQHELHCRKWEKKQNGKS KKVQAEAEVPEGVEKVLDRRVVNGKV EYFLKWKGFTDADNTWEPEIENLDCPE LD*SRFLNFSRKAGQRKRWVPRKSLSD VSESDDSQIHRKRDAADQPKEDFARGVL DP*KK*LAGHRPASGEVLMFLMKWKDS DEADLVLAKEANMKCPQIVIAFYEEKP TWHSCPVEDEAQ

998	9049	A	1943	1092	1285	IDVCVCLALLERLECSSVISAHCSLCS/SG SSDPPTSAS*VAGTTTACHHAQLIFGFFFF LKRWGF
999	9050	A	1944	76	532	LPRPRSRLTALPPPSFLQTPKSRALMAG LEVLFASAAPAITCRQDALVCFLHWEVV THGYCGLGVGDQPGPNDKKSELLPAGW NNNKDLYVLRYEYKDGSRKLLVKAITV ESSMILNVRTYKNSEELRSRIVSGIITPIH EQWEKANVSSP
1000	9051	A	1945	109	1008	ALPPPSFLHTPKSRALMAGLEVLFASAA PAITCRQDALVCFLHWEVVTHGYFGLG VGDQPGVNDKKSELLPAGWNNNKDLY VLRYEY*GWGPESFLVESHSWESSIDSS MLLGIMGSQQSWQI*PLNLG*LFSMAEH LGDFHRTYKNSEELRSRIGA\GIL\TPIHEQ WEKANVSSPHREFPPATAREVDPLRIPPH HPHTSRQPP\WCDPLGPFVVGEDLDPF GPRRVGMNVDPRLRSGLPRAFNDP\SSG LPNRL\PPGAVPQGAGDFPGPIGTSPPG \PNP\DHLP\PPGYDDMYL
1001	9052	A	1946	152	991	RKTKCVTRPAVVFSPLTSRSSRASACE VAFPRGQPRKGPKRDNWILGTRPSWVA VCSSPRLGLSR\EYKLVMLGAGGVGKSA MTMQFISHRFEDHDPTIEDAYKIRIRIDD EPANL\DILDTAGQAEFTAMRDQYMRA GEGFIIC*LLSRIRSFHEVPESLNQLIYR VRRTD\DDTPVVL/VWGNKSDLQTA*DRF TKGRKGLALAPENSSCPLFWRTSGCHTR \YYIDGCFPHAPVREIRRKEKEAVLAW EKKS*APKTSVWKEAKNHPFRKKKDSV T
1002	9053	A	1947	305	406	
1003	9054	A	1948	372	501	RPGAVAHSCNS\STLGGRGRWIT*GLEFE TCLANMVKLCLFHLV
1004	9055	A	1949	441	812	ITTHLYISKPLLCTPMKTYNYYLSIAKIF *FSLLRQGLALSPRECTSTITAHCSLNLP GFKQSSHSQPSE*LGTTDTHHHIQLVFLIL /AETEFCHVAQGG/LNIS*VQLIHLPQTSK VLGLQM
1005	9056	A	195	38	1222	EPESCSVTRLECSGVISAHCNFR/LPGFKN FPASASQVHGTTGTPHHAQLNLYF*VEE QGFFPMLAPGWILGSP*PLMDPAPSLALP QSAGDPQP*AHPHPGPSYLF\FKERENYE RPKII*LNPLPLAQGKKMEFALI\WVMKH TO*IRNNHIFSKROK/C*DL*SYMVA\YFW VGKK*EKNITSLTGNDTF**KILLSFPTRM IHCKAKIY\IAKFFFWRRSLTSVTLGWSA VWHNLSSLQPPPSGLKRLSHLNLNT/W DYRPPCPANLCFVVVVVLLFVFW*RW GF\TMLARLISNS*PQ/CDPPTSASQSAEIT GMS/HPCLAMGFVFH\TL*KPPFFKDYM KSFFQFFKYLIQG*CSLV*GVYRSSLIFF F/CFFETESCLVTQAGVQWRDLGSLQS
1006	9057	A	1950	2	370	
1007	9058	B	1951	209	524	MLLSLAAFSVISVVSYLILALLSVTISFRI YKSVIQA\QKSEEGHPFKAYLDVDITLSS EAFHNYMNAAMVHINRALKLIIRLFLVE DLVDSLKLAVFMWLMTYVX*
1008	9059	A	1952	3	463	

1009	9060	A	1953	49	1129	RDLIEFSCRILFLPSLPPRISFHPSPTLAR VAMAEPSAATQSHSISSSSFGAEPSPAGG GG\SPGSLPRPWGPKSCSSSICAVHDLIFW RDVKKTFVFGTTLIMLLSLAVFSVISV VSYLILAL\SVTISFRMYKFVIAVQKSE E\GHPFQKPNWNVDTLSSKSFSINNMNA AILHINMFLKLIIRLFLVEDLVDSLKLAVF MWLMTYVVGAVFNGITLLILAEFIFSVPI VL*RKYKTQIDHYVGIARDQTKSIVEKIP SKTPLGIAKKKGRIKYMETR NATSYLKH HLISYNVVTCTMKENTQCQLEPAFQAFF LIWCFLPSFPNPQSSSTKIDGLIKDLFLD LRRRNQIS
1010	9061	A	1954	46	519	SQTPMGHTEEDKATINTSLWGKVNVEV DAGGETLGRLLVVYPMPGQRF*PALG NLSSASAIHGQPPKSRAGQEGC*\RSLG\ DAIKAPGIDLQRAFFQA*\SELALVDKLA MWDSLNRNFKASWGKFCFLVDPFLAIPFSA KEFHPLRCQVFLGQKDG
1011	9062	A	1955	1	747	
1012	9063	A	1956	1	813	MKEENLCQAFSDALLCKIEDIDNEDWEN PQLCSDYVKDIYQYLRQLEVGLQSNPH FLDGRDINGRM/RAILVDWL\QVHVKFR LLQETLYMCVGIMDRFLQSLPAEDREA LGTSSPQHSGALGDVGYKSGFILSPHPC MSKIEPEDEKLSFLFIGPFLKNPSPRANG DPMFLCLNEDEAQLEETKWTGCQKQL CDPLSEEVKTGEKLVQTKGERTSRIREV QFLAQNHTRRWQSWDLGTSSLTPEPVF SLEINVREORDEDNIQVLRG
1013	9064	A	1957	1	1390	EATASKIPSAAGSESSPNGASYASVPPFS VRVPPWAGLALLPSPSLMALLRRPTVSS DLENIDTGVNSKVKSHVTIRRTVLEEIG\ NRVTTRAAQVAKESSGTPKFQVQPTKTT NVNKLKPTASCQTQYQMGKVWLPKG PSPTPAEDVSMKGRESLPLKFSALLCKI EDIDNEDWENPRLCSDYVKDIYQYLRQ LEVGLQSNPHFLDGRDINGRMRAILVD WL\QVHVKFRLLQETLYMCVGIMGSD F*QVQPVSRKKLQLVGITALLAPKYEK MFSPNIEDFVYITDNAYPSAQIREMETLI LKELKFELGRPLPLHFLRRAS*\AGEVDVE QHTLAKYLMELTLIDYDMVHYHPP*\G*\ PAAAS\CLSQKVLDKGMEL*\SQYYHK DTQENEVLEVHASTMAQECGAK*\MENL NLNSIGHQRIK\YAKQTP*\KISMIPQLNS KAVKDL\ASP\IGRS
1014	9065	A	196	526	835	FNLNFTVSLRTHSPLIPFFSSNERIKPGKS TIDGPWTRRTRL*\RKNLWMIQ*\LWDFLF/ VLFETDSSSVARLECSGAISVHYNFHLP SSDSPDSRSMPIVDRQ
1015	9066	A	1964	33	513	
1016	9067	A	1965	1	503	GHESDNLLFVQITGKKPNFEVGSSRQLK LSITKKSSPSVKPAVDPA\AAKLWTL SAN DMEDDSMDLIDSDELLDPEDLKKPD PAS LRAVASC GEGKKRKACKNCTCGLAEEL\ EKEKSREQMSSQPKSA\CGNCYRGAMPS GCASC PYLGMPAFKPGKEKVLLSDSNLHD A

1017	9068	A	1966	29	1270	PPFWPAVFQVCQYCTARMADFGISAGQF VAVVWDKSSPVAEALKGLVLDKLAQAF/TP GNEGRVSVENIKAAVAAILPTKNPSFGHY FVQ/CLVPGKAPLWWSA*DFWAGNPPGF LRPGWMFFFLKEPVETAVR*Q*AKWKT ASKL\CSAL\TSLGLV/EKLELQREPLTPE EVQSVREHLGHESDNLLFVQITGKKPNF EVGSSRQLKLSITKKSSPSVKPAVDPA KL\WTL\SANDMEDDSMCIFCGCSLTHRW PLEHVQVE/IMMDQPKRRTRVDTFFTP RTPKFPSRSPASHFSFSIKQKT/TRPVSLIA LNTL\QDLIDSDELLDPEDLKKPDPSLLR AASCGEKRRKACKNCTCGLAELEKE KSREQMSSQPKSACGNCYLGDAFRCAS CPYLGMPAFKPGKVKLLSDSNLHDA
1018	9069	A	1967	3	498	LANRAIMSHKQIYYSDKYDDEEFYRLV LAREQLATGRELWPLRAQGISNRN*GDR IGACVRDMSCCPKDIKLVPRTHLMSES EWRNLGVQ/QRSGWVHYMIHEPVEPHI LLFRRPLP\RKPKMKLGKLTQPSFYT AGPYLPNIFLDNIYVGLLVFFTFDI
1019	9070	A	1968	1	690	RRKAFPKRLPKMAEVQVLVLDGQGH LGRLAIAIVAK\QVLLGRKGGCSYACEGI HISGNFLQNVCSLAFPLQARMNTNP\ SQGP\YHFGIAPSRIFWRTVVRGMLPHKT KAEARPLDRLKVFDGIPPYD\KKKR\ MVVPAALK\VVRFAYTESFAYLGRLA PEVGWNAIRPVTAPPGGERGKRKAKIH YRKKK*L\MLR\RKQAREETWRKKIDKY TEVLKTHGLLV
1020	9071	A	1969	2064	2561	KRFWSFALFYLLKLL/CIDSIVRIGTILY STVFFIFLKFKV*LVLITFIQIAIFFGSET F*QVGV*FLLIPNFFSRVLLILSEGKVI*VC QLIVLLGLNFHIVFTVYGEVVGIIYSILN K/AVIHFFIKV/YFHVKFLFLYVLLLSYIT QFLF*KSSFVEVLVKN
1021	9072	C	197	7	276	MQWRDHNYCIFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXLARPFI*
1022	9073	A	1972	786	1502	PPPTKKEMFVPYSPEQRIETSIPPPFKGTG RP/PGQGRWTWERPPFSLEGKAGALPPLS PRTTKGEDPSETLAQSGQEGDCLNRW QHLH*SAFRPSSAEPFTRKLEGGPAPLR YPGAGNEPGRDAEGRP*GALAGRPRWP PSHGRPPAPCHPASRGGTARKTP/GRST KPPRFPPPLGDATSGKAIPANGRKGGA MSPHRGAGPASPSRFFSHIKQGRAIPHVS SRLHFSPSSSGSR
1023	9074	A	1973	8	234	SAQMAVTTADPRVRPRVRTQLCSLASLI QTLLVHLTPEEKSAVTALWGKVNVD VGGKALGRLLVLPWDPKRSFQSPLGES VPTP*MKVGGKALGRLLVLPWDPKRS F
1024	9075	A	1974	1	169	NLYISNLPLSMDEQELENMLKPFQGVIST RILRDSSGTSRGVGFARMESTEKCEG
1025	9076	A	1975	2	219	
1026	9077	A	1976	17	795	HSTAKLY*HSTFAKRSHRNQHPYVP*IS KSLTSSINSSTSSNSGWDQLSKTNLYIRG LPPHTTDQDLVKLCQPYGKIVSTNAILHK TTNKCKGYGFVDFDSPVAAQKAVSALK ASGVQAQMAKQEQDPTNL YISNLPLS MDKQELENMLKPFQGVISTRILRDASGT SRGVGFARTESTEKCEAVMVQSPSWTQ PQPYILQHPGAVLTPSMEHTMSLQPASM ISPLAQQMSHLSLGSTGYMPATSAMQG AYLPQY

1027	9078	A	1977	3	1421	CLRRRLHEFGTRPPPTPLPSSPERERQESP RLGNPKVSATLHGRLPSSFMGKVWKKQ MYPQYATYYYYPQYLQAKQTLVPAHPM APSPSTTSNDNHR\SISSNSRWDQLSRTN LYIRGLPPHTTDQDLVKLCQPYGKIVS TKGNFGIRTTNNCKGYGFLDF*QPMQQ LKKAVS\ALKASGGSSSKWAKQQGQDP TNLY\SNLALSMD\EQELENMLKPF\GQV ISTRILRDSSGTSRGV\GFARMESTEKCE AVIGHFNGKAFIK\TPPGVSCPHRNLL\CV LSFAGWEGQEKGDRTPNKYIPNGRPPWA *EEGRGETLLGLTLT/YTDPPTAAIQNGF YPSPYSIATNRMITQTSITPYIASTVHAFQ VQSPSWMQP\QPYILHDPGAVLTPSMEH TMSLQPASMI\SPLAQQMSHLSLCSTGT MPATSAMQGA\LPQYAHMQTTAVPVE EASGQQQVAVETFNHSPYTFQPNK
1028	9079	A	1978	2	1440	NSGPSSFMGKVWKKQMMYPQYATYYYYP QYLQA/KVWKAFGNTK*KGRVKNRKMML VGWQTL*TLLFLVGQKNQSLVPAHPMA PPSPSTTSSNNSSSSSSNSGWDQLSKTNL YIRGLPPHTTDQDLVKLCQPYGKIVSTK AILDKTTNKCKGYGFVDFDSPAQAQA VSALKASGVQAQMAKQQEQDPTNLYIS NLPLSMDEQELENMLKPFQGVISTRILRD SSGTSRGVGFARMESTEKCEAVIGHFNG KFIKTPPGVSAPTEPLLCKFADGGQKKR QNPKNKYIPNGRPPWHREGEVRLAGMTLT YDPTTAAIQNGFYPSPYSIATNRMITQTSI TPYIASPVSA\YQVAKETRENKYRGSIAK VQSPSWMQP\QPIYFYQHPGAVLTPSM KHTMSLQ\PSMIQPFWPQMSPSVH*G QHPEPYHALQPSLCKGALLGPQYCTYC RLTAVPC*GRQSGQTGRLAVRGRNLDPF SIYRFNPNK
1029	9080	A	1979	104	340	TGQSYKKRKFVKWLQINRYLTSFLF/VF KEIRSHSVA*TLEHSGAIMAHCSLKFLGL SNPPASASQVAGTSGVQYHTSLI
1030	9081	C	198	2	28	MIDTHTPS*
1031	9082	A	1980	118	528	
1032	9083	A	1981	1	864	
1033	9084	A	1982	3	4258	
1034	9085	A	1983	44	1360	VWDCPGLRWASFYLRLSWRAHRPQCGT ISFVTVNAAEQEKQFVSSRTKQKAKEEK LEKCGEDDETIPSEYRLKPATDKDGKPLL PEPEEKPKPRSESELIDELSEDFDLSECKE KPSKPTKTEESKAAAPAPVSEAVSRTS MCSIQSAPPEPATLKGTVPDDAVEALA DSLKGKEADPEDGKPVMDKVKEKAKEE DREKLGEKEETIPPDYRLEEVKDKDGK LLPKESKEQLPPMSEDFLLDALSEDFSGP QNASSLKFEAKLAAAISEVVSTPASTT QAGAPPRDTSSDKDLDDALDKLSDSLEQ RQPDPDENKPMEDKVKEKAKAEHRDKL GERDDTIPPEYRHLLDDNGQDKPVKPPT KKSEDSKKPADDQDPIDALSGDLSCPS TTETSQNTAKDKCKKAASSSKAPKNGG KAKDSAKTTEETSKPKDD

1035	9086	A	1984	159	2467	EKKGSYEEKKAASLGSSQSSRTYAGGTAS VTKVSAFSGATSKSYSNMPTETKAIPVS QQMEGPHLPNKKKHKQAVKTEPEKKS QSTKLSVVHEKKSQEGKPKHETEPKSLP KQASDTGASNDAHNKKAVSRSAEQQPIS EKSTEPKTKPQDMISAGGESVAGITAISG KPGDKKKEKSLTPAVPVESKPKDKPSGK VSGMDAGL\DDLDITLGGPEETEEENTTY TGPEVSDPMSSTYIEELGKREVTIPPKYR ELLAKKEGITGPPADSSKPIGPDDAIDAL SSDFTCGSPTAAGKKTEKEESTEVLKAQ VAGTVRSAAPPQEKKRKVEKDTMSDQA LEALSASLGTRQAEPELDLRSIKEVDEAK AKEEKLEKCGEDDETIPSEYRLKPATDK DGKPLLPEPEEKPKPRSESELIDELSEDF DRSECKEKPSPKTEKTEESKAAAPVAPVS EAVSRTSMCSIQSAPPEAGTLKGTVQDD AVEALADSLGKKEADPEDGKPVMDKVK EKAKEEDREKL\GEKEETIPPDYRLEEVK D\KD GKATPCPKSLKEQLPMSSEDFLLD ALSEDFSGPQNASS\NFEDAKLAGAISE VVSQNPFRSTT/TQAGAPPRDTSQSD\K ALGD\ALDKLSDSLQ\QRIQDPDG*GTNQ WEG*S*REKAKAEHRDKLGRKRWTLFP PEYRHLL\DDNG\QDKPVEGHLTKKSEN QRNPG\DDQ\DPIDALSEDL\DS\CPSTTET SQNTAK\DKCKKAASS\SKAP\KNGGKAK DSAKATEGTSK\PKDD
1036	9087	A	1985	2	788	EFSASIVGICTMPWALLLLTLLTHSAVSV VQAGLTQPPSVSKDLR\QTATLTCTGNS DNVGYQGAAWLQHHQGHPPKLLFSRN NNRPSGIHKKRFYGSNSGTTATLTISGLQ AMDEG\DYCNSRDSSGNHLRVFGG\GT QVDPSLRVRQGMPPWVNFVPGPSSEEAS SPNKAHTGVVFISDFLTPGNP*QVA\WKA DSQPPFKAGVETPPHPPKQSNKYTDSIS YLSLTP*PGGSPHRSLQLARVTH*RGAPL EKTVAPTRMFH
1037	9088	A	1986	226	401	TSGDHWNIAVAPHENS DLLLVQGH DYK YRYFGLIVCVL*QAI VTPEEPQSIVPRLRT R
1038	9089	C	1987	211	285	MFYPFFNPRYFSVGFIAMNRHTD**
1039	9090	A	1988	107	192	
1040	9091	A	1989	1	285	YIYIYIYIYIYIYIYIYIYIYNLDQSW FAPLLVCGP**AQVVTSELGNRN*SEKTF TWRICMRNIGRCSLGMLQDYFKPFD KVM LVV
1041	9092	A	199	780	888	NKRNQGGSSRVGTHL*SQLL/RRLRQENH LNPEGRGCS
1042	9093	A	1990	27	437	IAEGNWCVYMPDIIWVFPQAEAEEDCH SDTVRADDDEENESPAETDLQAQLQMF RAQWMFELAPGVSSSNLENRPCRAARG SL\QKTSADTKGKQEQAKEKL SIIDIVT NYIFFFWHMEIFTDTVSRHYNQTFGT

1043	9094	A	1991	25	1488	GGSSAAASGVSSRADAPVLAQSPASAGN GRPSTPRVPGSRRHPSAPRSGPLPREDGC RTPGPQLLPLPGALLRPRTLSSAAEDK ARSRHPDTQHPSSGGRCRGGTESPSSAA GRPASMAEAEVEDCHSDTVRADDDDEENE SPAETDVQALIPMIQAQWKLEPAPRVTS SRLENRPCRAARGSLQKTSADTKGKQEQ AKEEKARELFLKAVEEEQNGALYEAIKF YRRAMQLVPDNEFKITFTRSPDGDGVG NSYIEDNDDDSKMADLLSYFQQQLTFQE SVLKLCQPELESSQIHISVLQMEVLMYIF RWVSSDLDTSLVEQLSLVCARGFLTSC ARDP*KYARPGPALKVWGQKACIKLVS VTRPGREDVF*ERPPVS/RFDGVYISKTT YIRQGEQSLDGFYRA\WH\QVEYYRYIRF FPDGHVMMMLTTPPEPQSIVPRLR\TREYQ GLDAIPTGVITRLSPRHRTIRTQSIWLLIT KEKRKEKPL
1044	9095	A	1992	242	433	
1045	9096	A	1993	243	549	
1046	9097	A	1994	81	436	AKQGISPEGVMDVNTALQEVCLKLA\LIH VWT*TRGNSRS*PKPLDKRQAHLCVLA SMCDEP\MYVKLVEALCAEHQ\NLN*GL IDNNET/MGEWG*GLLLKFDRGGGKPRK SWFG\CSCC
1047	9098	A	1995	3	452	
1048	9099	A	1996	3	484	PTLLVPTDSERTHPWLLSPADKTTVK/AP AWGKVGAAHAVRSMCAEALERMFLSFPT TKTYFPHF\DLSHG\SAQV*GPRARKVAD AL\TNAVAQRGT\IAQRAVPPLSDL\HAH KL\RVGPGSTFKLLKATGLLG*PWPGPPS PAEFNPWRLQRLPWDKVSWVSC
1049	9100	A	1997	797	1049	SEEECCSCLPSPAGSDQRLCTHLP CVI VNSEWGVARY*LNVCS*PVFFSVG\PK QYPYNLYLERGGDPSKEPERVVHYEI
1050	9101	A	2	25	619	EFHRLRENPPWCSSPADKTNVKAAGWK VGAHAGEYGAEALERMFLSFPTTKTYFP HFDLSHG\SAQVKGHGK\KVADALTNA VAHVDDMPN\ALSALSDLHAHKL\RV\D PVNFQSS*SQLPCLGEPWAAHLP\AEFQP LAVATSSLGTFKPGLSVEAPLLTFQITFK GWKPRVGHAFFALWASPQPLLPFAPVP PWSLK
1051	9102	B	20	103	282	EDTAAQSSPGRGEEAEASAAEAQGGEQ AYLAGLAGQYHLERYPDSYESMSEPIIA HLLRP*
1052	9103	A	200	224	552	KVLRVARCGGSLLSRPSTLGGQGGRLM RSGVRDQPGQHSETPSLLKMQKLAGHG G/RAL*SQLLGRLRQENHLNPGGRGCSEL RSRHCI\SRVTV*DSISKKRRKKVL
1053	9104	A	2000	546	882	CHVPPTLGTGRQGTHQDPFFPHSPGAP APCPPPA\LLGPPRPFPSPVPGPGENRK PFTSAP*A*VFPRTPLGALS RG*GSPVVG RGATPSPTPSPACGPLKCWWHLIKN
1054	9105	A	2001	43	311	
1055	9106	A	2002	178	817	SPASGHCRNLNGAAVAMFGCLVAGRLVQ TA*QQAEDKFVFDLPDYESINHVVVF MLGNNP\FPEGMGGSVYFSPDSNGMP VWKLLG\SVTNGKPSAIFKISGLKSGES QHPFGA/NEYCPNLHLLRLGISGELLDS MAQQTPVR*CCWYPQFDSFTQFTQKML DNFYNFCASSFVSAQMTPS/SI*KCSFR PNVVLKWYEAFSVSNIAFYN

1056	9107	A	2003	283	840	TLPAGFTDVISIHKKTGENFCLICGNGRFA VHCITLLEAKYKLCKVRKIWFHDAHTIH YLDSEVKVNDTV*TGKITDFIKFDTGNLG RIGVITNRKKHRGSFDDVHVKDANGNRF APWLSNIFVTGKCNKPWISLPRGKGIRLT IAFHSDKWFCSDISVQNLCKRFSQGGDTGI KNSEARRCSNLQV
1057	9108	A	2004	1	966	GRPAPEDGGPLSLPNAAMARGPKKHLK RVAAPKHWMLDKLTGVFAPRPSTGPHK LRECLPFHFLNRNLK\YALTGD\EVKK\N CMQRAFIKADGQVRN*YNLPLLGFMDV\N S\NEKTGENFFP*SN*HPRGPLLL*HRITP\N EAKYK/VCAKMRKIFCGPTKGIP\HLVTS *CPAPHPAYPRNPLIQGEMNTHSR\ILET GQD/ITDFHSKFDHLVTL\CMV\TGGANL GRNWVLITQQRRTGPSFDRWFT*KDA NGNKL\ATSDFS\NIFWLLGKGNKPWISL VPRGKGIPPHHLEERDKRLAAKQSSWV KWGPVWTWSDLLVP
1058	9109	A	2005	1	383	RIRKLCNICVGESGDRLTRA\KVLEQLT GQTPVFSK\VREYELRKNNFSDTGNFGF GIQEHIDLG\IKYDPSIGIYGLDFYVVLGRP GFSIADKKRRTGCIGAKHRISKEEAMRW FQKYDGIILPGK
1059	9110	A	2006	3	224	
1060	9111	A	2007	176	384	
1061	9112	A	2008	2	669	IMAQDQGEKENPHAGNFAFRKLV\LNIC\N VGESGD\RPTRA\AQVLEPAQQGKTPCVF PKA*HTPVKSLWASRR\NEKIAFPTATSS EGAKARRNLCRRGLKRFSEYGVQDNTT FSGYWETFGFGI\QEHIDLG\IKYDPSIGIY GPGTSYVV/LGVRPGFQHPQTKKPPQGGQ CIGAKHRISKEEAMRW\FQKYDGIILP GOINSPFLSKKSNKKFSVNKKNNKKITL
1062	9113	A	2009	688	884	CSCVWNL\SFHGNAFHLKTPYSRIKKAKH /WMAHVYSPITLGGRGGWIT*SQEFETSL SNIKPCLY
1063	9114	A	201	41	320	
1064	9115	A	2010	442	780	IEFVIKKIFFPF\SHCLICLAIDLQ\Q*YMG VPR\WMLKTCYVRGKYRGVVLEE\QNIL WK*IH\PLQVREDGRPC\PLRKLGGKGG GGGEPLNQHGDPVQGNPPYFLFCHMRN P
1065	9116	A	2011	136	219	DPAREGHPVCCAGQRPCVDGHGQEKGF LKA\LEVELGASNP\SW*DTEVKPQSALP QASALT\WVS\YQQGVLSATILYEILLGKA TLYAVLV\SALVLMAMV\KRKDF
1066	9117	A	2012	3	762	TLRGAVLRGAAGRLGGGLLVLGAGRAM GLSAVGRTRAESGTAERAAPV\VLGLQA VSTDTQMFGPGTRLT\VLEDLKNVFPPEV AVFEPSEAEISHTQKATLVCLATGF\FPD HVELSWWVNGKEVHSGVSTDPQPLKEQ PALNDSRYCLSSRLRV\SATFWQNP\RNHF RCQVQFYGLSENDEWTQDRAKPVTQIV SAEAWGRADFGFTS\VKSYQQGVLSATI LYEILLGKATLYAVLV\SALVLMAMV\KR KDSRG
1067	9118	A	2013	1	1010	RYSFFKAVMGIRLLCRVAF\CF\LA\VLVD VKVTQSSRYLVKRTGEKV\FLEC\VDMD HENMF\WYQRQDPGLGLRLIYFSYDV\KM KEKGD\IPEGYSVSREKKERFSLILESAST NQTSMYLCASSLFNSGYQETQYFG\PGT RLLVLEDLKNVFPPEVAVFEPSEAEISHT QKATLVCLATGF\FPDHVELSWWVNGKE VHSGVSTDPQPLKEQPALNDSRYCLSSR LRVSATFWQNP\RNHFR\CQVQFYGLSGN DEWTQDRAKPVTQIVSAEAWGRADCGF TSVSYQQGVLSATILYEILARGRPTLYC

						LCW*APLVLMAMVKEKGFLKAALEVE LGAF
1068	9119	A	2014	344	463	
1069	9120	A	2015	1075	2102	QQKPGQPLFLGSISPCKSFKTRKQKSSSK AEYNLTACKCLLCKRKYSSQIMLKRHM QI/RPQDNSFWNKL*KRKR**YCQQFRN KS*S*TSRFCRIFTPFHYPFSTE/CN*REQII QMKKRTHRQHRKIKLNLTK/CPKSTSP SAAGGQKTRKPKLSAGDFKQLYCKL CKRQFTSKQNLTKHIELHTDGNNIYVKF YKCPLCTYETRRKRDVIRHITVHHKSS RYLGKITASLEIRAIKKPIDFVLNKVAKR GPSRDEAKHSDSKHDGTSNSPSKKYEVA DVGIEVKVTKNFSLHRCNKCCKGAFACK TYLEHHKKTTHKANASNSPEGKTKGRS TRSKALV
1070	9121	A	2018	1	408	SNPRVRGGGTHRSQGAFANMCRGGR MFAPT/KTWRRWHRRVNTTQKRYAICS ALAASALPALVMSKGHRIEEVPPLPLVV EDKVEGYKKTKEAVLLLKKLKAANDIK KVYASQRMRAKGKK/RCGR*ERKEGC CWC
1071	9122	A	2019	28	1437	EERGCFSLPPLACARPLISVYSEKGESSG KNVTLP/AVFKAPIRPDVELCSNPNLRK NNRQPYAVSEL\AGHQTKVAESWGTGRA GGSKFPEVRGGGTHRS\GQGAFG\NMCIR GGRMFAPTKTLGRRWNRRVNTTP/QK RYAICS\ALA\ASALTSNWVMSK\GHRIEE VPE\PLV\VEDKVEGYKK\TKEAVLLL KKL\KAANDIK\KVYASQRLRA\SKGKM RNRRRIPGAGGPCIY\NEDNGN\KAFRNIP GNYSA*M*AKLNILK\LAG\GHGG\RFCI WTEKCFSGKL\DELYGTWR*S/RASPQRS NYHSFPLHK\MINTD\LSRILEKPQRSQRA PPGHHAKKIHR\VLKKNPTEKTLR\IML KLKPHMQKTHAAGTTSSPRPRNHKLR VDKGKLLHQRHLQAKSDEKAAVAGKK PAVG\KKGKKAP\VGKK\QKKPLVGKK\ AAATK\KPAPEKKPAEKKP\TTEKKPAA
1072	9123	A	202	80	518	VGPLTPNSVLPRGSV/LPTEVGLDALGEG LKGLCGPNPVVETTNQGFPMQGVLT GRVR*ET*DQSTQDSASCYSTCPAAQTA AYCSE/ASSVPRKIKRLQNMNFWPRE* RRLRSARNKLRRDADFPLCELLLSLN PVRNKIF
1073	9124	A	2020	1	2196	
1074	9125	A	2021	1	207	
1075	9126	A	2022	1	1062	
1076	9127	A	2023	171	476	LPRFQTLRNTETEDHSCCSGRRRFAAA VASRSQ*GNPASLAGSSTTGARSCAPVA RTQRCPRCAACGCWRWRTRWICSAKG WFAHSQFSARIDWLOFLEW
1077	9128	A	2024	1	781	

1078	9129	B	2025	1	1602	MGYRARIRI...WLATQNHSTLVTERSA VPFLPVNPEYSATRNQGRQKLGRFNARE FGNLIIDILSESKRRQQAARAEQPHSAAAA DGVTFSPVPTPHTFRHSYAMHMLYAGIP LKVLQSLMGHKSISSTEYTKVFALDVA ARHRQPTRRKAPAVLGQCRAIATRERPG WFHVAEVRASRRGRSPTPQCADPGWASI SRGVLCDECCSVHRSLSGRHSIVKHLR HSAWPPTLLQSGFPGPSRRAAPRAARGP TPRTEEAAWAAMALTFLLVLLTLATLCT RLHRNFRRGESIYWGPTADSQDTVAGSP DHGLLAFAHYHRLVRFLWVLCPGWAFF LVNSSRGGVFNPIHPCPRHGQARFAGV GRAEDVTFLYHPCAHWPWLKLQALLAY ACMANPSLTPDFSLTQDRVDIEQLDPRG RTPHLATTLGHLECARVLLAHGETWA RENRSWGTVLQEAIVSTQDLELVQLVLR YRDYQRVVKRLASIPVLEKLRKQRSYL PGRPLARLRRSVNSSGAVGMIKSESMDR WVFGP*
1079	9130	A	2026	2	692	ENRSGFQSRRIYSISKQKKLTFFDVKD NT*SWNAVASREECYLGVT*SRTLGRS *TKDRLRRT*SMPCYSDSM/ISMQELEFR HLNTIQKMRCELIRLQHQTETLNQLEYN KRRERELRRKHVMEVRQPKGLKSKEL PNKKSSFQGYLQNSQTRQYKALRNHLE TTPKSEHKAVLKRLKEEQTRKLAILAEQ YDHSINEMLSAQVSLFLGQNKFSAPFL PPPE
1080	9131	A	2027	1	2933	MDDIPQEARQYRHNQAYAYSIIQGDGAE DDDERIVRFHTRVINHKKRKNSPRIVQSN DLTEAAYSLSRDQKRMLYLFVDQIRKSD GTLQEHGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNPYAMRLY ESLCQYRKPDGSGIVSLKIDWIERYQLP QSYQRMPDFRRRFLQHIFVLRERPET
1081	9132	A	2028	6994	7054	LISTSDLYFL*DL*VRCKQTGVLPWFHTT TIPRSSLEVNPRFTYHLCEL/SASYLTSW YLSFLIWTMG*LLHLHHTELL*G*SNKSC *VLCMEPDVTVAHSAVCTQFW/SNVDKN NNVISLRKSFLFF*QSFALVTQAGVQWR DLGSLQAPPPGFTPFSCLSLPSSWDYRRP LPRPANFLYF**RQGFPEFGFHHVHHVG QADLELLTSGDPPTLASQSAGITGVSHH VQPGEGFCNCCCVVESGPFKERVG
1082	9133	A	2029	411	713	TNSLYGLNIYLEIDQHFRNMKIYRSNSLI LILILLHLYCIFALSDL/CSH*PQVAI*KEIN WPGAVAHTCNPSTLGNRGRWIV*GQEFE TSLVNMAKARLY
1083	9134	A	203	63	552	
1084	9135	A	2030	3	84	SGSTHASGGLQASRWRRAGTSRCSVSSL TSTSTASLRGLPTVATGLRSGSWTSHHG VAG*GRPTRPVGSRRRDGGERVRVGAL CQA
1085	9136	A	2031	3	519	SRWRRAGTSRCSVSSLTSTSTASLRGLPT VATGDYPPPDQASSNLTLSPPPGHTHCG NRGQPWPVLGRGGANAAASSSRPEQG GGS/SSFARLSSTHGTGGGEGVKAVSSA *GPAGGLPGTLNLVGGGDVTDASLSALT GGLEGILEKP*AGRCPIITDGNPREEGREP RAG

1086	9137	A	2036	247	1294	MPNTAMKEKRCLLMGERSGSGKNQAM RSIIFAKLPFARDTRRLGATIDVEHSHVR FL\GNLVLNLWDCGGQDTFMENYFTSQR \DNIFARNVGSFDFK\VDVESREL\EKDMH YYQSCLEGHPPRTL\PD\AK\FCL\VHKMD/ LLVQEDQRD\LIKEREEDLR\RLS\RPLEC ACF\RTSIWG*GRFYKAWVQAFV\YQLD FPNVSAAGRLNLRDFA\QI\NEAD\EVLLFE RS\TF\LVISHY\QCKEQRDVHRFEKISNN K\QFKLSCSKL\PASFQSM EVRNSNFA\A FMRHLFT*NTYVMVVM\SDPVD\PFGLPL LINHSQCPGNHFEETGRELNGPQATVFP YGVEYCNALSEKA
1087	9138	A	2038	311	458	
1088	9139	A	2039	1271	1540	
1089	9140	A	204	1	69	SGVKNGRGYVVGISGGTTNKVSP*SRVS *PMAVSACY*VKNGRGYVVGISGGTTN KVSP
1090	9141	A	2040	176	552	MRSSQMKPNFPRCSITVLSVRGMVLF LTLACPRFKMSSRTDFRFGNPQVT*GSTI CSIFRLPSILSMRTTK/DQGMFIWQFQGM RFHF*SSETHLVTFLLPPGIM*E*FQSLKPE PFSFLLSCYCH
1091	9142	A	2041	204	401	WHEFTGAENHCKTLPKENF*WCLCKSH PSEPKNAAYNRTLCDLGISKSEVSLGTSF EMWTSQGQE
1092	9143	A	2042	123	311	PSRRLLGHPRWALSPHLLLPQRFCSWVS FAPASCPC/DLFISRDRSSVSVGLMKHRM LGLAELL
1093	9144	A	2043	2459	3030	TSPSTSLRPAPIPSPSPSSRPSSSQTTSAA SSPSSAWPKAASRQGA*RCRE*LP\SWTS QSSPPLKSWGLDSAPPPPLSTCLSASTTR GAGAAATPQCSAPCLHR/CDKVPGFAVA QCINQHSSPSLPHSRHPPAGAPAAAGA PATATLEAPARPPPPPPQPRVQQSGVAGK DADECSACRRPTVMAATGF
1094	9145	A	2044	1125	1695	DFFSKIDDSHLQVLFFENQLLILFFPHFHLN DCSNSFLFFSEMESRSVAQLECTG/AILA HCNLRLLGSSDFPALASRVAGTTGTCHH TQLIFVFLVETGFHHVGQAGTCMQSQLI KGLRENHLNPGGGGCNEPRSRPLRSSLG NRVRLSQREKQNP*DAQVSEKGLNTLEL QAKF*GVSHVFPGER/VSLISQNP*PFWK KVIKQVSRLRFKKPQDPFRASQSLRIFQS HH*KSWNTYSQQRQVILFLCLSSYVYFK SFSKQGPRTLQIQLCPWAWSTCCRSRE PCTNARVTHLPTLNPIEDATKQDSFLH GMVPIVRQGGQHRM*ENAGEFFPWELGL WMRGCFAHGTIRLLSFL*PFLSSF*R*SR K*SSLKMLDKNSQNNKTHASTSLIKNLP/ HLAPKSMATATKSNFKELRFLQQNR*FT SSSP/CLKISY*YYSSLISI*MTAAIVFCF/C FSEMESRSVA/QAGVHWCNLSLQSLPP GFKRFSCLSLSSWDYRHAPPHAHCIF SRDRVSPCWPGWSQSPGPHGLPAWASP KCWDYSREPPRPGQOYSFSVTRTSLSPIT LRLCIAPCPNQAFDPSRVLHLFVPASSIP PNLKVTLY
1095	9146	A	2045	1	577	PLKRS DGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVNVD VGGKALGRLLVVYPWTQRF\FESFGDL STPD\AVMGNPKVKAHGKKVLRGAFSDG LAHL\DNLKGTF\AHEVSLHC*QACTW DPGELQGSWGNVLVCVAGPITFGKRIST PPVAGLPNQENWLAWCWLNALGPQVIT
1096	9147	A	2046	16	370	
1097	9148	A	2047	1	1125	

1098	9149	A	2048	1	1941	MWKHLWNWVIGSGWKTLDVLEEDRKT KENLVLLRDFSSGCDQSIDRNMDSVQA DEFSDRNEEVIGNWSKGQPCYTLAKDLS ALCPYPKALWKVELKSDDLGEIPLELQR LVHGGQVNLDMEDHQDQEYIKPRLRFK AFSGEGQKLGSLTPEIVSTPSSPEEEDKSI LNAVVLIDDSVPTTKIQRILADGSRLIQR NSTHRRRAVNGPSNQLPDKPGSPSPFCL APLITVCPAADDPSPALWLHLVAARSTS QRNGQVLCYLPRKWGAVAVCTSVEACC WVFWLLERQNDSGMQLGGPPPSAIFRW LAAPAADAPAATSGAGCLATAGGAKTR KLALAELEYDEVKCKSSKSNRPKATVFK SPRTPPQRTVKNWFQLIAPNAGEDAEQQ ELAFIAGGTAKWYSHFGRPFGNLLQRAT WNVSRKLLRTTQISGLRYWGFPGFQAK VAATLAKQEVIPPYLSLGRGAEFKGLSQ NSLQAPLHGTSQGGKNDYPETA VLPKLP REKVSRRKRLASSRCLSLGTCMSEEA FLVITNSSSCSCEGGFPYLIAGKYAQDFG LVEEACFPYTGTDSCKMKEDCFRYYSS EYHYVGGFYGGCNEALMKLELVHHGP MAVAFEVYDDFLHYKKGIYHHTGLRDR PFHPFEL
1099	9150	A	2049	1	2077	MTYPENIQIKKITGVQWMVPLKYKEEGS KVTTYCNETMTGWVHDVLGRNWACFT GKKVGTASENVYVNIHLKNSQEKYSN RLYKYDHNFKAINAIQKSWTATTYME YETLTGLDMIRRS GGHSRKIPSSVPLCSS APLDVQLLVSPAKILGLYGGRMGMA GQKAPFLRAPVIGVSFADSFQPSRLQDSP QLFNQGQLLSAAQVGSSGSQRDVNCSV MGPQEKKVVVYLQKLD TAYDDLGN SG HFTIYNQGFIVLNDLQVGLPFFKYKEG GAARVTTYCNETMTGWGA*CVWGRN WAICFTGKKVGTASENVYVNTAHLKN SQEKYSNRLYKYDHNFKAINAIQKSL TATTYMEYETLTGLDMIRRKWWATSR KIPRPKPAPLTAEYSQKI/LLHLPTSDW RNVHGINFVSPVRNQASCGSCYSFAS MGMLE/ARGIRILTNSQTPILSPQEVVSC ISQY AQGCEGGFPYLIAGKYAQDFGLV EEACFPYTGTDSCKMKEDCFRYYSSSEY HYVGFGFYGCNEALMKLELVHPWGP WEVCFLEVYDDFLHYKKGDPTPHTGLK RPFSTPFELTNHAVLLVGYGT* LKPLG MEY\WIVKNKLGAPAWGLRNGYFRIPR GTDECAIESIAVAATPQFLNFRGRLPSIFI NGSASSCKGGIGIFTDCRLSTSIFRSLQID FP
1100	9151	A	205	379	540	IKKVRNLGPKHPRFSVLLHVS CSTNGG VLL*RSSVPRKIKKRLQNMLNFWPRE
1101	9152	B	2050	59	466	MSAAMRERFDRFLHEKNCMTDLLAKLE AKTGVNRSFIALGVIGLVALYLVWLPSL HLCGFLWCMAPSPSNGAELLYKRIIRPF FLKHESQMDSVVKDLKDKAKETADAIT KEAKKATVNLLX*
1102	9153	A	2051	1	915	
1103	9154	A	2052	1	3180	FRAAVAAPVYPALGTAPGGETVPEWMTA AMRERFERILHDKNCMTDLLAKLEAKT GVNRSFIALGVIGLEALYLVFGYGASLL CNLIGFGYPAYISIKAIESPNKEDDTQWL ITYWVVYGVFVSHC*NSFSDIFLSWFFP* LHG*KCGFLVGWCMAPPELLNGG*NCS KRRIIRSFSFGSTKSQIGQVLVKDP*RPR PKETADANH*KKPKKSLP*ILLG*KKKKK GGR
1104	9155	B	2053	171	256	XVDPASSQAMELSDVTLIEGVGNEVMV VAX*

1105	9156	A	2054	187	437	PWS*LGSLPT*QTAVQAPGRYCVSRRI RPPPGACGPPGGTANGNPEPTELPHPSEG NDEKAEAEAGEGRGDSTWGGWSWGC
1106	9157	A	2055	2	165	NQHHHTLPPPSPHYHPQ*G*HQRAPWP GCWQGPRCRNKGQHQAEPEGLQPL
1107	9158	A	2056	1	506	SPASQHCHHYPLMMGSSVVRGAFGLPP VGPHAPGVGRMCRLLTQ*RPAGACYRC LLRR*RAKLGPRLESAPPHLPPSPHYPH PQ*G*HQRAPWPGCWQGPRTAR*GGV PHPFSEAKVPLLDGPIPSALDWGPWAHP NRRAAWPQPP**DQLSRPVRSRVG*GGH KP
1108	9159	A	2057	496	1092	QPAPGQLLCHLATHPPPGACGPPGAG QGKPEPTELPHPSEGNDKAEAEAGEGRG DSTGEAGAGGGVEP/RP*ASP*HPRPAQK TSRCRQQSRGPPEI*G*HLPPSQPWPHH CAAQIPQ*YRGAGCG*ARGYRGCPPEEQI LPWTRKPDETDLPGPPATRPSPTAFSEH YRQLCDSLPLTPRVSCSRPLSLLGPLGH
1109	9160	A	2058	155	701	PGLFRRGLPHPGTGPVQSPFNFP*/PPR/GP EAPPP/RSPAPPRSLRGVDGL*PP*PTLLLT GRDNWSYPEAGARQPFSGSGPMDPSPA PRE*DHPKAEPSPQKKGAGPLLTVRSRY GQGRSQAEGQSKDP*GRTPGVLPGPSR EFPVSVPIVFVFLCRRFFSCKSWIMTLTFL PSGVSCGCDK
1110	9161	A	2059	1	506	DRDAEFYKFLQENDQSQLNFSDDSSEE EEESFHSLPYVLEEAAAFRAAVATT/RGD QESAEANKFQVTDASAVFNALVFNALV TFCIRDLTGCLQKLLIGKVAKDSSRMLQ PSSSLLWGKLRVDIKAYLGSVIQLVSCV AETVVLAAVLWHISVLVPCFLTTPKQCS RE
1111	9162	A	206	287	449	IKKVRNLGPKHPRFSVLLHVSCTNNG VLL*RSSVPRKIKKRLQNMLNFWPRE
1112	9163	A	2060	9	2295	VGCTLRVGVMAAAGSRKRRLAELTVDE FLASGFDSESESESENSPAETREAREAA RSPDKPGGSPSASRRKGRASEHKDQLSR LKDRDPEFYKFLQENDQSLNFSDDSSE EEEGPFHSLPDVLEEASEEEDGAEEGEDG DRVPRGLKGKKNVPVTVAMVERWKQ AAKQRLTPKLFHEVVQAFQAAVATTRG DQESAEANKFQVTDAAFNALVTFCIRD LIGCLQKLLFGKVAKDSSRMLQPSSSPL WGKLRVDIKAYLGSAIQLMSCLSETTVL AAVLRHISVLVP*FLTTPKQCHMLLKRM VVVWSTGEESLRVLAFLVLSRVCRHKK DTFLGPVLKQMYITYVRNCKFTSPGALP FISFMQWTLTLELLALEPGVAYQHAFLYI RQLAIHLRNAMTTRKKETYQSVYNWQY VHCLFLWCRVLSTAGPSEALQPLVYPLA QVIIGCIKLIPTARFYPLRMHCIRALTLLS GSSGAFIPVLPFILAEFQQVDFNRKPGR MSSKPINFVILKLSNVNLQEKAYRGGL GWSSCYDLNPGSYLHSAHCIGFPELVL PVVLQLKSFLRECKVANYCRQVQQLG KVQENSAYICSRQRVSFGVSEQQAVEA WEKLTREEGTPLTYSHWRKLRDREIQ LEISGKERLEDLNFPEIKRRKMADRKDE DRKQFKDLFDLNSSVEEDDTEGFSERGIL RPLSTRHGVEDDEDEEEGEEDSSNSED GPDAAEAGLAPGELQQLAQGPEDLEDL QLSEDD

1113	9164	A	2061	203	1383	MSSFGYRTLTVLFTLACCPGSDKVF EVHVRPKEAGRLSPKGSLEVNCSTTC NQP*SGVGLGDLSD*GFCWDEQVQLGN NYLGLKHFPIDTVLQCHFTLASGKQESM NSNVSVYQPPRQVILTLQPTLAVAVGKS FTIECRVPTVPEPLDSLTLFLFRGNEILA LWRTFRGRAAPAPQGGPQPHSNSTADR RGLAHRKLSPLAVLADLMSRGGWNIFHK VHSAPKMLEUYETCVRTSPDWSSLVTGG VGVACPLFVTSVLLCFIFGQHLRPASG MGTYGVRAAWRRLPAQFRPIATHGVA WPHTTVVTGTQCDSSGLRYQPWLKDCD RQQRGLTLPFLARIQTPGLSPVPTVSPGI TMAREGSHHGGLSLDASLPTLSFTGWH EA
1114	9165	A	2062	503	1808	TTVQEESTVDSQPVPNIDHLLTNIGRTGV SPGDVSDSATSDSTKSKGWSGSKDQYS RELLVSSIFAAASRKRKKPKEKAQPSSE DELDNVFFKKENVEQCHNDTKEESKES ETLGRKQKIIIAKENSTRKDPSTTKDEKIS LGKESTPSEEPSPPHNSKHNSPTLSCR AILKESPRSLLAQKSSHLEETGSDSGTLL STSSQASLARFSMKKSTSPETKHSEFLAN VSTITSDYSTTSSATYLA*PGLQSTEP*GA VSAESKGDEADDERSELISEGRPVEDS ESEFPVFPTSLDFREAFPRKTARSYTKSSR RNSEGESELCTEGSLTSSLDSSRRQLFSSH KLIECDTLRKKRSARFKSDSGSLGDAKN EKEAPSLTKVFDVMKKGKSTGSLTPTR GESEKQEPTWTKIADRLKLRPRAPADD MYE
1115	9166	A	2063	2	527	DPEADSIRAEMSRVALAVLALLSLSGLE AIQRTPKIQVYSRHPAENGKSNFLNCYV SGFHPSDIEVCLLKNGKRIEKVHEHSDLS FSKDWSFYLLPYTEFHPQLKKDEYALP V*THVTLSPAQR*FKWDRGHVKQHHGG LKMPHLGWNDKFLACFFNIDMLITLT LLCTKM
1116	9167	A	2064	3	163	
1117	9168	A	2065	611	1432	TPLHLAVITNQPEIAEALLGAGCDPELRD FRGNTPLHLACEQGCLASVGVLTQSCCT PHLHSILKATNYN/GYVCLPALPHPLGGQ VTWRRGRWANLRSPGKSLNS*HLEG*E NMACAKCLLDAFIKFFQNPDCGFLKFR* DYLPHKRIGERSEG*NRWVYFFPFVLP HTCLHLASIHGYLGIVELLVSLGADVNA/ QGWCFLPPTH*VRLVLML*AEIPNAAIS ISNSFWFQPCNGRTALYLAVDLPNPD VSLLLKCGADVNRVTYQGYSP
1118	9169	A	2066	1	1332	MVQLSPHYRGDSSEDGRKRMVRQRTKPV LFFWSDWLGNSPSLTPPQRNPQAFIGRR GGAAEPTAVRAAVPPASAPARKQRAAR GPAHPQQRQLVRAMFQAAERPQEWA MEGPRDGLKKERLLDDRHDSDGLDSMKD EYEQMVKELQEIRLEPQEVPRGSEPWK QQLTEDGDSFLHLAIHEEKALTMVIRQ VKGDLAFLNFKTNLQQTPLHLAVITNQ PEIVEALLGAGCDLELRDFRGNTPL*SL ACEQGCLASVGVLDSSLAPPPQLVHSILK GYPTTMGHTCLHLAFYPMGYWGHRSF LVFLGVLDVKCSRSPCKWPLPIHLAVD LQNPEPGCSLLFESVGADVQQLPTQGY SPPTQPHPGPPQAPRIQQQLGQLTLENL QMLPRE/SPDEESYDTRVQSSTGVSPED LAPMDDCGVFGGPRSDVMSAKGLKET
1119	9170	B	2067	169	251	XPQKEPYVIPFTGCVTQKGGVAGDAGW Q*
1120	9171	A	2068	33	445	
1121	9172	A	2069	1	1428	

1122	9173	A	207	263	525	IKKVRNLGPKHPRFSVLLHVSCTNNG VLL*RSSVPKKNKEEAAEYAKLLAKRM KEAKEKRQEQIAKRRRLSSLRASTFKSES SQK
1123	9174	A	2070	1268	2807	LPLESLAVQVKQHIDAVARFTGIKNCYF GFGGMSTQKPARGC*TRRPEIVVATPGR LWELIKEKHYHL\GNLRQLRCL\VVDEA\ DRMV\EEKGPFWELELLHSCFRDASNDSIQ YNPKRTKRLFFLATLTLVHQAPARNPFH KKHTKKMDYTAQL\DLLMQIGHEGAS PKVIDLTRE*GPRWETLTETKIPL*DLIEK DFLLVTTFLMQYSRAAA*CFANSIS\CIKR LASGLLKV/LLDIMALGPWHGLVWHQEG RGLRNLGSILPRL\EDCVLL\ATDVGSSGV WDIPK\QHVHPFTRVPRTSEIYVHRWS SNLLRSYQLTGLKS*LLIWGLKDVINFKK IYKTLKKDEDIPLFPRADINTWDVV\KERI RLARQNEESEY\RNFOACLHNSWIEQA AAAL\EIEL\EDMY*GEGKADQQEERR RQKQMKVLKKELRHLLSQPLFTESQKTK YPTQSGKPPLLVLAPSKERVCFLSCLSQ GRKEEGRTKEARGGPQPGTATAKLQVQ FNCPGQVCQ
1124	9175	A	2074	1	408	SNPRVRGGGTHRSGQGAFFANMCRGGR MFAPT/KTWRRWHRRVNTTQKRYAICS ALAASALPALVMSKGHRIEEVPELPLVV EDKVEGYKKTKEAVLLKLLKAWNDIK KVYASQRM RAGKGKK/RCGR*ERKEGC CWC
1125	9176	A	2075	3	1434	FPVAAAGLRGAWLSPLSAMACARPLIS VYSEKGESSGKNVTLPAVFKAPIRPDIV NFVHTNLRKNNRQPYAVSELAAGHQTK\ AESWGTGRAGGSKFPEVRGGGTHRSVG QGAFGNMCRGGRMFAPTQNLGRRWN VRRVDT\TQNR\YAVCS\ALA\ASALTSNW VMSK\GHRIEEVPELPL\VEDKVEGLQE EPRKLFLLKLLKAWNDIKK\YASRR MRGGQRQNGETVRRIPGAGGPCIYNED NGNIKPF\RNIPGN\YSA*M*AKLNILEALL PG\GHGGTFLAFGT*KLPRK\DELYGT WR*S/RASPQRSNYHSFPLHK\MINTD\LS RNLEK\QRSQRAPP\GHRGKREDPIRRVL KKNP\LKNLR\JMLK\LN\PKG\PCCR/RHPF FAQAQESQSSGVDKGKLLHQRLQAKS DEKAAVAGKQPVVGKTKGKGCLLVFK NQKKPLVGKK\AAATKKPAPER\SLQRR NATTEKKPAA
1126	9177	A	2076	275	652	TVNLCFSTFLWTVLYFTFFFAKCFQIHLL RIYLR**LKTNSWFMLY\UMHVLLVQG QN*NKIFSVKQIYLLCTFIYTGIFW*YHT KG*NTFTM*NSMYIFGYLHTLKPCKGI KRKHLFATTIC
1127	9178	A	2077	63	290	GGILLSISRPHYKTKPTHGIGKYKHLIKAEE PKKKKGKVAVRAINLGTDYNYGVLNIH LTA\YDMTLAESYAQYVHN
1128	9179	A	2078	315	1092	RPRSSKRMSGTSEKVLCLRNNTIFKQAFS LLRFRTSGEKPIYSVGGILLSISRPHYKSKP THGIGKYKHLIKAEEPKKKKKGKVE\RAI NLGTDYEGV\LN\HLTA\YDMTLAESYA PLFSTTF\CN\SLSH*KSEESYAMPTQNHKK WLPVCRDQ\GQPKCLLGLKCLP\THERV\ VQISGLSATFARKFSWKIIPKPVLP*RESG LFS*REHTERKTSRGRFQRFDELGRFTW AKFEVATVDPFHCQ\QWSYLSAKEKSL GS
1129	9180	A	208	68	280	
1130	9181	A	2080	61	346	LSLFFETEF\CS\CPGLECSGVILAH\CNFR\ LPGFK*FSCLSLPSSWVYRYP\PD\ANFL VLVETGFHHVGPGLVLNDPLIFNLDTCY

						SAKRQFLE
1131	9182	A	2081	88	386	PHRFGKRRNKTHTLCRRCGSKAYHLQ KSTCGKCGYP*AKRKRKYNSAKAKRP KYHPEPGRMRHLKIVY*RIQGMGFREG TTP*TQEGQAVASIQVHL
1132	9183	A	2082	187	913	STNKRSTRPPLGFEMASPHQEPKPGDLIE IFRLGY*EHWALYIGDGYVIHLAPP*SEYP GAGSSGVFSVLSNSAEVKRG*RLAEDVV GGCCYRGQQTAWDHGVSPRALEG*SF SSAKEMVWFRRLKIYSIVSRNCEALCSP SLRYGQVPAVKQVGKGRFEVG/VLATA LGILVVAGCSFAIRRYQKKSDSLKQPQN PVLEAAVGVPVEMSLPRCLQQPDPRLS QAFSRSFPLFPSLAGKSMI
1133	9184	A	2083	1	423	
1134	9185	A	2084	2	390	PRVRYRGVITDPQPLMEQPGLGDSRYWL SSRLRVSATFWQNPРНHFRСQVQFYGLS ENDEWTHDRAKPVTQIVSAEAWSKADC GFTSGN*QQGVLSATILYEILLGKATLYA VLVSALVLMGMVKRKDF
1135	9186	A	2085	2	1027	HLPDAAMGPQLLGYVVLCLLGAGPLEA QVTQNPRLITVTDKGDVPEGYKVSРKE KRNFPILILESPSPNQTSLYFCARSFEQGY EQYFGPGTRLTVTEKRNFPILILESPSPNQ TSLYFCASSSSQGRSPGFNYGYTFGSGT RLTVVEDLNKLFPEVAVFEPSEAEISHT QKATLVCLATGIFPDHVELSWWVNGKE AHSGVSTDPQPLKEQPALNDSRYCLSSR LRVSATFWQNPРНHFRСQVQFYGLSEN DEWTQDRAKPVTQIVSAEAWGRADCGF TS\VKSYQQGVLS\ATILYELARGRPTLY CLCW*APLVLMAM\MVKEKGFLKAALEV ELGAY
1136	9187	A	2086	1921	1991	SFVIFDANIFFQFIG*SLLSLWM*ALLCLL VTEHLYLVSIGHLWCVCVCVCVCVCVY DFLIPSHFSIDCFAKAIYILRIIFVIFDAN IFFQFIGCLLILCFR
1137	9188	C	2087	105	392	
1138	9189	A	2088	38	230	LYWQKRKGKLLNNLTQGIVADPVR*KK FHFКCPSNCPKIHNTESAYAVSFMKYSA HVLGSLYEM
1139	9190	A	2089	487	747	
1140	9191	A	209	465	1444	KKGEKDYSWTDLILTVSPPPGQKELARI \GQTFPISLKKMMSASML*ESPLNKG*E T*GPKAPKIQRLVTPCССSPNGGRIALK KQRT/TRKIKKRLQNMLNFWPRE*RRLR RSARNKLRRDADFPLCELLLLWCPPAT E
1141	9192	A	2090	1	1350	
1142	9193	C	2091	179	649	MFLLVGAPKANTTQPGIVEGGQVLKCD WSSTRRCQPIEFDATELHRELKENQNH YSLKSSASFNVIEFPYKNLPIDITNSTLV TTNVTWGIQAPAMPVPVWVILAVLAGL LLAVLVFVMYRMGFFKRVPPQEEQE REQLOPHENGEГNSET*
1143	9194	A	2092	274	423	
1144	9195	A	2093	1	3849	MCGGVFATEELAVSAGLKRКMCSVVEK RHGDFQVELLLDKLKQKGAIRRALFLYS RSPSHSKNMTISRGGLMQCEELIAYLRD ESEFRDKLTPITIFMEYRLDYRTAADTTG LQPILNQFTPANISRQSGFVLLTCSДQKKI YIGDDNPLTLIVKAQNQGEГAYEAEIIVS IPLQADFIGVVRNNEALARLSCAFKTEN QTRQVVCDLGNPMKAGTQHLLSPCTQF SMQVFLFHYTASSSVVALDSHRSKPVCV N

1145	9196	A	2094	1126	2034	RCWRPRTLGFASPPTRPCSPHAPGCEM TPRDWHRVLSFASPLRIEIEFQGYDKTFG LKNKKGAKQQKFIKAVTHQVKFGQ/SKS TSGSTE*SWKRKLKDDKKELQELNEL FKPVVAAQKI/RVKGADPKSVV\CAFFKQ GQCTKGDCKCKFSDLTGKMEKRSVY IDARDEELEKETKSSLIQADTMNDWDEK KLEEVVNKKHGEAEKKPKTQIVCKHFL EAIENNKYGFWFVCPGGGDCMYRHAL PPGFVLKKDKKKEEKEDEISLEDLIERER SALGPNVTKITLESFLAWKKRKRQV
1146	9197	A	2095	1	213	
1147	9198	A	2096	2	170	
1148	9199	A	2097	3	764	PAVVCGRRLISVLEQIRHFVMMPEINTN HLDKQQVQLLAEMCILIDENDNKIGAET KKNCHLNENIEKGLLHRAFSVFLFNTEN KLLQQRSDAKVTFPG/LVLRNTCCSHP LRQSSRALRESDALGS*/GARQHRGRLES LSLGIPLEEVPEELII*HRIHYKAQSDGI WGGHEIDYILWWRKNVTLNPDNEIKS YCYVSKEELKELLKKAASGEIKITPWFKI IAATFLFKWWDNLNHLNQFVDHEKIYR M
1149	9200	A	2098	1	299	GIPDQEVIGTGYGILDQKASGVKYTKS/D FRSPRPDDLSSFQL*VTSHWDLRLIEVTE TICKRLLNIACTRRGPAAIDLPRACQRPL RHYTTWYTKGSRW
1150	9201	A	2099	1	631	MDSMPEPASRCLLLLPLLLLLLLLPAPE LGPSQAGAEENDWVRLPSKCEVCKYVA VELKSAFEETGKTKEVIGTGYGILDQKAS GVKYTKSDRLIEVTETICKRLLNIACTR RGPAIDLPRLDSGLSFIRSGVRPACILVC LLVHRQKCSTVAAPVGT*RH*NGENSAR STMCRKVG*ARCQRTPRACQRPLRHY TTWYTKGSRW
1151	9202	A	21	918	1872	AEKGPPSPGVPSTCLANSPPPSAGSAAV PHSAPPGAAPRRSSRQRPCSPRRCWQEG AGVRAGQDGLGGSATRSAAQQSHQRQT GP/EGSTGKAKARGSTGRKR*AMGGSAA GDGA/PHVLGTGQPRAPPSTGDGARAG NWLAAQSAPTHRRWSTCWEFASPLPA SSNCCTHTWTRNCPGTAPSGTALPGLPG RPAPHPEPPPPMPPPP/PPRPGL/PLGSCVF L*VERPIWREVLSPAPPRACVDTSGHE/ ASGPSVPVAGTEPSRPWLKQPLCPPQQP RSWLTRRPE/AELHMPPTPLPAYLPGS/G VPQSHS*PPATLLR
1152	9203	A	210	87	904	GGWVAPETPSDPWFPVQRGVGDASVPG IGKNVVCEKAATSVDAPFRMVTASRYYP QLMSLVGNVLRFLPAFVRMKQLISEHYV GAVMICDARIYSGSLLSPSYGWFCDEL MGGGGLHTMGTYILDLLTHLTGRRAEK VHGLLKTFRQNAAIRGIRHVTSDDFCF FQMLMGGOVCSTVTNFMMPGAFVHEV MVDVPLL YLKGVMVYMQALRQSFQGG GDRRTWDRTPVSMAASFEDGLYMQSVV DAIKRSSRSGEWEAVEVLTEEPDTNQNL
1153	9204	A	2100	171	825	RANPTKPIGCAVRGPWSALKAGCGCQR RAGGRLAVVVVARRHVCSPGSGEGKLL RARPREEEPPGLGSGPGRAMDSMPEPA SRCLLLLPLLLLLLLLPAPELGPSQAGA EENDWVRLPSKCEVCKYVAVELKSAFE ETGKTKEVIGTGYGILDQKASGVKYTKS DLRLIEVTETICKRLLNIACTRRGPAAIDL PRACQRPLRHYTTWYTKGSRW

1154	9205	A	2101	2	527	PGRAMDSMPEPASRCLLLPLLLVMLVL LPAPELGPSQAGTDENDWVRLPSKCEVC KYVAVELKSAFEETGKTKEVIGTGYGIL DQKASGVKYTKSISDPPDQDDLSSFQL* VTSHWDLRLIEVTETICKRLLNIACTRRG PAAIDLAKVGFGIVLHPLWGPGLQCNLS VSAGL
1155	9206	A	2102	3	1203	SSAAEAMRVLVRRCWGPPLAHGARRGR PSPQWRALARLGWEDCRDSRVREKPPW RVLFFGTDQFAREALRALHAARENKEEE LIDKLEVVTMPSPSPKGLPVKQYAVQSQ LPVYEWPDVGSGEYDVGVVASFGRLLN EALILKFPYGILNVHPSCLPRIWRGPAPVI HTVLHGDVTVTGVTIMQIRPKRFDVGPIL KQETVPVPPKSTAKGIGKAVLFKDWGA NMLLSVLEKFGLESLSNGRQQPMEGAT YAPKISAGTSCIKWEEQTFEQFRLYRAI GNIIPLOTLWMANTIKLLDLVEVNSSVLA DPKN*REQALIPGSVIYHKQSQILLVYCK DGWIGVRSVMLKKSLTATDFYNGYLHP WYQKNSQAQPSQCRFQTLRLPTKKKQK KNCCYATMH
1156	9207	A	2103	3	215	
1157	9208	A	2104	2	341	SKPFSLQETYEAKRNEFLGELQKKEEEM RQMFVQVRVKEKEA/ELKEAEKELHEKFD RFKKLHQDEKKKKLEDKKKSLDDEVNPF KQRKTAELLQSQGSQAGGSQTLKRDK EKKN
1158	9209	A	2105	1	130	
1159	9210	A	2106	2	3449	
1160	9211	A	2107	2	1609	FVPPPFVEAYGWGCRKNWNWAGHRGK RRVKSAPSPYPTFKGWAVEGRLGLEQRR GGPSLAPPPTGLGRARSVTLSCRRSSSV SCAVAPVAAAPVAALADAGAMAATDIS RQVGEGCRTVPLAGHVGFDSLDPQLVN KSVSQGFCFNILCVGETGLGKSTLMDT LFQHQISKGEPATHTQPGVQLQSNTYDL QESNVRLKLTIVSTVGFGDQINKEDSYKP VVEFIDAQFEALLQEDPKVRRVLQTYH DSRIHVCLYFIAPTGHCLKSLDLVTMCK LDSKVNIPIIAKADAISKSELTKFKIKITS ELVSNQVQIYQFP/TDDSVAEIQLNP*TP HLPFAVIGSTEELKIGNKMMRARQYPW GTVQVENEACDFVKLREMLIRVNMED LREQTHTRHYELYRRCKLEEMGFKDTP DSKPFSLQETYEAKRNEFLGELQKKEEE MRQMFVQVRVKEKEAELKEAEKELHEKF DRLKKLHQDEKKKKLEDKKKSLDDEVNA FKQRKTAELLQSQGSQAGGSQTLKRDK KEKN
1161	9212	A	2108	1	618	
1162	9213	A	2109	1	427	HPVRRFFVHRGPH/VDFSLEVVSQWYELV VFTASMEIYGSAVADKLDNSRSILKRRY YRQHCTLELGSYIKDLSVVHSDLSSIVIL DNSPGAYRSHPDNAIPIKSWFSDPSDTAL LNLLPMLDALRFTADVRSVLSRNLHQHR L
1163	9214	A	211	217	624	GDELVKREAGMKMLPGVGVFGTG/ELPP EVLVPLLRAEGFTVEALWGKT*GGRRK ALLKEMNIAFHTSRTYDILLHQDVLVC ISIPPLTRQISVKALGIGKNVVCEKAATS VDAFRMVTASRYYPQLMSLVGNV

1164	9215	A	2110	2	835	WNSAELGRGPGAGGAGVIGMMRTQC LLGLRTFVFAAKLWSFFIYLLRRQIRT VIQYQTVRYDILPLSPVSRNRLAQVKRKI LVLDLDETLIHSHHDGVLRPVVRPGTPPD FILKVVIDKHPVRFFVHKRPHVDFFLAEV VSQWYELVVFTASMEIYGSAVGRNLW DNSRSIL*GGRYVYRQHCTLELGSYIKDP LLWFHRDLSGIVILDNSPGAYRSHPGY GGRADNAIPIKSWSVTPSDTALLNLLP MLDALRFTADVRSVLSRNLHQHRLW
1165	9216	A	2112	2	846	RFPLGCFPAQEPQGPVGPMPGAPAGNG HGS*SPHFHQGTGKRAALATWFNQPAP ERSPDVKAPAKPRARRIAPRPRVGVPIRP IVRCPTVRYHTKVRPGRGFSLEELRVA GIHKKIVARTIGISVDPRRRNKS\TESLQA KRAAG*REYRSKLILFPQSPRAPKKGDS SAEELKLAHPG*PGPGHAPSGTVYKKE KARVITEEEKNFKAFASLARMARANAPA LSAYRAKKSPRKPQKTDVEKPTIKPCLG TWNQSGSHAGSPRGVFRGNNWAWDGA SLL
1166	9217	C	2113	714	1010	MKSLNPHLDKIFPHKPLSSLASPSKTLVP GHLCDSTPFKFSFNYLLFPQNHPTSPH LPSPPKDKGISPIYTPHCLGGVITLILCMH FYRFVCHLSY*
1167	9218	A	2114	2	227	ERFRPPIARVIDVSNGKVHVAE/SCLEET GGLGVDIVLDAGLDPPDSHCLFLKGATL AFLNDEVWNLSNVQQGRYL
1168	9219	A	2115	3	487	
1169	9220	A	2116	1	489	
1170	9221	A	2117	2	221	
1171	9222	A	2118	353	512	
1172	9223	A	2119	1	1706	MPRAAIAQTPAPTAPAAAAARGPGRRLA ALSSPHLRAAEHDGRCSSETGCHGVLD LASPTPPFRSDERPDQWEQAGSLTKDW KVAVVKVQAVGAAQRQVSPGKRVLC GKRAFKRKVERCPTPCSPGEDGGSRR LTWDLFGPRPSLAEAAEGHFFLPHHFAV FGKQLVVIRCMWLLSQIGPLHYAKRRN HLERDVTMKGLYFQQSSTDEEITVFQE KEDLPVTEDNFVKLQVKACALSQINTKL LAEMKMKKDLFPVGREIA\GIVLDVGSK VSFFQPDDEVVILPLDS*KTPGL\CESL LRVHEPLLGFINPEKVTWTEAAGSISGM GVRAYYSFLHLSFFIFSPGGNQCLIMDGA KCHLRTIAIQLAHHRGAKVISTACSL QCLERFRPPIARVIDVSNGKVHVAESC ETGGLGVDIVLDAGVRLYSKDDEPAVKL QLLPHKHDITLLGVGGHWVTTEENLQL DPPDSHCLFLKGATLAFLNDEVWNLSN VQQGKYL*QSFQLRILKDVMEKLSTGV FRPQLDEPIPLYEAKVSMEAVQKNQGR KKPSWFQF
1173	9224	A	212	858	992	LKSPQRPGMVAHACNHSTLGARGGWIT/ R*GQEFKTSANMAKFHL
1174	9225	A	2120	230	535	

1175	9226	A	21	344	2631	GDREGTGR...EGAGAGMHFYDVEG VDWDRVQGP...MRGLSSSVQVGRFPAPK VSGPLSICVVRQLGLASSRFARSVPFGV WKKDLPLCLSLLSQSEDELTPFDMSIQVR LPFNLRQI*KQYWLGMVAHAHAGTEKDK NSVNFKNYVLQELDNPGQ*YFKISFSLI YENISTLIKEDMGHGS DYSLSEVLWVCA NLFS DVQFKMSHKRIMLFTNEDNPHGN DSAKASRARTKAGDLRDTGGHISPF*IG T*LLFFYFLFF*HISIAEDEDLRVHFEESK LEDLLRKVRACKETRKALSRCALSPGQL PTLPLNQKQAGRGGFKPPPIKLYRETNEP VKTKTRTFNTSTGGLLLPSDTKRSQVGR DAFCCCCF*DRVSLCRPGWRGLMLMGF KPLVLLKKHHYLRPSLFVYPEESLVIGASS VDHG*VTLTHSAVYGAALC/RYTPRRNIP PYFVALVPQEEELDDQKIQTTPGMWQ RYFQGF*TLPIWLNHPWTPQGGGTVRLA LDVSKKLETGTNCRQVKGLCWGNTGRN SKYRRAATTVLLSAVSVTHSATPEQ/VW GKMKAI VEKPRFTYR\SDSFENP\VLQQH FRNLRAALALDMEPEQAVDLTLAQCS Q*IKRLGSLVDESKGASLPQPDYNP\EGK SYPKRKNTNK*KGLGKKRKPWK*FK KEGA*RPHIKKGVRWGKVHCAPC*KEA CRGLRG*KSGLKVKQELLEALT KHFPGL DQRPAPALPAVLPGCPGLVLSQLKCV SPELGRVYPT
1176	9227	A	2122	599	1063	SCSEGLNAVNNLKASRKPKCLSLKWFL FYFP**IDSQAFYPLISKIVKRKMTFW TLYFMYLFLRQSLALLRPGWSAVAQSQL TVALGLL/VLRQSSYVSPPGTWNHRYMP PCPAF*NYFCRDGGLPILFRLVLSWV*A VLSRPLKMLRLQA
1177	9228	A	2124	142	461	
1178	9229	A	2125	145	904	VINLVYLISSPRELKPVDEKESEVVMKFP DGFEKFSPPILQLDEVDFYYPKHVIFSR LSVSADLESRICVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQHHV GAAGT*TFSACGNLLGTQVFLGRPEEY RHQLGFGMGISGELGHASSLPACLGGO EAEVAFCS DGLPCPNFLAL\DEPTNHLG HGRAIEALGPCLQTISGVGVILVSHE*SA LSRLVCRELVWC*GRRRHPGCKEGF
1179	9230	A	2126	39	2220	GASFPGVPEWNMATCAELRSEFPEIDGQ VFDYVTGVLHSGSADFESVDDLVEAVG ELLQEVSGDSKDDAGIRAVCQRMYNL RLAEPQSQGSQVLLDAPQLSKITENYD CGTKLPGLLKREQSSTVNAKLEKAEAR LKAKLRKRSEKDTLKTSNPLVLEEASAS QAGSRKESRLESSGKNKSYDVRIENFDV SFGDRVLLAGADVNLAWGRRYGLVGR NGLGKTTLLKMLATRSRVP AHISLLHV EQEVAGDDTPALQSVLES DSVREDLLR RERELTSQIAAGRAEGSEAAELAKIYAK LEEIEADKAPARASVILAGLGFTPKMQQ QPNPGVSQVAWRMLALAGALFARPD LLLLDEPTNMLDVRILWLENYLTWPS TILVVSHDRNFLNAIATDIHLHSQRIDGY R\GDFETFIKSKQERRAQQQREYEAQQQ YRQHIQVFIDRFYRNANRASQVQSKLKM LEKLSSELKPVDKES*VVMKFP*WV*EAL RRPFCSLDEVDFYYPKHVIFKRLSVSA DLESRICVVGENGAGKSTMLKLLGDL APVRGLRHAHRNLKIGYFSQHHVEAA WT*TSVLVELLARKFPGRPEEYRHQLG RYGISGELAMRPLASLGGQKSRVAFQA MTMPCPNFYILDEPTNHL\DMETIEALGR ALNNFRGGVILVSHDERFIRLVCRELVG

						MRRRR\VTRVEGGFDQYRALLQEQRRE GFL
1180	9231	A	2127	45	339	PPRTPSV PAG*LRAS/STPPRSSSSSSSSSP RKGLSLRPQEALPPPPCPSRSSAPSAPR GGRGETPNKGTGGSLCQSCHPPVDVQ AVLNKCFEAD E
1181	9232	A	2128	484	1879	FQQR MAGELKPSCNLEQSILLAKGTS\ GSSLTALISQVLKAP*VYVFGELLELCNV HELAE*ANAAYLQLLNLFA YGTYPDYIA NKESLP*LSTAQQNKLKHLTIVSLASRM KCIPYSVLLKDLEMRLNLEEDLIEAVY TDIIQ GKLDQRNQLLEVDFCIGRDIRKKD INNIVKTLHEWCDGCEAALLGIEQQVLR ANQYKENHNR/TLQQQVEADVILPQS GNDCRGLRFVSSLIGGVRCVHLKHKG D AVVWEAIEEGEALPGKYRLKGGRSVWA AAVRVCMQDVTNIKTLKATASSAQ EMEQQLAERECPPHAEQRQPTKKMSKV KGLVSSSPLGPAGAA GTHQAWVRWGG DTKGFPPLSTCSEFQTCSPHQRLPTLL VLFQKNCYSPSPTSPFSCSLQTQGLHQC HPKTGSDTAQLPSRRFLSLCKGLVSLPVF LLLPRHFVRLVISRRQL
1182	9233	A	2129	225	413	
1183	9234	A	213	1	126	FRAWTRSRSE RRRRRKRSSSGSEKFDSK K*KKNSSRKKQHEE
1184	9235	A	2130	356	1024	GRAEPEDLEN GESSAELDYQDPDATSL KYVSG*CHPPSGWG/HEDALIVHCVDDS GHWGRGGLFTALGKA/SPLKPRKIYELA GENEKTLSLGGVLLFPV***KIQDTKGKI CWP*LWLSIVNRSNVLSGI*DGSPIRRA* RRY/CLAAK KAGKSSVQPPHVLDMPRK GFKRVGVPEPTLFGKHPGLQRGHPQPYH ILFPLEGKSACPFHSQFFILPSLKDSWCP
1185	9236	A	2131	3	205	
1186	9237	A	2132	3	205	
1187	9238	A	2133	1	428	
1188	9239	A	2134	36	417	QAFRKFLPLFDRVLVERSAAETVTKGGI MLPEKSQGV LQATVVAVGSGSKGKGG EIQPVSVKVGDKVLLPEYGGTKVVLDDK VCKP**F*KEVRYLQLVVL TN GFFHLQD YFLFRDGDILGKYVD
1189	9240	A	2135	496	751	ISLLNKHPSFFKGGEIQPVSVKVGDKVL LPEYGGTKVVLDDK/DV**T**F*KEVRYL QLVVSTKGFFHLQDYFLFRDGDILGKYV D

1190	9241	C	2136	92	265	MSLVIIRFIKGEIWEIYMTERISGTSSGM GRHHVDAISNSDLFQSTVLSKNCNNL*
1191	9242	A	2137	330	875	AYAAGFGDSCLIAMSGRGKQ*GKVFAK AKSRSSRAGLQFPGGRVHRLLRKGNYA ERVVGAGAPVYLAADVLEYLTAEILAE GNAARD\NKKTRIIPRHLQLGHPATTEEL NKLA*GRVTICFRGGVPS*TSRAVLALPK KTESSPQGGQSDFDYLELPRKRYSNP KGSFSEAPLPFQRKS
1192	9243	A	2138	25	414	
1193	9244	A	2139	1	65	RTRGRTRGNLSFI*NHM*QIA
1194	9245	A	214	90	943	SPLADTFLLSGLGRTASPRPKAEARGTGR VRGLRAVRASPRMGRSRSSSRSKH TKSSKHKKRSRSDRDKERVVRKRSK SREK*RNRRRESRSRST/RHWPCPGAS GTGSAPRPRPTASTSSGARRASAGSLDE KQKARGGGEESGVPSGSEKFDK*KKN SSRKKQHEE*KNW*QKRVEEELEKRKDE IEREVLRRVEEAKRIMEKQLEELERQRO AELAAQKAREEEERAKREELERILEENN RKIAEAQAKLAEEQLRIVEEQRKIHEER MK
1195	9246	A	2140	293	444	SPSGYGR*SEASRRPTWCSQFQLRQPPHP EPPKSATWNQTPNIGNLSLPL
1196	9247	A	2141	544	1553	CQMRSCDRTECSFTTARICLSPLPTAFRT HTYGPKSCRSPACDVLGKGRSCRGWL RLASAWCSARVSAGSALRFPMESEM ETQSAGAEEGFTQVTRKGRRRAKQRQA EQLSAAGEGGDAGRMDTEEARPAKRPV FPPLCGDGLLSGKEETRKIPVPANRYTPL KENWMKIFTPIVEHLGLQIRFNLKSRNV EIRTCKETKDVSDDKRDQDFVK\AFILG LSGWKE*HLTLRL\DDLFE\SEITDVKP LKG\DHLSRAIGRIA\GAKEGKTKFTIEN VTRTTIVLADV\K\HILG\SFQNIK MARTA ICNLILGNPPSKVYGNIRAVASRADRF
1197	9248	A	2142	1055	1223	SSPGNLNVQEGFRITGLICY*KQYQY*MC FLFLL\SLYVCVDFLLLLCYKCGHPLH
1198	9249	A	2143	2	256	SPGRTAMRSWSCRPCGGGGLG/SSQGRS EPGSSRLGPAPS/CGLTHPCRRGPSCPHPC PAGCRTCGGICPGPHPTSRCPSPRNCGQT
1199	9250	B	2144	1	2848	MARRPRNSRAWHFVLSAARRDADARA VALAGSTNWGYDSDGQLLQVTCLSLTG SWLWDAGVPAGSAVFDCAACPVSPPNG PAVCCGQEHSDSDSDPEYSTLPSPISAV PVTGESFCDCAGQSEASFCSSLHSAHRG RDCRCGEDEYFDWVWDDLKSSATLL SCDNRKVSFHMEYSCGTAAIRGKELGE GQHFWEIKMTSPVYGTDMMVIGITSDV DLDKYRHTFCSSLGRDEDSWGLSYTGLL HHKGDKTS
1200	9251	A	2145	3	630	RSGGSASSGRAEARDCWGGRRSLPGDR TLEPCGGCNSCSGSPACCVAPA*GPAA AADPPACLPALAAAGAGGGSTGTGGK\IC AGTG/GG*PSCCSGPPWSTPSGRISC/CCS LVAATPGREGPSLYTSCS*KR*VCRARCP GARQ*WSPGRTATRSWSCRPCGGGGPC RRGPSCPHPCPAGCRTCGGICPGPHPTSR CPPSCRCRRRERS
1201	9252	A	2146	16	716	SVLESKGQRNKGQRKGPVPAQEGSSTG KSVRSGGSASLWQQGSRTAGVGGGRC PGDRTLEPCGGCNSCSGSPACCVAPA* GPAADPPACLPALGRS\CAGGGSTGT GGKWRWHRSG*PSCCSGPPWSTPSGRIS C/CCSLV/CCHTY/ITSCS*KR*VCRARCPG ARQ*WSPGRTATRSWSCRPCGGGGPCR RGPSCPHPCPAGCRTCGGICPGPHPTSR PPSCRCRRRERS

1202	9253	A	48	123	488	LKCNFRLDKYGTAMSGGEQKPERYY VGVDVGTGVSRAALVDQSGVLLAFADQ PIKNWEPQFNHHEQSSEDIWAACC/VCH KGDShrNVIMWLDHRAVSQVNRINETK HSVLQYVGGVMSVE
1203	9254	A	2149	2	321	
1204	9255	A	215	739	857	IIPSPNSNQLNPP***FPGNYY*YFNITQI NKDNYKTE
1205	9256	A	2150	257	565	INKDPIFVPGVWGPYFSA/MVPGFWLNE GGQSVTGKLDILSTNTPHPITILGNTNSIL KTQLQHQPFLITSPHIPKTPQTSRTDQA SFLCSPSSDSLQILSL
1206	9257	A	2151	1	291	VADLTCLKGMVTGLKLFQDLEYLAILYLA TVQAIALGTRFIIIEAMEAAGHSISTFLCG GLSKNPLFVQMHADITGSNGKNEQSWE SCVPETTG*KIL
1207	9258	A	2152	1	1690	FRDDPRVRARLRAESVYLKFNRLDKYC GGTALSGGEQKPERYYVGVDVGTGSVR AALVDQSGVLLAFADQPIKNWEPQFNH HEQSSEDIWAACCVVTKKVQGIDLNQI RGLGFDATCSLVVLDKQFHPLPVNQEGD SHRNVIMWLDHRAVSQVNRINETKHSV LQYVGGVMSVEMQAPKLLWLKENLREI CWDKAGHFFDLPDFLSWKATGVTARSL CSLVCKWTYSAEKGWDDSFWKMGLED FVADNYSKIGNQVLPPGASLGNGLTPEA ARDLGLLPPIAASLIDAHAGGLGVIG AHVRGHGLHL*GAASDVTLAVICGTSS CHMGISKDPIFVPGVWGPYFSA/MVPGF WLNEGGQSVTGKLDHVMVQGHAAFPPEL QVKATARMPEYILHI*TVTWDL*GRVQ PVGFSFTV*FYMFGPDFHGNRSPLADTL KGMVTGLKLSQDLDDLAILYLATVQAIA LGTRFIIIEAMEAAGPL/ESSTFLCGGLSQ E/YPLFVQMHADITGMPVVPVARGGSPF LCGA AVL GACASGDFASVTEAMAKMS KVGKVVFPRLPE
1208	9259	A	2153	1	479	AATSWGAAQTISSPILDKSLPADISIEDQQ CLVFRDVAPQAPVHFLVIPKKPIPRISQA EEEDQQLGHLLLVAKQTAKAEGLDG YRLGE*LLALGSPMNSHSYFSI*SSFFDL CHDPDSLTPSSISVINDGKLG AQSVYHLH IHVLGGRQLQWPPG
1209	9260	A	2154	284	604	RERRDIGGCWSSSAWGNPREWGFLGN DQGRCTGSLRGPTSREHKTLAGPHKRIV SWGGSCPRIREDGWGCSPRSWLAGAL ATFIP*KAPFPRIIPG*RRRPAATYVPPLS L*LLGH LTPMWLSRQQLRGLGDGYRL VINDGKLG AQSVYHLHIHVLGGRQLQW PPG
1210	9261	A	2155	496	1579	NCLNSFSCSMNQMYLLIALMTIEYNLAY DSYYICHFIFIKIVYKLTDFFLQMR*ILM QIFW*GSLFLL**FQLIRDLPAFSLR*KL CPHLLKYKGILWKQIILVLC*R*ILILMC DLFALSGIIVFLSFIMRKFSHL*VTVKFIY MSIPRRPVQIL*EHLGLQDIIGI*ILISCY** ENRYSIVIPLF/CF/VILITHFGFFSLF*I*LL VFV**F*FNPNQYI*FI/CFLSNLTTFFL CFLVGG*/CFVKGIIV*DHCFHTCFTLHVF *STFIY*AFGLE*FHQMNTFW*FVMSSSN CYTLLGT*Q*ICKGKRNNFLYSANLFI** IIHFFLKIVWIDCF*NTNLWLWFFFSSAFP ASK
1211	9262	B	2156	302	451	XEFLFKHPKRTATLSMRNTSVMKKGIF SAEFLKVFLPSLLSHLLAIGLG*

1212	9263	A	57	1	765	PPLSPGAHV APTSAFPPPAEAHPA ARRGLRSPQLPSGAMSQNGAPGMQEE LQGSWVELHFSNNGNGGSPASVSIYNG DMEKILLDAQHESGRSSSKSSHCDSPPRS QTPQDTNRASETDTHSIGEKNSSQSEED DIERRKEVESILKKNSDWIWDWSSSAGKI FPPKEFLFKHPEAARPTLQA*GNRAVMK KGGIFSA/ENFLKVFLPSLALLSHFAGPSG LGVIYIGKGVLTSTSTFWMKELGVLT R
1213	9264	A	2158	1	381	
1214	9265	A	2159	2	312	
1215	9266	A	216	263	425	FAFQKFYIYTYF*KHTL/WLGAVAHGCN PSTLGGQGGQIT*DEEFETTLDKMVKS
1216	9267	A	2160	1	576	
1217	9268	A	2161	2	313	VSYYHFHRMEKAHPEPGTWDSFLEKFM AGE/VWA*LEEGGCEAEGWWL*RTATL CRCPLPASLVSYGSWYQHVQEWELSR THPVLVLYFYEDMKEVRPTVMLPPM
1218	9269	A	2162	901	1848	RRNMELIQDTSRPPLEYVVKGVPLIKYF AEALGPLQSFQARPDDLINTYPKSGTT WVSQILADMIYQGGDLEKCNRAPIYVRV PFLEFKAPGIPLRMETLKDTPAPRLIKS HPLAALLPQTLLDQKVKVYVAAQRKR SVAVSYYHFYHMAKVHPEPGTWDSF LGESSLVL*KVVLADSWYQHVQEWEL NRTHPVLVLYFYEDMKENPEKGRFQKDP WSLGGRSLQEKTGDFQVQHTSFKEMK KNPMTNLHPTVPPGSSMDHSISPL*GK GMAGDWKT/TFTVAQNERFDADYAEK MAGCSLSFRSEL
1219	9270	A	2163	3	287	
1220	9271	A	2164	75	301	AHKKLRAAPLAPMTGTH*KVVFVAGD KVKAGNPSWVMFPMKMEHTIKSPKDG TVKKVFYREGAQRHHSFSRV
1221	9272	B	2165	63	368	MKGGRSPASPAKADGSHCDPKTAPKAK EAPAPKAEAKAKALKAKKAVLKGVRS HTQKRRSACHSPSGGPRHCDSGGSPDIL GRAPPGETSVATMLSSKFR*
1222	9273	A	2166	153	370	LIAGAFRKASGGNNIFRRPKTL*LRRQPR *PQKSTPRRNKLGHYAIKFPLTTESAVK KIEETNTLVFTVLV
1223	9274	A	2167	842	1770	CTPEKCLPAVHRRNWLRNAEPPVWKRH LSPICRKRQGRATKPKRRPYTTPPTRR VRDVALRPYSRH/GRQPHAKKIRMSLT FRPKTLRLRRQPRYPRKSTPRRNKLGH YAIKFPLTTESAVKKIEENNTLVFTVDV KANKHQIRQAVKKLYDSVAKHTEERR HDEQNNILTREAKNRNDNTRNRARTETN TETQKNSGYQALISFHSYSDTSDNKAH LVSYQSGQCTYDRLGWNLLIRMTCSL QHTYDIQSTQIASCFHPVSVRVNLRLYC ANYGGISAVFMPLRKELLILTRSSNSKVS QLRI
1224	9275	A	2168	3	281	
1225	9276	A	2169	353	605	EMAPKAKEAPAHPKAEAKAKALKAKK AVLKGVRSHT/RKKKIRMSLTFRRPKTLR LRRQPRYPRKSTPRRNKLGHYAIKFPLT T
1226	9277	A	217	2	660	FVTRPDAGVMRLPLVLLAVLLAVLCK VYLGLFSGSSPNPFSADVRRPPAPLVTDK EARKKVLKQAFSANQVPEKLDVVVIGS GFGGLAAAAILAKAGKRVLVLEQHTKA GGCCHTFGKNGLEFDTGIHYIGRMEEGSI GRFILDQITEGQLDWAPLSSPFACIMVLEG P/KWPKGVPHVQWRESLHSGPQG/GSFH RRKLSLTSI*SWLRWYPVEPLMPSC

1227	9278	A	2170	301	946	PGSYLKPLSWIVALSRLRPGFMSRWPCQR LTWQRRSVTQASGASGASLCASRLPRDK TAPKAKEAPAPPKAEAKAKALPKKAV VERCPHTHAKKRIRMSPTFRPKTLRLR RQPRYPRKSTPRRNKLGHYAIKVFPLTTE SAGKKNKKNNTPLVHCGC*RPTRHQJR QAVKKLYDSDVAKVTTLICPDKEKKA YVRLAPDYDALDVANKIGH
1228	9279	A	2171	1	1602	
1229	9280	A	2172	243	620	LLTSSKVMNLSLLEVFS/VSSSQSPSPGP NHTSNSSNASNATVVPQNSSARSTCSLTP ALAAHFSENLIKHVQGW PADHAEKQAS RLREEAHNMGTIHMSEICTELKNLRSV RVCEIQATLREQR
1230	9281	A	2173	3	688	QRSFLRVPQSPPIPLLQDPNLLRQLLPAL QATLQLNNSNVDISKINEVLTA AVTQAS LQSIHKKFLTAGPSAFNITSLISQAQLST QAQPSNQSPMSLTSDASSPRSYVSPRIST PQTNTVPIKPLISTPPVSSQPKVSTPVVKQ GPVQSATQQPV TAG/PGPRS/SEPVSRR SSALK*PEKSITWVPIHTSNSSNGIQMAT VVPQEFFLARSTCSLTAGTSSTLQ
1231	9282	C	2174	1	1038	MEDFTTPLSTLASSMRQKVNKDIDLDS ALQQADVIDIYRTLHPKSTEYTFFSALHC TYSKSDHVGSKALLSKCKRTEITTNCVS DHS AIKLEFRIKKLTQNR TTTWKLNNLL LNDYWVDNEMKAEIKVFFETTQHDQNF TKARCIQEHRTYPYSQSFKLKAETRDPSF TKNVQKMKRVRDADLAVAALSRLRGK VWVKAWPPLRGCRV LGCCFLAFCIRSL MDVKHSCPVCQRELFYHRLPRSPRSA YLAVRDIGPKMARDTVNLWPQARDPSE NASPALLQTHAEKVLVRRVGSGLGTTLP RRGDDPTPERQISFLKCLLKKLSHGFGSE GAMPEEISH*
1232	9283	A	2175	1	1312	MGRNQSRKAENSKHESTYSPKDHSSSQ AMEQSWTENGFEKLGFRKEALYYLDL TASCQSQELFQLYAGMSVVGTSMPVQA VCPYCGNRIITVTTFVPGALTWLLCTTLF LFGYVLGCCFLAFCIRSLMDVKHSCPVC QRELFYHRLRQME LASSARTVVAPSRP CAGREGRGDANGKNSSPTAGSAMSSEPP PPQPPTHQA\GVGLLDTPRSRERSPSPL RGNVVP\SPLPTRRTRTFSATVRA SQGP VYKGV\CKCFRSQRAIGFNYPAGWAG PDIF/LWHIS*LWKGGVIVPSGKGDEGHP NKMCSHPHPKE*R\IAARPVKVVHHLTL APQAPKHETWS\GHVISSLGGLVESTPLS LCFVGDFAGRRQQTLEDDILPHETGLQR GNGPSQVSPGGKGYGGAGVGCGVFP AIS TAYGPLQQPLHHLKSIKSI
1233	9284	A	2176	75	411	PIITKEHLFYVILVPSSGLDGIQG*SQKEG RGLAVPTPVSAAGLPAASMAEEAADQ VGRAALAWLCPAGRRRGFGGEVMRAL VASRPDLLTSSASSG WALGSEGRVKASA D
1234	9285	A	2177	1	361	GIKRRSGREATRALITSPNPFRRPAGQS QARAARPTWSAASSAMEAAGSPAATET GKYIASTQRPDGTWRKQRRVKEGYVPO\ RRSQYMKTSM*SF SRVNQSCPQG*ALRP LLSPHPGPEGGEPLQGQPNVNLEGE REKEAAAGKRKERAEGLSKDS*LRCPW EETAQLPSAPQGSRAAPTAASDQPD SAA TTEKAKKIKNLKKLRQVEELQQRIQAG EVSQPSKEQLEKLARRRALEEELEDLEL GL*GLSPEATAPVTPSRA
1235	9286	A	218	151	414	ERERESVCVCMCVRVCVCLRERERQ RQRDKRLCGEMRKIQYVNNKLHYI/SKYL YIYKYVILQT*TFIHIYIYLYK*ICIHTQMY

					AVY
1236	9287	A	2182	3	140
1237	9288	A	2183	365	2078
					NLVHCHCLDIFINQAFDMQRDLQITPKR LEYTRKKENELYESLMNIANRKQEEMK DMIVETLNTMKEELLDDATNMEFKDVIV PESGEPVGTREIKCCIRQIQELIISRLNQA VANKLISSVDYLRESFVGTLECLQSLEK SQDVSVHITSNYLKQILNAAHYHVEVTFH SGSSVTRMLWEQIKQIIQRITWVSPPAITL EWKRKVAQEAIESLSASKLAKSICSQFRT RLNSSHEAFAASLRQLEAGHSGRLAEKTE DLWLRVR\KD HAPRLARLSLESCSFTGC LCLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEF HYMRS LPKHERLVDLHG SVIDYNYGGG SSIAVLLIMERLHRDLYTGLKAGLTLETR LQIALDVVEGIRFLHSQGLVHRDIKLNK LLDKQNRKITDLGFCKPEAMMSG SIVG TPIHMAPELFTGKYDNSVDVYAFGILFW YICSGSVKLPEAFERCASKDHLWNNVRR GARPERLPVFDEECWQLMEACWDGDPL KRPLL GIVQ PMLQGI/L*NRLCKSNSEQP NRGLDDST
1238	9289	A	2184	2	468
					GPEAVPHRACSLWLPTSPGPTCPATRHS EHEFTFQMWPGCASSLLCVGTPGEARA DHRCMRVTPVHLGLPGWVGAGARPH CCESATPGGPRGCPTP/DDWVA AHIPPSF HK*GNPGCIRGDPRGLLWPLCPMTCVAS DKAPALLGSACCSVWSVR
1239	9290	A	2185	170	1224
					PVWRGPAGPTPGIPSTTEKHTRLPSANM MVLKVEELVTGKKNGNAGEFLPED FRDGEY*AAVTLERQEDLKTLLAHPVTL GEPQLRKRETHERAELKKKKLEQRSKLE NLEDLEIIQL*EK/RKKSRET KVPVLKDP EP*IHYGTCWECPTFLKA/SLWENNL PVV EKFLSDKNNPDVCDEYKRTALHRACLE GHLAIVEKLMEAGAQIEFRDMLESTAIH WASRGGNLDVLKLLLNKGAKISARDKL LSTALHVAVRTGHL*GCAEHLIACEADL NAKDREGDTPLHDAVRLNRYKMIRLLI MYGADLNIKNCAGKTPMDLVLHWQNG TKAIFDSLRENSYKTSRIATF
1240	9291	A	219	4	328
					HGVSLFPRLCNGTISAHNLRLLS*SD SPASASQVAGITGMHHARLIL/YFLVEM GFLHVGQAGLELPTSGDPTLPWSPKCW DYRREPTSPGPQTYIITQSKSSP
1241	9292	A	2190	93	458
					LLLWTMSVIFACVVRVRDGLPLSASTD FYHTQDFLEWRRRLKSLALRLAQYPGR GSAEGCDFSHHSIIQKVKWHFNYVSSQ MECSLEKIQEELKLQPPAVLTLED TDVA NGVMNGHTPM
1242	9293	A	2191	1077	1818
					LLLWTMSVIFACVVRVRDGLPLSASTD FYHTQDFLEWRRRLKSLALRLAQYPGR GSAEGCDFSIHFS\SGDVACMAICSCQC PAAMAF\CF\ETLWWEFTASYDTTCIGL ASRPYAFLEFDSIIQKVKWHFNYVSSQ MECSLEKIQEELKLQPPAVLTLED TDVA NGVMNGHTPMHLEPAPNFRMEPV TALG ILSLILNIMCAALNLQPVQHVYLGQLDLG AH/HRKSFIGREKGNILVF*VDMIQ
1243	9294	A	2192	1	999
1244	9295	A	2193	1544	1928
					QKVRGQIREGCLEEVALGSSRPPAHVCL GLPTGQTADGKSYVKYQVIGKNHVAVP THFFKVLILEAAGGQNELRTYVMPNAP VDEAIPLEAFLVPIESIERASGLLFVQNIL ARAGSLKAITAGSK

1245	9296	A	2194	2	1068	ARGWVPRPKPLAVFVSGREVTLSAAPA ALCPRWIPRRGSFKSLAGRPLGRSPAM RALRAGLTASGAGLGAVVEGWRRRRE DARAALGLLGRLPVLPVAAAAELPPVPG GPRGPGLAKYGLPGLAQLKSRESYVLC YDPRTRGALWVVEQLRPERLRGDGDRR ECDFREDDSVHAYHRATNADYRGSFDF RGHLAAAANHRWSQKAMDDTFYLSKV APQVPHSNQIAWNNLAEKYSRISLTRSYQ NVYCLH*GHFFLPRTADIGKSYVKYQV IGKNHVAVPTHFFKVLILEAAGGQIELRT YVMPNAPVDEAIPLERFLVPIESIERASG LLFVPNILARAGSLKAITAGSK
1246	9297	A	2195	204	507	GSPGTRSETREPGAMSQPPAPPPLPPPPP PPEAPQTPSSLASAAAASGGL/*SGETGESF PGAARIRSVRRVYFSRPPVLSASSVPSAA SGTSSNSCWGLRR
1247	9298	A	2196	1	460	EFKQLIHIEHQPNNGASVIHAYSNELSHL SPMEMERFARKSLVGS*CSSENENSGSFP T*WGIVHGAATYLPDFLDYFSFNFPNS PVKMEILGKKDIETTTMSNFHAQSLTVL QPGRQSETPSQKKRKKFMIMLSSRWEGE TKNKYRRLTN
1248	9299	A	2197	199	769	
1249	9300	A	2198	182	2889	TEKGAAAGTAGSCSRRQHASPQSYGSPA SWSFAPLSAAPSPSSSRSSFSAGTAVPS SASASLSQPEPRKLLVPPTLLHAQPHLL LPAAAAAASANAKSRRPKEKREKERRR HGLGGAREAGGASREENGVEVKPLPRAN DKTRSFDDFSPDQAAAECLSIRKRILKG SCQTGYLRKALFSDTVTLGIKASTYGFV GGMISIVKGLAETFNFWIHWELNDLQ YISALFACSEMPDYHLEKQLADKIKDKI KERDKEKEREKKKHVMNEIKKENGEV KILLKSGKEKPKTNIEDLQIKKVKKKKK KKHKEKREKRPKMYSKSIQTICSGLLT DVEDQAAKGFLNDNIKDYVGKNLDTK NYDSKIPENSEFPFVSLKEPRVQNNLKR DTLEFKQLIHIEHQPNNGASVIHAYSNE LSHLSPM/EGWERFAEEFVG/*VFSENE NSAAFYVMGIVHGAATYLPDFLDYFSFN FPNSPVKMEILGKKDIETTTMSNFHAQV KRTYSHGTYRAGPMRQISLVGAVDEEV GDYFPEFLDMLEESPFLKCTLPWGTLSL KLQSRKDSDDGPMWVRPGEQMIPVAD MPKSPFKRKRTTNEIKNLQYLPRTSEPRE MLFEDRTRAHADHIGQGFERQTAAVG VLKAVHCGEWPDPRIKDVICFHAEDF LEVVRMQDLHEPPLSQCVQWVDDAK LNQLRREGIRYARIQLYDNDIYFIPRNVV HQFKTVSAVCSLAWHRLKLYHSEEDTS QNTATHETGTSSDSTSSVLGPHTDNMIC AVSKASLDSVFSKLSKYELQIKHEPI ASVRIKEPVNVNIPEKTTALNNMDGKN VKAKLDHVQFAEFKIDMDSKFENSNDK LKEELCPGNLSLVDTRQHSSAHSNQDKK DDDILC
1250	9301	A	2199	2	122	
1251	9302	A	22	10	284	
1252	9303	A	220	436	777	IYSYGKTGPV*KRKNCQSRIKEQNPIICW LQATHLKCKETYKLL/MRKICQANTNQ EEIGIL*NSRLYSKNYYQG***KGSILQED MTILNMYAPKNRSGGYMRQKLIELQGE
1253	9304	A	2200	1130	1437	LSRIMKAWFPLFFKIPFRDKVFFLSPPAW SAVAQSRLHCSLELVGSINSSISAS*LGW EYRCAPQCPG*FLAFFCRD GALPCCPSWS QVICLP*PPKALGLQA

1254	9305	C	2201	279	449	MHPVSCWVIMSCRPLCTRLILSDSPGPP SDICVSRKNPSNYPAMVLPQCFTICH*
1255	9306	A	2202	1	1173	
1256	9307	A	2203	1	2112	MGVELFTPASVMGVKRCCCSIPGQLSGN GEPRFSEIDSSVSVRGGWQPRWFLLCGGI LSYYDSPEDAWKGCKGSIQMAVCEIQV HSVDNTRMDLIIPGEQYFYLKARSVAER QRWLVALGSAKACLTDSRTQKDKEFAE NTENLKTkMSELRLCCDLLVQQVNKTK EVTTTGVSNSEEGIDVGTLLKSTCNTFLK TLEECMQIANAAFTSELLYRTPPGSPQLA MLKSSKKVNQKYITNKEEFTTLQKIVLH EVEADVAQVRNSATEALLWLKRGLKFL KGFLTEVKNGEKDIQTALSFSSN/SCT/CI WRLGPGDVLTL*RKRL*LANAAL*LQ* SQPVSAFSSLSSP/CGTIFNGKEKGCKFD IFVLMFRLISKKTQTQALRRFFEKCLH NSYSEPVGSLMHSSGIMVPFSHFVPAFI SRDITLFEMREDNAYGKTLRQHGWVV RGVFALALRAAPSYEDFVAALTVKEGD HQKEAFSIGMQRDLSLYLPAMEKQLAIL DTLYEVHGLESDVLYPLGCLDCCPEGE QSWFQKKNVFGCLSQLPVGRGVQLPCG HEGPAKENRVWLCMLAITPESAEQNR DNHLWSSVVRVDGELMNDGLTSALRT QITFGMICCVNALSSSENKVASLLTLVRF TAAPSLPTLHCVSRHLQVEDPHLVMSVC ECGTTISLPEPRSQLQCSTAVSQLEDSRR MAEH
1257	9308	A	2208	132	509	NMVQTTCPGLMSTPCTGPAQARR*K/ WLVECLSLTGMGPGEGRGQGAEEAEP N*VLGTPAGGSGPCPPGIQQTTPSPHQP SQVLSSLSPTRICPGFLAYLLSLFTPREE LQLTQNDTFLAPRV
1258	9309	A	221	212	275	FLILNCNSF*KIYPKYKSLIR
1259	9310	A	2218	491	812	
1260	9311	A	2219	2	948	IFKIAFAKFGVWAGEWGREGMGRKWS ARAAAQRAEPRSGRQVRPRALRPPARQ PRQLEPSRPPAAAPESPSSSAMAGWN AYIDNLMADGT/CVTGAIVRYQDSEPPF WHAVPGK/TRFVNITPAEVGCPWLAKTR SSFLR*MGLTLWGGQK\CSVNRGLHCLQ EWGIIACDLRYQEPPGGAPHLISVTCPR LNKDAKSWLMGQRKVSHGGLTNKKCY VEMASHLSGFPSTDLRLVPFPLSPFPTAFA PLSLPIHTQTNFYFLGPLHTPYCCQNHM GLGGQGLMGQTPSPTHIPSRVWLEKLLF FGVFFFSE
1261	9312	A	222	770	1573	NHLEIVNLCNVGISQSFPQI*LKAQATKE KINCIPKLTFG/TEKYIKNVKRQYIE*Q KISANHLSDKRLVFRIYFLKTITVQY*KD KPIIK*VKDLNR/HFSKEDT/YMTNKYMK RC*KSSSTIREM*IKTTMR*TLPHYRWNIK KTDNNNC**GCG*TGNIHCWLECKIMY P/IFRTV*QFPEKVKQHYPSSDAAILLGIY PRNMK/SKCLPKNYTRMFITELLILKK*K QLKC/PIN**W/K*NDKMW*IHMICYSA IKRHRVLINA
1262	9313	A	2221	259	941	PVSWSLNSCRFFFF*DSQLSPVV/QAGS GQ*RNLDL\QPLASRFK*FSSSRL\SSW DYRHMATMARLIFILVEMGFMTLARL VLNFLTSSDPPTSAFFKWGLGQGVKPN RAVGFN**LGYYSIILYHSNSPGTDLVFIL FIYLFYFLRQEQNSAAQARVQ*WHNL GSLQSPPPGVH*FLCLSLPSSWDYRCAPP HQANFCIF*RDGVFCWPWGSRTPDRL

1263	9314	A	2222	343	600	MSPLSQFVDGTLKIQCYYGTFEHSVA RLECIGMISAHCNLCPLGSSNSPASAS*IA GIIAP/CHHAPLIFVFL*RQGFTRIYFFK
1264	9315	A	2223	142	583	
1265	9316	A	2224	163	1603	IQAGQCGNQIGAKFWEV\ASDEHGIDPTG TY\HGDSDLQ\LDRI\VVYNEATG\GKY VP\RAIL\VDLEPGTMDSV\RSQFPGQIFRP DNFVFGQVWGQVTTWAK\GHYTEGAE LVDS\VL DVVRKEAE\SCDCLQGFQLTH SLG\GGTGSGMGTLTYQQGFKEYPDRI MNT\FSVVP\SPKCLDTVVEPYNATLSVH QLVENTDETYCIDNEALYD\ICFRTLKLT TPTYGDLNHLVSATIE\CVVTTCLRFP\GQ LN\ADLRK\LA\NMVPPRL\HFFMPGFA PL\TSRG\SSQ\YRALTVPELTPARSDAK NMMAAC\DP\RGQPINFNRGLSSRGSGC PMKEGRMKQML*RCKNK\NSSYFCGNE SPNNVK\TAVCDIPTSWASKMAVTFVIGQ *HSPSQELFK\RI\SEQFTA\MFRRKAF\H WYTGE\GMD\EMEFT\EA\ESNMNDLRL*S IKQLPRMPTQEEEEDFGEEARKRRPKGR APNQLKASQFP
1266	9317	A	2225	234	1374	KSGGLRRRQRPGRSAAVGEEELPPGMEK FKAAMLLGSGDALGYRNVCKENSTVG MKIQEELQPV\GGLGHLV\SPGEWPVSD NTIMHIATAEALTTDYWCLDDLYREMV RCYVEIVEKLPERRPDPATIEGCAQLKPN NYLLAWHTPFNEKSGSGFAATKAMCIG LRYWKPERLETIEVSVECGRMTHNHPT GFLGSLCTALFVSFAAQGKPLVQWGRD MLRAVPLAEKYCRKTIRHTAEYQEHWF YFEAKWQFYLEERKISKDSKNKAIFPDN YDAEERE*TYRKWSSEGRGRRGHDA MIA\YDALLAAGNSWTELCHRAMFHGGE SAATG\TIAACLFGLLYGLDLVPKGLSQD LEDKEKLEDLGAALYRLSTEEK
1267	9318	A	2226	139	366	AMAYQLYRNTTLGNSLQESLDELIQGS NTYRFCDNVWTFVLNDVEFREVELIKV DKVKIVACDGKNTG\SNTE
1268	9319	A	2227	160	588	AMAYQLFRILPLETSFQESLAD*LIQSQQI TPPTCPFKFYQLDRA\NAALA\QVRN R\VNFRGSPKYGTRFC\DNVGDVWYRND\ VEFQRG*PEPIKRG*K*KLVACDGKNTG LPIPT\WNRKKYDFFYTHLLLFI\AFEREA
1269	9320	A	2228	918	1085	QEKLF*VLCFNFFSFFFFFFCFL\VD*F*FL FGKGAV*TLFVSSASHRYRQGKTR
1270	9321	A	2229	145	365	
1271	9322	A	223	86	427	SPQIRKQEISI/SLLTDGTILYIENPKESPPP KLLKVIKFNKATRFKINMQKSVVFLHPR N/QFENEFFKILSFGTEPS/RSEYLG\NITK EV*NLNTKN\DIV\KMKELLSKWKD\SPC
1272	9323	A	2230	2	750	ILGFDLQPPGRRWAAPAV\SGLS\RKVRC FSTG*VRPFA\KLVGPSVQVYGIEGRYA T\ALYSAASKQNK\LE\QLEKELLRVAQN PRRNPKVACFLNPLCESRSIKSEKALN\ DITSKRRFSPPSTTQ\LLNQFCLAGKMG PI*ANNPKGVV\SGLFLTMDGVFHSRERV PLHSGPLASSFRKESHTLLNLKTVLKEFP KVKGQVLELGAK\TDPS\LGGMIVRIGE\ KYVDMSVKTK\QKLG\RAMREIV
1273	9324	A	2231	100	468	ATEPLAPSERREVSIPLLVAPLPPPPRP VPSRTRTRPWRRP*ACFPMTLAASCGPT RSPWPSQQIPQAPVG\PGNIKT\LGDAY EFAVDVRDFSPEDIIVTTSNNHIEVRAEK LAADGTVM

1274	9325	A	2232	228	721	LWQLHAAPLGAPGLPRQVIRALRGGEV HREGTSAPGRHRRRCGCPVGLQVLHSL QPCVATKTDVATGTDVAMKTGNIKTLG DAYEFAVDVRDFSPEDIIVTTSNNHIEVR A/REA/ERP DGTVMNTFAHKCQLPEDVD PTSVTSALREDGSLTIRAWRHPHTEHVQ
1275	9326	A	2233	3	605	KKLTPVVRSRVERDPRVRRGLRPHVLS SLRPPGQGPAPSVDEPQNLFLHSPGEKIP FLFLLLLLFTPPRPPVLSRPRTWPWRP* ACFPMTLAAICGPTSPWPSQPAPV/VAG NIKTL*DAYEFVVDVRDFSPEDIIVTTSN NHIEVRPEKLAADGTVMNTFAHKCQLPE DVDPTSETALGEDGRLTIRARGHPHTE H
1276	9327	A	2234	229	510	KGIWYINMEEQFVI*IHFL*TRSQFYFVNI TFKYIYTHIYVQLYIHVH/MICKFIFIYNI *IDICRQVIDYRDPKQLNNCSKFSSSLTA GV
1277	9328	A	2235	203	334	SRRDHSFIL*ILHLSIYIHTYMYNYIYMC YMYQRKQYGKTNP
1278	9329	A	2236	1023	1470	TPKTKHNSNPFVPHAHKFACSYFFFCCLC VFMGSKLNLLAIYKNVNSKLYLLRNVI F*FIFTQLFILIYFFYTVLNTQTYFLFMIFL SCSHGICFPILFSLISITGWDLTNNNVRGR KYFATVDYYTLKFYIMKIYNSLYASKKK KKA
1279	9330	C	2237	226	450	
1280	9331	A	2238	3	449	LLRRVSVTAVAALSGRPLGTRLGFGGFL TRGFP/KAAAPVRHSGDHGKRLFVIRPSR FYDRRFLKLLRFYIALTGIPVAIFITLVNV FIGQAELAEIPEGYVPEHWEYRVKELE VRKLMHVRGDGPWYYYETIDKELIDHS PKATPDN
1281	9332	A	2239	3	635	HASAHASAMSLRRVSVTAVAALSGRP LGTRLGFGGFLTRGFPKAAAPVRHSGD HGKRLFVIRPSRFYDRRFLKLLRIHLAL TGLPVTIFIALVNVFIGQAELAEFPEGYV PEHWGILLRHPISKMGFAR*FLMIGPEK DIMERNNGPSFQIGSLKKAGIYGVKGSW EVRKI*WHVEEGDGPWVLLWRPFDQGT LLDHSSRKPTPWTN
1282	9333	A	224	35	397	FLTGTQWKG/DSPFNTWC*DH/WNIHRN LDLYLIPYIKINLKQLTGPNLRAKTIKLPE QNIGENLCDL*LSRERYSTKSITIRIKL/D TLGFIKIKNKCISKDTIRKR*ATDWEKIFA NHVLKG
1283	9334	A	2240	811	1005	SNFTGKIHK*LTSFKIVNLFYIL/FFETGFH SLTRLECSGMILAHCNLRFPESRKLFFFG AIDSF
1284	9335	C	2241	256	540	MSPAKATEMLIFGKKLTAGEACAQGLV TEVFPDSTFQKEVWTRLKAFCKLSPNCL EIFKEVXRKRERXKLXAVNAEECNVLQG RWLSDECTNAV*

1285	9336	A	2242	602	2067	SSSSGLALGMQRPLLARLRTGTPGRALSA PAATGFAELRAAQGMAMAYLAWRLAR RSCPSSLQVTSFPVVLHNMRTAMRASQ KDFENSMNQVKLLKKDPGNEVKLKLY ALYKQATEGTCKMPKPGVFDLINKAKI WDAWNALGSLPQGSCPG*NYVDLVSSL SPSIGNPPS\QVEPGTERDNQLGFETLVVT SIEDGITKIMFNRPKKKNAINTEMYHEIM RALKAASKDDSIITVLTGNGDYSSGND LTNFTDIPP/GVGVEEKANTNAIVLLRIEF VG\CFINDFPKPLDCSGSMGPSCGASPVTL LGAYSMPVLLHLDRTGTFHTPF*SP*AQS PEG\CSSYTFPKIMSPA\KATEMPFIFGKE VNQREEACASRDLFTEGFPWIALFRKKV WDQG*RAFCKSFPPQMALEEFSEKIVIRK REREKLHAVK\AEECQCPFGKWLSDE C\TNA\VVNFLSQIKNCDDHLQHQHSM SQGRMCCSLCLSSTGTK
1286	9337	C	2243	2163	2402	MSQAAASHKSKLTPKNQRAPFTLLRKSQ CQDPSRGESEEGWWPIQRACRSMETFLP QMFQSWHQIYKNVSRDQFFTLK*
1287	9338	A	2249	761	1178	LSTPLTSWCWMRRTTPGSPTRCSCSSA\ PGTQPLGGGHQ*RGCHQCVASSPR*AWP ASGPAKLQ*LQPKTQQRAPATGEHVPP VQPSAQ*PHSRFQSSETSRPADGSEQQPA RASGPGARRPPHQPRQVINCWLRR
1288	9339	A	225	832	1043	LLWWFRLRSSPCGTQQGPWHLVCVGY AG\GWAGPPWHTCPWDPSHCPGTE*CP WCVWFCFFCNTYLLVPN
1289	9340	A	2250	135	408	PHSRFQSSETSRPADGSEQQPARASGPGA RRPPHQPRFHPPPSA/RAISIECPA*AVMR SGSEPRARQEYSLGLWTPSQFLQGILYLA RSPT
1290	9341	A	2251	123	578	TTNIFKWAKYFKRHFSRDI*MANEHM KRCLTSLTIMEMQIKTTIRCHLT/PRMPII KKIIKC**GWRETGTLI/YAWWECKIVQ/P AFR/TVWQFLKRLSQHPTIPFP/GMCPRET KTHIHSKTY/TQMFMAALFIEARKWKQF KCLSTNEWTNVVRP
1291	9342	A	2255	209	531	
1292	9343	A	2256	1	308	AKRAQSYAERLRLGLAVIHGEAQCTELD MDDGRHSPPMVKNATVHPGLELPLMM AKEKPPITVVGDVGGRIAIIVWLYVIHV QRWHSWLLVSRLSTLGLYF
1293	9344	A	2257	2	1161	VRKGTDLGALPVPPAMNAARTGYRVF L\ANSTAVCSELAKRITERLGAELGKSV VYQETNGETRVEIKESVRGQDIFIQTIPR DVNTAVMELLIMAYALKTACARNIG\VI PYIPYYSKQSKMRKRGSI\CKLLASMLAT AGLTHIITMDLHQKEIQGFFSFPPVDNLR SLHLFLAFSIIQGRKFPNLQEMQVIVG*V FLDAGKGAQSYAERLRLGFWAVHSR GEGFSCTKLADMDDGRHSPPMVKNATV HPGLELPLMMAKEKPPITVVGDV\GRI AIIVDDIID\DVESFVAAAEILKERGAYKI YVMATHGILSAEALRLIESSVDEVVVT NTVPHEVQKLQCPKIKTVDISLILSEANR RIHNGESMAYLFRNITVDD
1294	9345	B	2258	80	402	XVPTVDTYDGRGDSVVYGLRSKSKKFR RPDIQYPDATDEEDITSHMESEELNGAYK AIPVAQDLNAPSDWDSRGKDSYETSQLD DQSAETHSHKQSRLYKRKAYDESH*
1295	9346	C	2259	272	409	
1296	9347	A	226	764	1016	LLQAGAHACNPSGFGEAKAGGSTDLRS GDQPGQHGETPSLLKVQKVA*RGGAFL* SQL/LRGGGGCSEPRSHD*IPA WMTEGDS V

1297	9348	A	2260	2	628	EH SIVGTRLVSGQLQPSQPNADQGKLT MRIA VICFLLGITCAIPVKQADSGSSEE KQLYNKY PDAVATWLNPDPSQKQNLLA PQTLPSKSNESHDMDDMDDEDDDG PCGDSQDSIDSNDSDVDVDDTDDSHQSDE SHHSDESELVTDFFPDL PATEVFTPVVP TVDTYDGRGDSVVYGLRSKSKKFRRPDI QVNPLTDT PDGSD
1298	9349	A	2261	67	1276	SHASGRRQSTASSGPD SVSGQLQPSQPN ADQGKLT TMRIA VICFLLGITCAIPVKQ ADSGSSEKHFYNKY PDAVATWLNPD SHKQNLLAPQNAV SSETNDFKQETLPS KSNE SHDHMDMDDED DDDHVDSDSI DSNDSDDVDVDDTDDSHQSDESHHSDES DELVTDFPTALPATEVFTPVVPTVDTY DGRGDSVVYGLRSKSKKFRRPDIKYD ATDEDITLHMESEELNGAYKAIPVAQDL NAPSDWDSRGKDSYETSQLDDQSAET HRVHQQ\SRLYKRKANDESNEHSDCDW* ARTFPKVSREFHSHEFSSPWRFLFVAP KSREEDNTPLEFRYSQELDSASSGGQLK GGKNTISPLCHLVQKKNGFIAKMKENHE MLLSPVYWLKCVSI
1299	9350	A	2262	1	651	MTAFNSGKVDIVAINDPFIDLNYMVYMF LYDSTHGKFHGT VKAENGLVINGNPIT IFQDQDPSKIKWAP/LAKVIHDNFGIEGF MTTVHTITATQTINGPSGNCHVMAAGL SRTSSL SLLA/LAKPVGKVIPELNGKLTG MAFHVPTANVS VADLTCRLEKPA/KYDD IKK\NTHSSTFDAGAAIVLKDHSVKLISW YDNEFGYSNRVVHLMAHNASKE
1300	9351	A	2263	2	5264	
1301	9352	A	2264	56	1357	IRLSVCSSCSTVSRIFCVASRATSLRTPM GKVKVG VNGFGRIGRLVTRAAFNSGKV DIVAINDPFIDLNYMVYMFQYDSTHGKF HGT VKAENGKL VINGNPITIFQERDPSKI KWGDAGVAEYVVE\STGVFNQPWKKA GAHLQGGAKR\VIISAPSLMPPMFV MG VNHAEKYDNSLKIISNAFLQPPTCLAPL AKG*FHDNFG*SWEGLIDHSSMAITGNP RKTVD\GPSRG\NCGRGWAAGLSRTSSL GLYWALPKA\VGKGHP*G*TGKLTGMA FPVVPNCQNVSVVDLTCRSRKTLPQYD *HQGRVVKQA\SEGPPQGAILGYTEAPR WVSSDCNSGPPVFPFDAGAGIALNDH FVKLISWYDNEFGYSNRVVDLHGPHGL QGSKTPTGTEPQARGTRGRDETLTAGES LPHSDPHHTESPLLTVM
1302	9353	A	2265	34	476	LSGGPRRAASCASSAGLLVLLPFMPMFI VNTKLHRASLPEGFLSKLTQQLAQAN RQAPPN*FAFNVPDQVVSFGGSSEPCA LACSLHSIGKIGGAPDPAPYSKLL\CGPAG RSRLPIQARTRVYIN\YDMNRGQMWA GNNFHLSP
1303	9354	A	2266	63	470	QOPPPERPAHQFARPPAPFTMQPASAKW YDRRDYVFIEFCVEDSKDVNVNFEKSKL TFSKLSFLSNDVK*SFTQLNNFDWLVS LKLLLIFVSLKRLNSFFIILYSLGGSDNF KHLNEIDL FHCIDPNVSSLYA
1304	9355	A	2267	2	854	RAFCCVTSRRPASPLVCTHARSFSVLAP LFLHFLLPDRRSRSFRAVHFWGPRSSPP HAAVRLREARRGRDRREKAESPTGEKST SPSSRRRQRGPPTKVRRPPAPFTMQPASA KWY\DRRDYVLKWEFVFLNTRLRDVNV NFEKSKTYNFSCLESGSDNF*GI*MEAD LFHCIDPNDFQGLKGTDRSIFMFVLRKR RIWASSWPGLTK\ERGKGLIW\SVDFN VWKDWEDSDSDMSNFD RFSEMMNN MGGD\EVVDYPEVDG\ADDDSDSDDE

					KMPYLE
1305	9356	A	2268	117	388
1306	9357	A	2269	66	354
1307	9358	A	227	748	1488
					RLTKRPETFPRRHFKLPTLKTPTVAGATPL SPSHPDWPVFNPIPLTNRT*PPLQLQLRQ PSRSCPETTQGPASISEAELPVRSPPPFR LFPTPE/PGLSRQWP*EVEGTSRTFFKAE GQK/EGKVKEGKTEGPCSPSRRTILPPY SRLESGPVHWGEQGNRKS WPPPNLPDQ GF*QEREEAMGHIPSPPGIRQRHRTSVQE *GSEIKPK*CPEPGKAFNRPWGLGLT/TR PLPLHSQKSRQDS*NTG
1308	9359	A	2270	148	398
					RPAKRGAAAMDGRVQLIKALLALPIRPAT RRWRNPIPPETFDGDTDRLEFIVQTAS YPWPWARTRSSARPISSPPPETSCVLA
1309	9360	A	2271	356	1241
					KVTFLITRLTGPAQVGDPLHQEGEPPQ LITGAFWPEMKRVFGWGGGRGLLGRE LGPG\GGCSGEGPLCYWPPGSPPAPSF RASPPLEPPRCPLRSCSLPRSACLCSRNS APGSCCRPWASLWSEPPSPSSQPAPPM YIWTLSAPVAQS*APVTHWTDHPLPL PSPLLPTRLPDDLHFGPQTLRCQSHRW PSHPRQDCWLL/M*IWTHLGGI WAGH SPWTVIQTAGR\PPRDLSPSARPISSPIE TFCAPATWLPGLSCAWQAKFESLIFSLW TKLVFAHKRSIS
1310	9361	A	2272	2	178
1311	9362	C	2273	88	228
					MKVDKDRQMXVLEEEFQNISPEELKME LPERQPRLQRTTDDVCRE*
1312	9363	A	2274	3	382
					VDRTIMSDSLVCEVDPELTEKLKFRF RKETDAAIIMKVDKDRQMVVLEEEFQ FVVYSYKYVHDDGRVSYPLCFIFSSPVG CKPEQQMMYAGSKTRLVQTAELTKVQT GMWLQSVRERWCGSWV
1313	9364	A	2275	89	636
					KTAE LRKEEACGQNNHALPGSLRQSDSL VVCEVDPELTEKLKFRFRKETDAAI MKVDKDPARWWCLEGKNFKNISPQREL KMGFPRRDKPR\FVVYSYKYVHD\DG\R VSYPLCFIFPPRPVGCKPEQQMMYAGS KNRLVQTAELTKGVPKSRTT*LTSLRP WLQEKLSFLSLISGAGD
1314	9365	A	2276	2	2453
1315	9366	A	2277	1	1008
1316	9367	A	2278	1	884
					MVDKCRYHQSLHKVSNSESKISSGLL SRLQRRPRGRGDAELRRAGSVKRRQRG KMAAAVPQRAWTVEQLRSEQLPKKDII KFLQEHGSDSLAEHKLGLNKNV GKT ANKDHLVTA\YNHLFETKPF*GYLKV*S KVSEQVKKCERLMKINPKETKSERDPW NEG\PPK\YTKSCS*KRGDKTQLFPKRGD VVHACWYTGNTTKMGTVF*YLIFQ TSA KKKEKCPSL*GFKVRSRPKLSRGWDEA LLTMSKGEKARLEIEPEWAFGKKGLPD AKIPNNAKLTFEVELVDID

1317	9368	A	2279	3	510	AIRAVAYCADMAQSMNHTTLHQSRIWH RIGIKKPRSQTDQSLTGVDPMFLKNMRF AKKHNNMGLKRMQANNAKAMSARAE AIKALVKPKEAYL*IPNGVSRKLDPLAYI AHPKLAKRALARIAKGLKLCRPEALAEA RAKDQTKVQGVAPA*APAHAPKRTQAP TKASE
1318	9369	A	228	34	478	LSPRLECSGAI*AHCNLRPPGFKQFSCLSL SSSWDYRHAPPTQLIWFYFYFK*RPGF QLVLVQAGLEL\TL*IPPASASQKC\WD YQV*APH\WPALYKVSY*EKWFPIMFFA PFSWLSLGTEKFVRKVAVAGLGTLP TG WALCSLWKY
1319	9370	A	2280	9	674	IERLQVRIACSCRDAIPGSSHASAHASEA LREPLNGADMAKSKNHTTNQ\SRKW P\RNIGIKKPRS\QRYEFS*RGWPPQVSLR NMRFAQRSTNKKGP*RRLOANKLPRAM SATCPRLIKAPPLKAPRRFKPDPPKGVS RKLDRLA\YIAQPQGLGSVARCP*LPRGP RL\CPPKAKGQGGQAKAKDQTKGFKP RPRVQAPVSV\AQAPKRTQAP\TKASE
1320	9371	A	2281	417	822	RENCILLSTRAQSVFNAQGTALWSFQDP ATGEGGAGHGGRLMRPSLLPSQGASAC* /PRFGESKLAPVGKFKMCLLELPFLSHH LSRGCSGASEGQLCLLEVPATARVGVHK PSQSRGLEFSWVLMSDLCSPPL
1321	9372	A	2284	85	409	TCGLPMCQKQTVSWGGKTPSLRRFPQR PRPPRGQPPSGARWEH/PPPGTTAPRRSR RPSPPARLAGPEP*AKSPLHAANSRGQTK GHLWKTLLVLFKKPNFFFFNFHN
1322	9373	A	2285	193	609	NQINFCLNGKYTYICIDTLPLYMFIHTL KHINTSVIISLEFAI*HKGQVELHIKITYRS N*MWLGHNQRRN/LCPQEGEEIPNEA*IF SIHKRQSWPGTVAHACNLITLGG*DGRIS* DQVFKTSLINIVETPSLLKK
1323	9374	A	2286	117	433	
1324	9375	A	2287	2	1923	VETPPQGSVHSGHLGSVVGDPHTGTGN AGERGPRGKGARVLALDSGGMDSSPSLP LIRTPSSLHEALDQCMTALDLFTNQFS EALSYLKPRTKESMYHSLTYATILEMQA MMTFDPQDILLAGNMMKEAQMCLQRH RRKSSVTDSSFSLVNRPTLGQFTEEEIHA EVCYAECLLQRAALTFLQGSSHGGAVRP RALHDP SHACSCPPGPGRQHLFLLQDEN MVSFIKGGIKVRNSYQTYKELDSLVOSS QYCKGENHPHFEGGVKLGVGAFNLTL MLPTRILRLLEFVGFSGNKDYGLLQLEE GASGHSFRSVLCVMLLLCYHTFLTFVLG TGNVNIEEAEKLLKPYLNRYPKGAIFLFF AGRIEVIKGNIDAVSDGGPGRGWGSLGV SQTSRKSGTC\ILRDRIDWGRGGGPREN QPESRGRRGPSGRAAWEDKGGGICGA WDFDWEI*DCSIAVEGGGGRCLEAEVR KAHLFRA*RLGWSLVPLHYSSLLLHFH VTKNQSPRRGLYSPTSCKT*EVKPGLE ARSPGSWGPT*A*HRAGPLCPGGVPVCC GVGRFGGCRGVGAGWAPVRLTRRCLQ AIRRFEECCEAQHWKQFHMCYWEL MWCFTYKGQWKMSYFYADLLSKENCW SKVG

1325	9376	A	2288	1	1818	LGEGGGKKGLWDLVAGLHPLGGQQSP MGQKGHKDSLYPEGGTPESSLHEALDQ CMTALDLFTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGN MMKEAQMLCQRHRRKSSVTNSFSSLVN RPTLGQFTEEEIHAEVVCYAKCLLQRAA LTFLDENMV\FSIKGGIKVRNSYQTYKE LDSLQSSQYCKGENHPHFEGGVKLG GAFNLTL\SMPLTRILRLLEFVGFSGNKDY GLLQLEEGASGHSFRSVLCVMLLLCYHT FLTFLVLTGNVNIEEAELKLPYLNRY KGAIFLFFAGRIEVIKGNIDAAIRFECC EAQHWKQFHMCYWELMWCFTYKG QWKMSYFYADLLSKENCWSKATYTYM KAA\LSMFGKEDHKPFGDDEVELFRAV PGLK\KIAGKSLPTEKFAIRKSRRYFSSN PISLPVPALEMMYI\WNGYAVIGKQPKLT DGILEIITKAEEMLEKGPENEYSVDDECL VKLLKGLCLKYLGRVQEAENFRSISAN EKKIKYDHYLIPNALLELALLMEQDRN EEAIKLES\AKQ\NYKNYSMESRTHF*IQ AATLQAKSSIENSSRSMVSSVSL
1326	9377	A	2289	486	713	SKFYLFYLFYFFVYTYVINIVYIKI*QQID LNFIYLFYLFYFWRQSRFLSKL*CSGA NMTHLSLNLPGSRNTPAPALQAAGTTG M*HHTWLIFVVFVETEFHHVGLKFLSLD\ IHPPWPSKVLG*QGGWIV
1327	9378	A	229	28	359	KGKIPWLCGI*PQNEKLM*HSKSLATVFC IYR/TN*KNKRIISINAEKAIDQIHTFMNF LKNF/MKTVRKLKMDGSILNIIKEICERP TNM*DGELLDDFPKIGDEAQRPP
1328	9379	A	2291	1	774	
1329	9380	C	2292	214	483	
1330	9381	A	2293	701	1033	
1331	9382	A	2294	440	1383	SSSWNRAFSRKKDKTWMHTPEALSKHFI PYN\AKFLGSTEVEQPKGTEVVRDAVRK LKFA\RIKKSGGQKIPKVELQISYIGSK NS*DPKTKREV\QHNCQLHRISFCADDKT DKR\IFTICKDSESNKHL\CVFDSEKCA EEITLTIGQAFDLAYRK\FLESGGKD\ETR KQIAGLQKRIQDLETENMELKNKVQDLE NQLRITQVSAPPAGSMTPKSPSTDIFDMI PFSPISHQSSMPTRNGTQPPVPVSRSTEIK RDLFGAEPFDPFNCGAADFPPDIQSKLDE M/QAPEMEGFKMGLTLEGTVFCLDPLDS RC
1332	9383	A	2295	412	842	GKVSP\GL*GP*GEQG\PLG\PSGAATGLP HSLCPEAFASPR\SV\YR*DQAQLALWAV PL*EGPL/PDLVRGVVPGSPVKVP\GDEV R/T/CHSCGRFPRALGQSKTLPPNLPLTTRR GVNSEDLPSPVYRAADRGNRFP\GAVGG SCHR
1333	9384	A	2296	1036	1429	GRAWRTCP\RAHQ\PRRSHLRPSSCSTLQ RG*SPPPGRSSSPVQ*CA*ARGWGSQPG *HWTCLFLAWQSPQCTGPQICQYPRPLR SPRPAGPPGGTSGHSPPDARAPRRRPAP CGREC\SSSSGRNAAPLG
1334	9385	A	2297	44	396	
1335	9386	A	2298	298	409	

1336	9387	A	2299	123	1221	KRQLFPLSWAMAASGSRMAQKTWEWLA NNMQEAQSIDEIYKYDKKQQQEILGGEA LD*GVRSHHYFKYCKISALALLKMMVM HARS/GEKNLEVMGLMLGK/VWDGETM IIMGKFFFCLVEGTETRVN/SLQAAAYEY MAAYIENANQV\GSPENAIGWYHSHPGV YGCWLSG\DVSTQML\NQQFQEPFVAV\ VIDPTRTISAGKVNFGAFWAHPK/GGYN PPD\EGP\SGVPGLFPLNKIEDLGVHCKQY YALEVSYFKSLLGSQNCLELLWNKIWG GIRWSS/SLAGLLNADYPTGQVL*FVLKK LEQSRSPSLGRGEFPCWGLETHDRKSED KLAKA\TRSS\CKLPIEANHGLMSQVIKD KLFNQINIS
1337	9388	A	23	3	438	LFISLLSISEKIIENCWV*LSAARS*ALRKL AFF*ATRSFF*ARDILGRFHLFF/CNFFLG LLFIDWILSYSSMSFLIHLHPAGQQQAS TICCSIICQANLHTIFWQFVCIRCADYHIP LYTGISNLTNDISVCHTNYHPVIGVW
1338	9389	A	230	1216	2017	HPRGAKYPETNPGFVTL SYVGPDPDSRQL THSRPSRSENACGHRPGELNWLNCSCGL LVPRGKRVWTETCNLVWKTEASGPPPG DPLPSLSSPITHQARPT/DTQAHCPAPCP PH*PLALNPQQNFCPEESAQVGGQGEED RTSRGWVHGSQPQVGAGK*PLSTGSKA QGARLTGGGVPSRPLR*EQALVRCRCRL CRLGSCVRSHSLKFIDEAGEAPSAAGLD GQGTGRAPGAPEARCPRAESGEGPGSG QAPAEQDPQPRAALRA
1339	9390	A	2300	2	433	
1340	9391	A	2301	1	2423	MAGALAGLAAGLQVPRVAPSPDSDDST DSEDPSLRRSAGGLLRSQVIHSGHFMVSS PHSDSLPRRRDQEGSVGPSDFGPRSIDPT LTRLFECLSLAYSGKLVSPKWNFKGLK LLCRDKIRLNNAIWRAWYIYVKKRKSP VCGFVTPLQGPEADAHKPEAVVLEGN YWKRRIEVVMREYHKWRIYYKKRVSSG GPGRPQSFPAAAGYRPPRKIPGKILTP ELAPLGPSIQSRADSATVWPQRLLAASLP RGRLRKPSREDDLLAPKQAEGRWPPPEQ WCKQLFSSVVPVLLGDPEEPGGRLD LNCFLSDISDTLFTMTQSGPSPLQLPPED AYVGNADMIQPDLTPLQPSLDDFMDISD FFTNSRLPQPPMPSNFPEPPSPVVDLSF SSGTLGPEVPPASSAMTHLSGHSRLQAR NSCPGPLDSSAFLSSDFLLPEDPKPRLPPP PVPPPLLHYPPPAKQETVPEFPCTFLPPTP APTTPRPPPGPATLAPSRPLLVPKAERLSP PAPSGSERRLSGDLSSMPGPGTSLSVRVSP PQPILSRGRPDSNKALLGSFLGSPNSLLPE TENRRITHISAEQKRRFNILGFDTLHGL VSTLSAQPSLKVSKATTLOKTAEYILMLA QQUERAGLQEEAQQLR\DEIEEL\NAAINL CQQQLPATGVPI\THQRFDMRDMFD\D YVRTRLHNWKFVVSSLKPMAGGLQ GLWQGSSLTWAQFSILIRPLFESFNGMVS TASVHTLRQTS\AWLDQYCSLPALRPTV L\NSLRQLGTS\TIL\TDPGRIP*/EQATRA VTEGTLGKPL
1341	9392	A	2302	1	535	
1342	9393	A	2303	155	276	
1343	9394	A	2304	1	477	

1344	9395	A	2305	221	2323	LGLQMHTTSGRIHQAMVTSLNEDNESVT VEWIENGDTKGKÆIDLESIFSLNPDΛVP DGEIEPSPAETPPPPASSAKVNKIVKNRRT VASIKNDPPSRDNRVVGSARARPSQFP EQSSAQQNGSVSDISPVQAAKKEFGPP SRRRSNCVKEVDKLQDKREMKRLQQQE LREIRAQDV DATHPNYEIMCMIRGFTGS LDYRPLASADPIDEHRIYVCVRKRPLNK KETQMKDLDVITIPSKDVVMVHEPKQK VDLTRYLENQTFRFDYAFDDAPNEMV YRFTARPLVVTIFERGMATCLAYGQTGS GKTHTMGGDFSGKNQDCSKGIYALAAR DVFLMLKKPNYKKLELQVYATFFEIYSG KVFDLLNRKTKLRVLEDGKQVQVVGVL QEREVKCEDVLAKLIDIGNSCRTSGQTS ANAHSSRSHAVFQILRRKGKLGKFSLI DLAGNERGADTSSADRQTRLEGAENKS LLALKECIRALGRNKPHTPFRASKLTQV LRDSFIGENSRTCMIATISPG/MWASCEN TLNTRLRYANRVKELTVDPATAAGDVRPIM HHPNQIADDLETQWGVGSSPQRDDLKL LCEQNEEEVSPQLFTFHEAVSQMVEMEE QVVEDHRAVFQESIRWLEDEKALLGD*L EEVDYDVDSYATQLEAILEQKIDILTEL DKVKSFRV AALQEEEQASKQINPKRPRA L
1345	9396	A	2306	264	451	VLPNLTVHASPTTIKIWAGKVTHAYNPS TLGGQRGRIA*AQEFKTSLSNIMGLRLSK KKKKK
1346	9397	B	2307	1	642	MLEEQLVRMLTREVMDLITVCCVSKKG ADHSSAPPADGDDEEMMATEVTPSAMA ELTDLGKCLMKHEVLSGTLADAVTWL FTSVLKGLQMHGQHDGCMASLVHLAFQ IYEALRPRYLEIRAVMEQIPEIQKDSLQDQF DCKLLNPSLOKVADKRRKDQFKRLIAGC IGKPLGEQFRKEVHIKNLPSLFKKTCPML ETEVLNDGGGLATIFEP*
1347	9398	A	2308	3	101	STHASESNFSICSILCFCLEAPISLMLSLSA SLEDQPWAWALCGGGRAPSTT*PPLSL* HL
1348	9399	A	2309	360	483	SMCLTVSMLVTACPADPCVT*A*NRSSF EVPPPWTSDLRFF
1349	9400	A	231	5	399	DGVSLV/SPRLEYSGAISAHCKLRLPRFK *FSCLSIPSSWDYRHVPPPPANSVFLVKT GFHHVGGAGLELLTSGDLPTSAPFKCW DYRCDHCAWAKD*KFKCVSVGRRGGP GEAVHQNSNRLSYWWEDGGKTG
1350	9401	A	2310	100	190	
1351	9402	A	2311	2	193	WRRRRRRFCPQPQSLIWSGMRSPKKLTP PR*NYLRQALRRNLSTLRRPFAQETAWY QWCFLGL
1352	9403	A	2312	103	237	
1353	9404	A	2313	3	1361	VETQEGKTTIIEGRITATPKESPNNPNPSG QCPICRWNLKHKYNYYDDVLLLSQFIRPH GGMLPRKITGLCQEEHRKIEECVKMAHR AELQRELQRLSPLPATQVYYQITGLGFLK ELFRANPNSTGPLAKAQGGYLTRWAP GSVKPIYKKGPRWNRGEANRKAHFSTV QWPAPSAIAHAKDDVSPLOPTQCLLDNI KKKVVPVLSGRPGNTDSTCQESRSIYLS QALAVTFTHTLTATAEAQEPSQLLSPPPG LGEKPPADLVLQW/SEAPRAKQHYCTSP SHPAQRVSSSDSSEHPAAASHPRPPRP GTNGWSRRGSCRASWSRDCSGVRSRRV ALGMAMDQVNALCEQLVKA VTMMDP NSTQRYRLEALKFCEEKKEKCPICVPCGL RLAEKTQVAIVRHFLQILEHVVKFRWN GMSRLEKVYFEEQWSWNLIAKGPFEHF GRGEPY

1354	9405	A	2314	138	397	SHCPLSMHVGGTRPSWWGGTGV*LWPR AC/RVGLLLPSTGAGGTLEALLSVSDTAS KVFEELARHCPSEGVNPTGHAHPVPSRG PFL
1355	9406	A	2315	16	546	QLNGRSIRHEVMISHRKFSAPRHGSLGFL PRKRSSRHGKVKSFPKDDPSKPVHLTA FLGYKAGMTHIVREVDRPGSKVNKKEV VEAVTIVETPPMVVVGVGYVETPRGLR TFKTVFAEHISDE/CRLPLRQKKAHLME IHVNGGTVAEKLDWARERLEQQVPVNP VFGQDEMIDVI
1356	9407	A	2316	2	451	PRAKAQKGSFVLWAQKSCPPKTTRALA KVAACIGAWHPARVAFSVARVGQKGYH PRTEITKKIYKIGQGYLIK/DGKLIKNNNA STDYDLSDKSINPLSLLVQTKRRALEKID LKFDITTSKFGHGRFQTMEEKKAFMGPL KKDRIAKEEGA
1357	9408	A	2317	1	625	CKFIRVMAHTRLRLPLRRKKAHLMEIQ VNEGTVAEKLDWARERLEQQVPVNPQVF GQDEMIDVIGVTGKGYKGVTSRWHTK KLPRKTHRGLRKVAC/KDGKLIKNNAST DYDLSDKSINPLGGFVHYGEVTNDFVML KGCVVGTKKRVLTLRKSLLVQTKRRAL EKIDLKFDITTSKFGHGRFQTMEEKKAF MGPLKKDRIAKEEGA
1358	9409	A	2318	1	1251	
1359	9410	A	2319	1	903	
1360	9411	A	232	481	525	AAGTYSL*IGKE*VKLSLSVDSMILYIDN LKTLPKTLTDDKFSKISEYNISVF*CIND EKAKEIRKTIPFTIIR*NTSDLTKKVKG LYKGNKTLMEINKWKDIPCA*IRRINI IKIVYPK*T*FKAISIKILLSFVTEIEKKIPK FI*NQKRIRIAKATLSCWNLFPMNSWHN RC
1361	9412	A	2320	1	1341	
1362	9413	A	2321	1	1131	
1363	9414	A	2322	10	1304	ESDGVTSHRKFSAPRHGTLGFLPRKRSSR HRGKAKSFPTDDPPKPGHLTGFLAYTAG MTHIVREVDRPGSKANTKEAGEAATIVE TPPMVSVGVGYVETPRGLRFTKTVFAE HISDECKRRFYKNWHKSKKKAFTKYCK K\WQDEDGKKQLEKDFSSMK\KYCQV\I RVIAHTQ\MRLLPLRQK\KAHLMEIQV\I NGGPCGPRSDWAREKLE\QQVPVNPQV F\GQDEMID\VIGGDPGAKGYKRGSPVR WHTKKAAPARPHPRACAKVGLVLGAW\I HPG\RVAFSV\ASRWGRKGLPFHRTEINQ GRIFKDWPRATLIKDGKLIKDQCLHLNY DLS*PRASNPLGGFVHYW*SDRNDFVM L\KGCVVGTKKRGAHPFRKSLLVQTKR\I RALEKIDLKFDITTSKFGHGRFQTMEEK KAFMGPLKKDRIAKEEGA
1364	9415	A	2323	138	737	TTTMSSKKAKT\TTKKRP\QRATSNVFA MFVHSQIQGVQRGPFNMIDQNRDGFHS DK/EKVLHDM\LAFSREESPLDAYLDAM MNEAPGPHQVSPWFLTMFW*ESLNRTD PLKIVIQKPPFA\CFD*KKATRHPPFREDYL /REELLTNPWGDRVYQIEEVG*TCTGEAP I*QKKGNFQITSEFHHGILTGRPPKHKDD LKELLA
1365	9416	A	2324	2	307	
1366	9417	A	2325	2	215	
1367	9418	A	2326	1	213	

1368	9419	A	2327	2	935	FRPRYEGRGRGCCGRVRLRLRGLHVD GKLGKLTSSCGKPSSNRMSLQWTAV TFLYAEVFFVLLCIPFISPKRWQKIFKSR LVGVVSVPMGNTFF/VLVLIVILVLLVIE CRAAKFREVMMDVDGKRVNLPGTIPGG HGEALSHMEAFSVAPGGNLLHWLGFSL LLSFLRLRLVTLISQQAITLLASNEAFK KQAEKC*VKAARKYMEENDQLKKGA PDEGKLNFEAELKLEEKINRELKANLQ KLKDELQALSKKLEKG*KTSFWPMRK QFMRGLTQ/ERYDRLLLEQPKAAGLQV DGPMD\KKEE
1369	9420	A	2328	2	1217	QARGASLRPSLLRIPSEYAFATMQLRFR LLLAALLVIVWTLFGPSGLGEELLTSL AFLPAPALPGPLALPRLLIPTQEACCGP GAPPFLILGGTAPENLNQRNAIRASRG LREARGLRVQTLFLLGEPNAQHPVWG SQQE*TGPSSEAAQGDILQAAFQDSYRNL TLKTLSGLNWAEKHCPMARYVLRDDED GIANVPELVSELVLRGGRWGQWERSTEP QREAEQEGGQVLHSEEVPLLYLGRVHW RVNPSRTPGGRHRVSEEQWPHTWGPFP YASGTGYVLSASAVQLILKVASRAPLLP LEDVFGVSARRG\GLAPTQCVKLA\GA THYPLDRCCYGKFLTSHKLDPWKMQE AWKLVGGS\DEKDCAPFAPWFPKSL GILRCR\AIA\WLQS
1370	9421	A	2329	1	395	AINYNEKIYELRMETKPDKAVSHIED MNVDFDAP/LGYKEPERQVQHEESTEGE ADHSGYAGE/LGFRAFSGSGNRDLGKKK GVEPSPSPIKPGDIKRGIPNYEFKLG EAGGRFVAFSGEGQSLRKKGRKP
1371	9422	A	233	20	129	
1372	9423	A	2330	1	1494	
1373	9424	A	2331	2	1062	GRAVGGVSSLHCPERSGVCQVVSIMFS NMFDHPIPRVFQNRFTQYRCFSLSML AGPNDR/SSIGEKEGKIIMPPSALDQLSR L*HYRIPMLFKLTNRNSDRMTALLQCLE FVADEGICYFPTL/WMMQNLLLEEGGLV QVKS\VNLSATLLPNFQPS\DFL\DTN PKAVFENALRNFACTTGDVIAANYNE KILRNCVVMETQTPTRPVSHH*SVNH*T V\DFDCFLPLPKNPGKTKSHHEESEQKV KADPTVAYAWKSLGFPRFSRSGSNRLD GKKKGVEPSP\SPIKPGDIKRGIPNYEFK LGKITF/VSRSRPLVKKVEEDEAGGRF VAFSGEGQSLRKKGRKP
1374	9425	A	2332	1	214	APARSALCSGSAPRTSGQPWGTAPPPS FHQRNTPCPWSAPPSGAAPWGSTKGQR LDGPCCAPFPGRGLSM*SKVPWWPA*TA PAPPSFHQRNTPCPWSAPPSGAAPWGST KGQRLDGPCCAPFPGRGLSM
1375	9426	A	2333	1	1515	MAPLQQHIAVLPDITADQVTTEDDGYT WTALQHVATAKEKRKSSQTMEESQDFP LHIPRAQGTQRAVARPSGPKAWTEAG PAKDAARSEKPGGRKAPGGRGQLTCRR SLSPVRQPPVSVVSDSLRRRSPCSPADW REAGATSLDRIPILVLMVDKLVVVF STGAQGGSVARILLEDGTFKVRVVT RNP RKKA AKELRLQGA EVVQGDQDDQVIME LALE\WAYATFIGTNYWESCSQEVEPT A/GSLDRIPILVLMVDKLVVVF GL\GTSRS*RQGDWPPRTLTAKGRWRNI SGTLAPP*PVWGFANLENLLQLFFPR KTPEGKELLCGACQVTFPWWMACPCLT WGPVVL\SLFEDARKIRRP EHRG*ALAGT RPRSTLPCSPSTPARSCTMPR*LPEDY EKG LGFP GARDLGQHV PFLCPET PTRDI/PSLT LRLNPKALTLDQWLGT AQRGLQPAVTL

						PASRPLVGIRQHQRGKKAPTSEIKPICSPK K K K K
1376	9427	A	2334	3	1037	ILRSVARAQRGRRSLRFHWSPPGGHGGRS EAGAAGP/VEMRRTAAPQGRVPGL/PS KLGIPDALPTVAAPRPVCQRCGQPLAAL VVQVYCPLEGSPFHRLLHVACACPGCS TGGARSWKVFRSQCLQVPEREAQDAQK QGNSLAAEDWCEGADD/CGK*Y*GGAFT TVYLGFW*EQQC/HKT*TGLLGSKTS/C LQDAVLGAAPVPPGLPLFLPYICVAD EDDYRDFVNLDHAHSLLRDYQQREGIA MDQLLSQSLPNDGDEK/S*EDHN*KVGG SRPF*QIP*KRNWLLVREQILRVFPGVES HSF*PAPTSEVTELSLQPVWEAKRIFEF QLMPALGQHASRVLI
1377	9428	B	2337	240	387	NGKERGTGDVKLLKHKEKGAIKLLMRR DKTLKICANHYITPMELKPNAX*
1378	9429	A	2338	1	152	
1379	9430	A	2339	1	830	MRRPRRRLCWLRLVECGPLQSRSAVG NSEEQRKAYVFFSSLSLVDTHEDHDTST ENTDESNDHPQFEPVSLPEQENKLEED EELFKMRACLFRFAENDLPEWKERG TGD\VKLLKHKEKGAIKLLMRR\DKDP *KICANPLPSRPLMGAESPTAGRSPVW VLETPHA\DFRPNCEPPSPPLGPPRFLN A*RMPQKFQNSFEELQGRSEGEKEE SRFQKNDL\HRKKCAEKPGSSLR*REE TKEDAEAEAINRLILLSFSSLSLS
1380	9431	A	234	16	370	
1381	9432	C	2340	392	631	MRTAESCRRLSWAALLGSHWRCCSHPC AAGQGPYPRAAVNGPRTPLAYLRFKEM FSSGLINVEFPQFLYLSHFHSLLLR*
1382	9433	A	2341	3	121	
1383	9434	A	2342	1	2970	
1384	9435	A	2343	48	1493	DGQYRIWWLIEWHVDGGCGDTETWKD R\WNHVKK\FLERSGPFTHPDFEPSTESL QFLDTC\VLVIGAGGLGCELLKNLAL S\GFRQIHVID\MDTNDVSNS*IRQFLFRPK DIGRPAEVA AEFLNDRV\PNCNVVPHF NKIQDFNDTFYRQFHINVC GTGLSCA RRWINGMLISLNLN YERMVS*DPSSIVPLI D\GGTEGF\KENARVILAPGMTACIECTLE LYPPQVNFPMCTIASMPRLPEHCNEYVG MLQWPKEQPFGEVPLDGDPAEHIQWI FQKSLERASQYNIRGVTYRLTQGVVKRII PAVASTNAVIAAVCAT*EVFKIATSAYIP L*ITWVFNDVDGLYTYTFEGRKGK\EN CPAC\SQLPQNISVFLHQAQLQEVLGILT NSASLQNEILPAITATLGGEKIGTLYQS VTSIEERTRPNLSKTIGRIGLLDGPKTG RLLDVTPQT VLFQTSILLK GKSP
1385	9436	C	2344	166	312	

1386	9437	B	2345	355	487	MLGLRSGIPAPVRLQLAVVLGNSLGNFG TEGPGLKGRMTMTGDPX*
1387	9438	A	2346	754	1035	GKVRTVKIKYWMLARSSGSSL*SQHFGR LRQADHEVQEIKHHPGKHSANP\SLK QKVS*LVSQAWWWVPVPAIREVEAGE WCEPGRQSLQ
1388	9439	B	2347	80	432	MANGPRAXFCENFQAALALSRVGLHKN PEKEPYKSKYSARALLEEVKALLGPAP DEDERPEAEDGPGAGDHALGLPVAQRA VRLAVIEFHLGVNHIDTEELSAGEEHLV CLRLRS*
1389	9440	A	2348	2	1060	HWLSTANVISDYDDKSSPTQDTAETV*D TPELYHQGKGEIARCWKYCLTLMQNA QLSMQDNI*ELDLKQSELIALRKKEDE EESIRKKAVQFGTGELCDAISAEKVS LRPLDFEEARELFLGQHYVFEAKEFFQ DGYVTDHIEVVQDHSALFKVLAFETDM ERRCKMHKRRIAMLEPLTVDLNPQYLL LVNRQIQFEIAHAYYDMMDLKVAIADRL RDPDSHIVKKINNLNKSALKYYQLFLDS LRDPNKVPFHEIGEDVLRPAMLAKEFRVA RLYGKIITADPKKELENLATSLEHYKFIV DYCEKHPEAAQIEVELELSKEMVSLFP TKMERFRTKMALS
1390	9441	A	2349	11	2571	VKCRKAEGRRSRLQTFEESQAVEAAM ANVPWAEVCEKFQAALALSRVELHKNP EKEPYKSKYSARANMAEEVKALLGPAP DEDERPEAEDGPGAGDHALGLPAEVVE PEGPVAQANRLRLAVIEFHLGVNHIDTE ELSAGEEHLVKCLRLRRYRLSHDCISLC IQAQNNLGIVWSEEEIETAQAYLESSEA LYNQYMKEVGSPLDPTERFLPEEEKLT VEQERSTRFSKVYTHILYYLAQVYQHLE CFETAHYCHSTLKRQLEHNAYHPIEW AINAATLSQFYINKLCFMEARHCLSAAN VIFGQTGKISATEDTPESEGEVPELYHQR KGEIARCWKYLF*LLMQNAQLSMQDNI GELDLKQSELRALRKKEDEEESIRKK AVQFGTGELCDAISAVEEKVSYLRLPLG FEEARELFLGQHYVF/ERAKEFFQIDGY VTDHIEVVQDHSALFKVLAFETDMER RC\KMHKRGLAMLEPLTVDLNPQYLL VNRQIQFEIAHAYYDMMDLKVAIADRL RDPDSHIVKKINNLNKSALKYYQLFLDS LRDPNKVPFHEIGEDVLRPAMLAKEFRVA VARLYGKIITADPKERAGKIWATSLAEH YKFIVDYC/EKRHPEAAQIEVELELSKE MPGRRSETPSLKERNKKDKIQAKTTSA PPAQLALATPQPVRMCRQLTRVISLGSS KGKASFAGPDRPPYEDPHIVRLQLYHPQ RERSCVTSSRRSCAKSPWTLSSRWPHGS SWEKSYELSDGQVITSSNKRHFCEALF QPSFLGMESCGIYKTTFSIVKCDVDIHK DLYANTVLSGSTTMYPGIALQDAEGDHC PGSQHEEDQDHCSF
1391	9442	A	235	1	1125	
1392	9443	A	2350	1	421	GTVVMGLPKYFISLSTKFPLSFSLSADEL HIASLFLWPRSKPFGVIQRSCASQLNALP EVLKNPGDPDKMLRFAESPRNLPAVL/ GDIWTDGKGSVSLQEQQVYHFLIRPTPGS *ARASFLSCG*EEFRRHGLTFSSTRE

1393	9444	B	2351	211	1632	MSTELFSSTREEGSSGSGPSFRSNQRKML NLLLERDTSFTVCPDVPRTPVGKFLGDS ANLSILSGGTPKCCLDLNLSSGEITATQ LTTSADLDETGHLDSSGLQEVHLAGMN HDQHLMKCSPAQLLCSTPNGLDRGHRK RDAMCSSSANKENDNGNLVDSEMKYLG SPITTVPKLDKNPNLGEDQAEIISDELME FSLKDQEAQVSRGLYRSPSPENLNRP RLKQVEKFKDNTIPDKVKKKYFSGQK LRKGLCLKKTVSLCDITITQMLEEDSNQ GHLIGDFSKVCALPTVSGKHQDLKYVNP ETVAALLSGKFQGLIEKFYVIDCRYPY LGGHIQGANLNSQEELFNFLKKPIVPL DTQKRHIVFHCEFSERGPRMCRCLREE DRSLNQYPALYYPELYILKGGYRDFPE YMELCEPOSYCPMHQDHKTELLRCRS QSKVQEGERQLREQIALLVKDMSP*
1394	9445	A	2352	200	1525	IMASAHLATSAFCTRSSSSGRSGSCKRGS WDSEQALIRAWTTLPSLHAADGSFAGG RGIPSKRWSWRAGQQSSLCLIMQTSSNC GNSFQLVSEGASWRGLPHCSCAELQDSL NFSYHPSGLSLSVRPSSPGNSPKEQFSQ VLRPEPPDPEKLPVPPAPPSKRHCRSLSV PVDLSRWQPVWRPAPSKLWTPIKHRGS GGGGGPQVPHQSPPKRVSSLRFLTSSQC LFSMCPSSQTLQPSFLQPGGPSSSRPCA ASPQSGSWESDAESLSPCPPQRRFSLSPS LGPQASRFLPSARSSPASSPELPLAT*G/L SATFPESRSQPCDLARKTGKVRREED PRRLRPSLDFDKMNQKPYSGGLCLQETA REGSSISPPWFMACSPPLSASCSPGTGSS QVLSESEKEEEGAVRWGRQALSKRTL QRDFGDLNLNLIEN
1395	9446	A	2353	2	280	
1396	9447	A	2354	2	971	
1397	9448	A	2355	604	876	SLHHKDFTGMLLLQFAHHLGEIGFSLIS PKSRQPRFLPSVRQCGAAAA/RRCYRL APRPVCSGKRRTPAGAGD*GGERARPPR ARVFCPR
1398	9449	A	2356	1	1042	DLFRRHFKSSSIQRSAAAAAATRTARQH PPADSSVTMEDMNEYSNIEEFAEGSKIN ASKNQDDGKMFIGGLSWDTSKKDLTE YLSRFGEVVDCTIKTDPVTGRSRGFGFV LFKDAASVDKVLKEHKLIDGKLIDPKR AKALKGKEPPKVFGGLSPDTSEEQIK EYFGAFGERENIEFSMDTKTNERRIGFCFI TYTDEEPVKLLESTYHQIGSGKCEIKV AQPKEVYRQQQQQKGGRGAAAGGRG GTRGRGRGQGNWNQGFNNYYDQGY GNYNSAYGGDQNYSGYGYGYDYTGYN YGNPMEYGTRGYGQTYQWPQQSTLMG KASVRGGGQSTQNNYPAHT
1399	9450	A	2357	586	1970	PQEFTPLRFSLLILFSQARVPSRVASLLA GRAAMEVPPRLSHVPPPLFSPAPATLASR SLSHWRPRPPRQLAPLLPSLAPSSARQG ARRAQRHVTAQQPSRLAGGAAIKGGRR RRPDLFRRHFKSSSIQRSAAAAAATRTA RQHPPADSSVTMEDMNEYSNIEEFAEGS KINASKNQDDGKMFIGGLSWDTSKKD\I LTEYLSRFGEVVDCTIKTDPVTGRSRGF GFVLFKDAA\VDKVLGT*KGHKLIDGKL IDPKRAKALKGKEPSPKRFLWSGLSPDTS VEEQIKEYFGAFGEIENIELPMDTKTNER RGFCFITYTDEEPVKLLESRYHQIGSGV KCEIKGCTTPKRYLGQQQPPKGCK/RG AAAGGRVGTGRGRS\QGGQNWQGFNN YYDQGYGNYNSAYGGDQNYSGYGGYD YTGNYGNYGYGQGYADYSGQSTYG KASRGGGNHQNNYQPY

1400	9451	A	2358	592	608	WLRWATYKAGQPQLEAQNPFYSFREGQ PFLRLDHLRTAGAEQNCAAAVWVRRL* RNMGFVLLTGAASFIMVAHLSHQCSQG PAKKVPKWEYPYPCTATEPLNNGHHPST CIQAKPHPRNTVGKV*PSPSLFFPSLLGG VYHPAV*ASWPWAWPWICWTEFLYA\Y GLLHGENPSKRSPRSPWGSIALAFGWG TTVCSGFPSILVWVKISGLGQVEPKC\CH LKKL
1401	9452	A	2359	857	1343	SFRISFSGIITFKIVSFGIMAQTHAMGQFF ERNSVP*LTQGEIENLNRPIPVKL/ESITNN LL**KAPGLDGFTDD*SNI*EINL*PRNISL KFFFLRKKSQYQFSTIASKKIEAKGTHPN* L*ETSITLILKSDKDMTRKGKQLSLINIDA KILNKILANQMQ
1402	9453	A	236	426	2173	MRAQTHNRAVDIALGTAGAHLEDPGAQ QGQDRCSWQVCRSARRRRRREAAGGRR AARRAQHPCCREPSGNQSLSAHLHTGAT KGPASSLLHEHLWKPIARSARLPGNSSPL FSAPCSMGAGPSLLAALLLLSGDGAV RCDTPANCTYLDLLGTWVFQVGSQSGSQ RDVNCVSMGPQEKVVVYLQKLDTA\Y DDLGNF\GHFTIYNQGFIVLNDYK\WF AFFKYKEEGSKVTTCNETMTGWVHD VLGRN\WVFTGKKVGTASENVYVNTA HLKNSQEKYSNRLYKYDHNFKAINAIQ KSWTATTYMEYETLTLDGMIRRS GGHS RKIPRPKPAPLTAEIQQKILHLPTSWDWR NVHGINFVSPVRNQASCGSCSYFASMG MLEARIRILTNNSTPILSPQEVVSCSQY AQGCEGGFPYLIAGKYAQDFGLVEEACF PYTGTDSPCKMKEDCFRYSSEYHYVG GFYGGCNEALMKLELVHHGPMVAFAFEV YDDFLHYKKGIYHHTGLRDPFNPFLT HAVLLVGYGTDSASGMDYWIVKNSWG TGWGENGYFRIRRGTDCAIESIAVAATP IPKL
1403	9454	A	2360	84	326	DKAYQCSDCDK/ELHSVTLVSR*SVLSM HQSIHIWKKKLCFLK/CHKAFSQ*SALII KQRIHVAQII*ICCIWESLQPEVVL
1404	9455	A	2361	635	1170	RLFKCILGLLTFPPDSSHQPLPGESPGSFE KSRCPCGWPHPAQPHQSRWA\GPACSSY SGVLQG*EPQI*SLQHGRGGGGRTGGLE KETRTGSRISDTALGG/EAGPCPCGQLPH LPGPPAAHDAGPYIP/PKGPGGSGYLHP HGSAKLGSNQGAMKQAGRTGSAGSQG SAEFHKAALWT
1405	9456	A	2365	2	333	EPVCATWKNRTPEPTRQCRPAEKQRASA TQHQEGRPQGWKPRRSSDPPHRPRGFSS THDVSD*PK\TNCREAKGEEAGSGLPTGT GIGGSKPSNRLRSTHTTTPGTVFNT
1406	9457	A	2366	208	491	KQSQVWCVLWSEGLLGLDPPNPSACG GDRLS/RTSAVPPVP*S*NSSAHGPGGRP GKPQGWG*TVTSGRSVAGKPGVPSNRR CFLPPHPWLLDN
1407	9458	A	2367	2	1010	PQPAQPCPGKELRTVNGSQMLLVLLVVL SWLPHWGAL\SLAEVASRA\SFPGP\SELQ LRRTSKIPKSLRKRIYEDLLNPGCGPNQS WEDSNTDL\VPAPAVRI\LTPEVRLGSGG HLHLRISRAALPEGLPEASRLHRLF\RLS PTASRSWDVTRPLRRQLSLARPHGPALH LRLS\PPPSSQSD\QLLAESSARPQLEHL RPQAARGRRRARA\SNGDHCP\LGPRCC RLHTVRASLED\LGWA\DWVLSP\REVQ VT/LCAIGACP\SQFPGRQKMHAQESKTN PAPALKAPNTV\PKRP\CLVPRQLQIPWVL HSKRPD\TGVC\FDL/SD*LVKPKTCHLH Y

1408	9459	A	2368	68	430	HVLTAPHPPHRLGPGPQGRSGMGREL GPTVCLSSLPRLAASFPRPP/VGLGPQQV QVVNGGCWPCRGYGEGTQAPQPPS*VG DPGEPNPQAPGAQSSTPKPAHIPPTQEA GRRWEGKWWF
1409	9460	A	2369	694	872	VCPGTGGE*GLWGOGLGPKETPLKPM DAFTGSGLRKRFDDVDVGSSVSNDSDEI SSSDSADSCDSLNPPTTASFTPTSILKRQK QLRRKNVRFDQVTVYYFARRQGFTSVPS QGGSSLGMAQRHNSVRSYTLCEFAQEQ EVNHREILREHLKEEKLHAKMKLTKN GTVESVEADGLTLDDVSEDEDIDVENVEV DDYFFLQPSA\PKRRRALLRASGVHRIDA EEKQELRAIRLSREECGDCRLYCDPEA CACSQAGIKCQVSDRMSFPCGCSRDCG GNMAGRIEFNPIRV RTHYLHAIMKLELES KRQ\GAAQQPQ*GALPDCQLQPDSTGP *DPLTWHLIPAWLQAHASGSQYSRQSQP HSSRRRMRARSSCFSSASIRCTPEALSRA RLRLVGRWLQEEVIIHLHIFHINIFI
1410	9461	A	237	3	463	GTRFLHSFLSSLKHGCGPSLLAALLLS PGDGA\VRCDTPANCTYLDLLGTWVFQ VGSSVGSQRDVNCSVMGPAQRKKK*VVY LQK\LDTA\YDDLGN SGHFTIYNQGF VLNDYKWF AFFKDVTD FISHLFMQLGT VGIYDLPHLRNKAGY
1411	9462	A	2370	2	295	
1412	9463	A	2371	2	345	
1413	9464	A	2372	156	1437	GIETRRPWGRPYVAWLLVMDALVEDD ICILNHEKAHKRDTVTPVSIIL/PGDESVA SHFALVTPYEDIKKRLKDSRKRTSFLKK RIRFLEEKLI/GSDLKKKQVT*GRE\QVNK AYHAYREVCNDR\NLKSKLDKMNKDN SES\KVLNEQLQSKEVELLQLRTEVETQ QVMRNLNP\PSIQTGEVGVGAGDLKIH GFGNQELELMRKECSDLKIELQKAKQTD PYQEDNLKSRDLQKLSISSDNMQHAYW ELKERKCLNLHLVTSSYKLELLRKT*KT STAIKKVACAPVGC\VEDLGRDSTKLHL DGFLLATYARHPPLLPNGKALCHTTSSP LPGDVKVLSEKAILQSWTDNERSIPNDG Y/DAFREHSSYGQNSLEDNSWGIFQSPPK /SQSETAFGETKTKTLPLPNLPLHYLDQ HNQNCLYKN
1414	9465	A	2373	28	405	FLYDPAPPFLSIYP\KELKVES*IDTCTLFI AALF/LIGKRWK*PKYPLTDEWINK/VWY INTIEYY/SHLKRKDILTHYTTWVNREDLI LSEISQSQKINTVESTYMRKYISNS*ISIG TSYKSHRV
1415	9466	A	2374	1414	1607	DRVSLWLPRLECSGAISAHCNLCFSGLS NSPTSASRVAGTTGACHHTLLI*FLFV VVVFETES/HLWLPRLECSGAISAHCNLC FSGLSNSPTSASRVAGTTGACHHTLLIFV FLVEMGFHHVGK
1416	9467	A	2375	558	985	KKDPRWALYSLYVYKFLHFSYSSAKNP DGCFFQKVLNGFTKFFCKEQYCKLLKLY FYRLFALLWILCLSGFLKFFFYSEIMELV LAAAGALLFC/GNFIYDTHSLMHKLSPE EYVLA AISLYLDIINLFLHLLRFLEAVNK K
1417	9468	A	2376	664	937	VLLILFSNINIFL*SLPYSSFFIGEDNGSWV LAAAGVALLFCGDSSMDTHSLDGINWS PEEYVLA AISLYLDIINLFLHLLRFLEAVN KK

1418	9469	A	2377	1	739	DPTVTPRSSLKNDSTNGSSVASATVHIE WAFRLKVYSILSLQVLLTTVTSPVFLAYF ESVRTFVHESPALILLFALGSLGLNFALT LNRHKYPLNLYLLFGFTLLEALTVAVV VTFYDVYIILQAFILTTTVFFWFDCVYS YQSKKDFSCKFGAGLFALLVG*LCLSGF LKVFFFYSEIMELALA\AAGAPPPVDFII YDTHSLMHKLASPEEYVLAASLYL\DI NLFL\HLLRFPQSOLNKK
1419	9470	A	2378	272	1668	AMSQGSVTFRDVAIDFSQEEWKWLQPA QRDVYRCV\MLENYGHVLSLAGLSISKPA DVVSLLEQGKEPW/VWGKREVKRDLS VSESSGENQGLFHQKNVIYDGLHPSI*IM ERNISKVKAPVYSSFKGGWKCKDHTEML QENQGCIRKVTVSHQEALAQHMNISTVE RPYGCHECGKTFGRFSLVLHQRTHTGE KPYACRACGKTFSQISNLVKHQMIHTG KKPHECKDCNKTFSYLSFLIEHQRTHTG EKPYEECTCGKAFSRASNLRHQRIHIGK KQYICRCKCGKAFSSGSELIRHQIHTGK PYECIECGKAFRRFSPLTRHQSHTTKTP YECNECRKAFRCHSFLIKHQRIHAGEKL YECDECGKVFTWHASLIQHTKSHTGEKP YACAE*NKAFSRFSLSLILHQRTHTGEEP YVCKVCNKSFSSWSSNLAKHQRTHTLDN PYEYENSFNHSHFLTEHQ
1420	9471	A	2379	1322	1644	HLELFLGIRGIKMFVGWVTNE*EEKAGLN GSRL*SQHFGKPRWVDH/LRSGVRDQSV GQHGTSSLQKNKTTSWAWWRAPVVP AT*EAEVGGWLEPRGGGCSEAVSGAF
1421	9472	A	238	12	362	DRVSLSPRLECNSAIPAHCPNCLP/GFK QFSCLSLPSSWG*RCLPPRLANFLY/SLVE IGFHHVGQAGLKLLTSCDPPTSA/FPKCW DYRHEPQ/WPDL*LTSF*GYRYEDSDFL PKVPI
1422	9473	A	2380	319	724	EASLDLAPNISPPKTSCLPTGSCCSFTQT WMPQSKVFIHGPEQGPWDWALGTDLTA LPFKARNMPNLDTAGLPSIALRLTVNHR RSPGSQELSCLPDSCLSQ/PPQPC*GSLLP LEYKCTPKEALRK*KRLSFLFV
1423	9474	A	2381	38	704	SSEEEQSRFSSSHQGDPAVTVKWLKP VPPRWRFSHFPLDSPWHLLQTAVTPLP QISAAPPKPLLPPTSPLAFFSSLLTDLPLY HPQGFSAGATA\NKASHNRTRALQSHS\ SPEGKEEP*TPYPPELEYIP/RKRGKNPHG KLVTGLGHSAFFCGYSFLFHPSPKRG GTRDRVEGRLKARQNRVCSNN/AGEYE EARRFKGLSSQSGPVPDPVAGSGVQT
1424	9475	A	2382	107	449	
1425	9476	A	2383	68	422	
1426	9477	A	2384	54	859	LRRGRSRETNEEPPPTVQVQGPQREE KQKTKMAKFVIRPATAADCSDILRLIKEL AKYEYMEEQVILTEKDLEDGFGEHPFY HCLVAEVPKEHWTPEGYSL*LRHVHG VYMDGRGGN*KILYTIK*MIMINEDTAL VGFAHVLIYPMNPWDWQSYLYLEDFSIV MSGYKGLGIGSEILRNLSPGCQ*RCR\CS SKHFLVAEWQ*THPITFYKRRGASDLS Q*RRGWETCSKIGQGSTWLKIGQPEGVR ECCLLGWTTSHSYF
1427	9478	A	2387	112	861	NPGAAMPAYHSSSLMDPDTKLIGNM/A HLLPIRSQFKGPAPKRDTRIPDIVDEAIFL PSGPNVFF\KNYEIKNEADRTLIIYITLYISE CLKKLQK\CQFPKAQGEK\EMYTLGIPLN FPIP\GEPGFSHFNANLCPNPANK\QEDEL VMRAI\YLPSTSLRPRTLGLKTL*EKFFGPS RMDKPQQSGWTWLC*RDSEFMNKSLSG PWTIEREPGAHRLPRGPAAFFQQDVT QSFCLYFSKVFIQRRRACLYLKNS

1428	9479	A	2389	1	395	AKAKMADVLDLHEAGGEDFAMDEGDG ESIHKLKEKAKKRKGRGFG/SR*VWGKW GRVA**GRSYGFWSPPHRRNNGRKEEF SVISCM SLIEGSRARMREDYDSVEHDG DEPGPQRSVEGWILFVTGVHEEA
1429	9480	A	239	3	153	
1430	9481	A	2390	146	831	CLSGTDEISIEGEMADVLDLHEAGGEDF AMDEGDGDESIHKLKEKAKKRKGRGFGS EEGSRARML*DYDSVEQDGDVPGPQRS VEGWILFVTGSP*RKPPEEDIHDKFARIM GEIKNISSSTFDRRTG/YILKGYTSLNIET YKEAQAAMEGLNG\QDLMGQPISVDWC FVRGPPK\GKRRGGRRRSRISPDRRPSLT GPLLRC SLQDSIW TMAALGQIGLGWEL CCVYI
1431	9482	A	2391	2	442	FYVILISVRELYLCHHLPFLCAGVYMTNS AMKVFLIWL VIVKITVLEFKKLSWP GAV VWF*GLILYTHI*TL\NTHI*VQNV CYIIL QRNK*FHRFCINIKSWLGAEPHACNPSTL GG*HS*IT*AQKFETSLGNVRPCLYKKY KN
1432	9483	A	2392	2	425	RRANPPSISPSAQDSRVTVPGEGPGSP/G* PSRPVS/GPA/PGSGGLRGSSAPATPLGE APSPSAIGPTALQPCDPGAGP/GTARPG QTASAAPAPLPPRRGAGAPPQAGREGG PCGEEERPPSGREKVSC*KRQTGPGQRR ADK
1433	9484	A	2393	2	662	ACTAADLIAGTTISEAGPHMENQP/GEVA GPAGPPTPSWAPRIPLAPPWRAAAGRDP AT/GQEDSQ*PTPGCPSWPPWPTQLSPSA AGSPIHTVPIQGFHSQLLS*RSPGTEEP*E ANKLPPWTGHREPEHPGLPGHPCAAGS IGHWHL LLLCPLATLHGERQRHLHPGQR SGCGVQGRTPPGSAQIQDLPAAPSSILQN LSTQLCSAARPRSM PASRMRM
1434	9485	A	2394	115	187	
1435	9486	A	2395	93	584	KHSASAAQALPGTLGACTGSGGLRGSS APATPLGEAPSPSAIGPTALQPCDPGAG PVLPGQVKLPQQ/PPAPLPPRRGAGAPPP PEIPSGSSFQGYWEGGAQTPGLLPAQRPL PPFPALGSGCSALEEG*ATGTRGHKGG CS*GLWGEPGRAGKHPPHLL
1436	9487	A	2396	46	438	LQKRVGDWLGEAPPWGWVGS HR CRAR TARPGQTASAAPAPLPPRRGAGAPPLAR VPAPPCCAQRAPSSSQGRNQ**AASGP WRPPR/PGREVGTGCEERPASGREKDS C*ERQTGPGORRAVKMTQIR
1437	9488	A	2397	455	1241	ARELRAGGFYVPHRGLEMPETALEAG VSGVGLQHLP/HLGEAPSPSAWPD TQR CSRVIPVQGPVLPQGVKLPQQ/PPAPLPP RRGAGAPPLRLARVPAPPCCAQRAPPS SSQPGRNQ**AASGPWRPPRQAEKESNC GEEERPASGREKDSC*ERQNGARSAAGR QAKESPQTSRPPDGEPACEVAGPAGPPTP SWAPRSLAPPWRAAAAARDPATGRRTV SDPHRPAHHGLPGQHSYLLQLQDHL SIH SPIQGFHSQLLS
1438	9489	A	2398	2	328	PLFSDNGKKRGLALDGK LKHEDTNLASS TIVKEGANKEVLGILVSYRVKLVVSR GGAPETDVPVDTNLIEFD TNYATDDDIV FEDFARLRLKGMKDDDYDDQSTRP
1439	9490	A	2399	2	417	EIRAFCAKSLE*KSHKRNSVRLVIRKVQF APEKPGPQPSAETTRHFLMSDRSLHLEAS LDK/EVRQYADICLFSTAQYKCPVAQLE QDDQVSPSSFTCKVYTITPLSDNREKRG LALDGK LKHEDTNLAFSTIGKEGGH

1440	9491	A	24	497	752	DGVLLLLPRLECNSAILAHRNLRP/GFK RFSCLTLLSPWDYRHLPPRLAIFVFLVY VGFHHVGYAGLELLTSR*SARPRPKIA
1441	9492	A	240	3	423	GSTHASARMAVMAPRTLLLLSGALAL TQTWAGSHSMRYFYTSGRPGRGEPRFI AVGYVDDTQFVRFDSDAASQRMERAP WIEQEGPEYWDQETRNKAQSQTDRVD LGTLRGYYNQSEDGSHTIQIMYGCDVGP DGR
1442	9493	A	2400	188	340	GGALLKDPLGGPNLPGGGKDKFFSFWG AF*NPPGDFWEGTFFLGGGILGP
1443	9494	A	2401	117	457	
1444	9495	A	2402	39	447	
1445	9496	A	2403	3	1359	FPGRRFRGGAGILAAGEEAASEPRTERA AGARTMGEKPGTRVFKKSSPMCKLTVY LGKRDFVDHLDKVDVDPVGVVLVDPD/Y TMKDRKVFT/LSPCAFRYGRELDVL GLSFRKDLFIATYQAFPPVPNPPRPTL QDRLLRKLGOHAHPFFFTIPQNLPCSVTL QPGPEDTGKACGVDFEIRAFCAKSLEEK GHKGTSVRLVIRKVQFAPEKPGQPQSAE TTRHFLMSDRSLHLEASLDKELYHGEF LNVKCSFTNNSTKTVQGRFKVSC*GQ/ YADIWPLSGTAQYKCPVAQLEQDDQVS PSSTFCKVYTITPLSDNREKPCCLALDG KLKHEDTNLVSSITIVKEGANKEVLGILV SYRVKVKLVVSRGGDVSVLPFVLMHP KPHDHISLPRPQ\SAAPETDVPVDTNLIEI DTNYATDDDIVFEDFARLRLKGMKDDD YDDQLC
1446	9497	C	2406	933	1070	MKRKNILYYGTNKLNTNLLNNFINI LVSSLGLSERSFYRIL*
1447	9498	A	2407	138	1166	VVAMAQVLRGTVTDFPGFDERADAETL RKAMKGLGTDEESILTLTSTRSNAQ\WQ EISCS/AFKTLFGRDL\DDLKSELTGKF EKLIVALMKPSRVL*MLIELKHALKGA GTNEKVLTEIIASRTP\EELRAIKQVYEE EYGSSL\ED*RWLGDPGGYYPAGCWLVI LLQANRDPDAG\IDEA\QVEQDAQALFQ AGELKWTDEEKFITIFGTRSWSSF*GK VFDKYM\TISRISKLR\ETIDRETSQGFRSQ LLGCCGILFRRYTSPTLQETFIYAMKEA GTDDHTLIRVMVSRSEIDLVIYPGREFR KNFCHPPPYSMIKGRYIWGTIKKALLAL CGEDD
1448	9499	A	2408	1	498	
1449	9500	C	2409	14	394	
1450	9501	B	241	1	540	MPVNHK\HRD\TIAESLITPNVTDSVKD CIKELGNRLFLWTQGCSSHVATVAPPTA PRGLRVRS\AVRPLPLGGWAAAMEGEPP PVEERRRLQEELNEFVESGCRTLEEVTAS LGWDLDSLDPGEEEAELHQIRCQESWE FASSPFCALKLDTSDWDSTNSRIKGCHQ EVTGNSCGH*
1451	9502	A	2410	2	353	
1452	9503	A	2411	1	349	
1453	9504	A	2412	123	195	SWKPSFSAN*HSNRKPNTACSHS
1454	9505	A	2413	240	743	
1455	9506	A	2414	284	672	GGWEGLTDSYRRAPAGIRPVLQRKEQT VIFAVLQPLLVIPR*TASGVDLQQT/GRP AEERPVRRTKKQNATTSKSTKGTPQK PHSNVIRFKDERDMDEAGNHHSQQTNT GTENQTTTCSHSYVGVEQ

1456	9507	A	2415	579	1383	VGSCAFYLAVSVFLAPRPFLHLLQLGAD EARSWDFLRSPPEEFNTNMDIRPNHTIHI NNMNDKIKKEELKRSLYALFSQFGAHVV DIALKTMKMRGQAFVIFKELGASTNA LRQLQGFPFYGKPMRIQYAKTGSDIIS KMRGVTADKEKKKEKKKARTVDQTAT TTNKKPAGQGTTPNSAIPQGNSTTQIPQVP DYPKSLNFYSLNKLQRETNEMMLSHA V*ISSTWPSSEVPSGYPRGHDIAFVEFEN ADGQAGAARDALQGF
1457	9508	A	2416	1186	1451	DLLKVLHEKPKLARRSGSHL*PR/HFGRL RWKDCIKPGVQDHSGQYRESPSLQNIKK KIIWAWWCMPIVPTTQAVKVGSLELK RLRLQ
1458	9509	A	2417	1	412	
1459	9510	A	2418	298	532	MGSWSLPGRTLWKEKVRFLKSKERTNP GSNFFSFPQSQHTREERSQECLSLPVLPS YLATRLSLPDSCPLKGRKAH*QRHSEI*L MGFEPGWPGKL*GWIELAFLGCLHLTL PLPCPTPLPPKSTKSGCFSLSIALCFNKQF AVTK
1460	9511	A	2419	5	977	VRGGLAAGRGRGSAGAAPVVVAAMLG AWAVEGTAVALLRLLLLLPPAIRGPGL GVAGVAGAAGAGLPESVIWAVNAGGEA HVDVHGIHFRKCIPL*GRVGRASDYGMK LPILRSNPEDQSCYQTEARSNEETFGYESP IQREGGLTCWSLKFAE\VFYFAQSQQKVF DVRLNGHV\VKDLDFDRVGHSTAHEI IPMSIRK GKLSVQGEV\STLYTGN SNME/F VKGYL*PIPKVCAL\YIMAGTVDDVPKL QPHPG*ERKKGEEEEEEYDEGSIPKKNR PIKNGGQSGP\RHNP\TP*ASDNSSLMFPIL V\AFGVFIPTLFLCRL
1461	9512	B	242	232	387	MEGEPPPVEERRRLQEELNEFVESGCR LEEV\TASLGWDLDSLDPGEEEEAAE*
1462	9513	A	2420	1	453	RNSEKEVEKRKVALQEAKLKAKGLNPD GTPALSTLGGFSPASKPSSPREVKAEES PISINAKTVKKEPEDRQQASKSPYNGYN NRRSRSGTYSSRSR\SRSHSESPRRHHN HSSPHLKAKHTRDDLQSSNRHGHKRRK SRSR\SQSKSR
1463	9514	A	2421	19	434	QRGNY\SF\IVAMACINLASKIEEAPRRIR DVIN\VFHHLRQLRGK\RTSYIYQSLGDVE WYIEMKLSSWQQT\PSPLILDQNYINTKN QVIKAERRVLKELGFCVHV\KHPHKIIVM YLQVLECERNQTLVQTAWV\VDGIT
1464	9515	A	2422	171	437	TSNFY\YLSYNNRRSRSGTYSSRSR\SR HSESPRRHHNHGSPHLKAKHTRDDLKSS NRHGHIRKKS\SR\SR\SQSKSRDHSDAG*KH RLE

1465	9516	A	2423	21	1855	FPGRFRFLRWACVRLAKTMASGPHSTA TAAAAASSAAPSAGGSSSGTTTTTTTT GGILIGDRLYSEVSLTIDHSLIPEERLSPTP SMQDGLDLPSETDLRLGCELIQAAGILL RLPQVAMATGQVLFHRFFYSKSFVKHS FEIVAMACINLASKIEEAPRRIRDVINVF HHLRQLRGKRTPSPLILDQNYINTKHQVI KAERRVLKELGFCVHVKHPHKIIVMYLQ VLECERNQTLVQTAWNYMNDLSRTNVF VRFQPETIACACIYLAARALQIPLPTRPH WFLFLGTTEEIEIQEICIETLRLYTRKKPN YELLEKEVEKRKVALQEAKLKAKGLNP DGTPALST/LGVGFSPASKPFIHQENVKA GRRKSPIFHLMWKDSKKEPGG*D/RQA FPKALYNGVKEKDS/RRRSRNSRSASRS RSRTRSRSRSHTPRRHYNNRRSRSGTYS SSPRSRSPSHSESPRRHHNHG/SPHLKAK HTRDDLKSSNRHGHKRRKSRSRQSRSR DHSDAAKKHR/HERGHHR/DRRERSRSF EEVP*KARHHGWPVRSCTWARAQGADL SSSLWSPAIOFLGFGPIYQCDGMGLNPKT IKRKTGLGDFLETPPRSS
1466	9517	A	2424	1	1566	
1467	9518	A	2425	328	889	GLRTPAAYLYCGTVRTAGVAAASRYQG DNIYVKNLDDSIDDERLQKEFSPFGTI*S AKGMMEGGHSK/GFGFR/ICFSSPEEASK AGTELNGRTVATKPSYVALAQPKKECQ AHLNQHMQRMASVRAVPNHVMNPYK PAPPSGYLMTGIPETQNRPPRPGAVGHPC NPSTLGGQEGKNTGSGDRDHPG
1468	9519	A	2426	1	2262	
1469	9520	A	2427	365	2419	FSIPVDFCPSALAPRSPPPGSGPQPRHLS SSHGKVAACGPAGSRAEMNPSAPSYPM ASLYVGDLPDVTTEAMLYEKFSPAGPIL SIRVCRDMITRSLGYAYVNFQQPADAE RALDTMNFVDVIKGPVRIMWSQRDPSLR KSGVGNIFIKNLDSIDNKALYDTFSAFG NILSCKVVCDENGSKGYGFVHFETQEA ERAIEKMNGMMLLNDRKVFVGRFKSRKE REAELEGARAKEFTNVYIKNFGEDMDDE RLKDLFGKFGPALSVMVMTDESGKSGF GFVSFERHEDAQKAVDEMNGKELNGKQ IYVGRAQKKVERQTELKRKFEQMKQDRI TRYQGVNLYVKNLDDGIDDERLRKEFSP FGTITSKVMMEGGRSKGFGFVCFSSPE EATKAVTEMNGRIVATKPLYVALAQRK EERQAHLTNQYMORMASVRAVPNPVIN PYQPAPPSGYFMAAIPQD*DRVAAYPPS QIAQLRPSRWTAQGARTHPFQNMPGA IRPAAPRPPFSTMRPASSQVPRVMSTQR VANTSTQTMGPRPAAAAAATPAVRTV PQYKYAAGVRNPQQHLNAQPQVTMQQ PAVHVQGQEPLTASMLASAPPQEQKQM LGERLFPLIQAMHPTLAGKITGMLEIDN SELLHMLESPESLSKVD EAVLQAHQ AKEAAQKAVNSATGVPTV
1470	9521	A	2428	2	237	
1471	9522	A	2429	68	866	GSTGAVTAATATAATAAGASAPLGLPV YLPAPRSTAPAPSPAASALLFLVLTTPSRP ERLPSHQPPSATMATAPYNYSYIFKYIII GDMGVGKSCALLHQFTEKKFMG*FVPH TIGCWNLGRINESLVGQIKLQIWGLR QQQERLRAVYT/RAYYRGAAGALMVY DITRRSTYNHLSSWLTRCQGISPNNKYW **FSIGN*SQIWRPQRDVTYEEVAKQFAEE NGLLFLEASAKTGRRIVEDAFPLRACPR KIYQNIQDGKLGs

1472	9523	A	243	1124	1394	ACDDWNRMDKSHLHPPPPFPRDPDYV GPSGTRSPPTSGSRSPRNRSAAPPAPAA PPQVQARPP*HSPDKRKRPNCRTRGSP PWFRS
1473	9524	A	2430	229	593	SLICFAVGVGDCAEFWVTRLAPRAEKRR LAPAVPPHHQDERGGTSTPHFHNLSHG WVTFPALLPOYDILPLNSFLHEIQEPSLG SGLGPFSCNTYLISFSSTCHLAPVINLWA LPGASIM
1474	9525	A	2431	594	829	PCALVPLRPYATK*GMLPWLLGLHLOS RAFAVALDHILF*VL/CHV*IPSILTKIFEN GYFVISVLLMRNILSSSALL
1475	9526	A	2432	1479	1734	LKVNISLGMVGHACNPSTLGSQE*ATVP LILYFLNKLAFTHCGITLNSFLHKIQEPS LGSRLGPLSCNYHATALQPQQSKALS
1476	9527	A	2433	30	508	
1477	9528	A	2434	338	853	EGRGFGRAGLPPLCIAALFQFKMNYMPG TATLIEDNDKKHLVLLRDGRTHIGFLRS IDQFANLVLHQTVRIHVGVQK/YTGDIPR GIFVVRIGENVVLLGVEIDLEKESDTPAQ QVSH*RKFLLEQKGWNQQTKLAEAEKL KVQALKDRGLSIPRADTFDKDLFFCPEA VGS
1478	9529	A	2435	357	893	TVFQIWANHPGQRPAPQLCPVHLLGGQS HQEPRHTSNSEPSRASASLRRLTPLKPTG IGPGSQILED RDFRAFT*WGDYFWGKGA PACLIQDGVKGQWAGPHSGVGGVWGP APRACPPVFSPPQSQSSACGCQYLSRP KAYPQGWGRGGDPPGQNVRSVCDLRC CMWTLNCTCSF
1479	9530	A	2436	233	566	RLFLVRKRMISFSAPPLMLPFSFYFFVC PAARTARKRKPSPEPEGEVGPCKINGEA QPWLSTSTGLKIPMTPTSSFSVPPPTA* PHSNRTTPPEAAQNGQSPMAALIL
1480	9531	A	2437	219	702	ARKVRARAAGLESRTGSTGPRPCATRC WRCTSTATRGPSRASFKKEPALTA VART ARKRKPSPEPEGEVRAPLRSTEKAPGC PHSTGLKIPMTPTSSFSVPPPTASPHSN PGPHRLESGPRMGQFPIGSPDLSSRQFRG QSCSKDANQVHSTTRNSN
1481	9532	A	2438	173	1136	ALEGAGKSRGFWRAGLGQQAQDRARH AAGRCTSTATSGPFESKFKEPALTAGR LFGVFEGQRGQGLKAVCKNSKKGKSP LPEPRKVKSGPLKIQRGSPSRRL/SPHPQR GSRSP*LLHPLLCLRHPLPHLIPTGPHRL KRPRMASPPWQP*S**QTMQGASHASKD ANPGSLPTTRKE*PTVGPSSVLL*TKERL GPKRGGGPREQATQEDWEPVHPASLPDF LFGQPVAPLCCTLCHERLEDTHFVQCP VPS\HKFCFPCSSQGIKQQGS\SGEVYCP SG\DKCPSGLPMSPPWA\FMQGEIATILA GDVKVKKERDS
1482	9533	A	2439	1	206	PTRPRTSYEKQGYLLPPVFSIVLEVLR AISQETEEKSVQMGKEEVKLSLAFVCVYI YA*ENPVESTK
1483	9534	A	244	171	512	CTVGVRCTVFPTEHKLPAVESHLIVSRSE SVINKI*ANQIWEH/IKKIIHHEEVGFILGM QGWLNIRKAPTEIYHINR/SKDKNHMIILT /D*EKAFDKI*HYFILKTLDKLGI*GNF

1484	9535	A	2440	611	1203	ERLLRVCLALGSAGTADDVKLHPVSCA DTARSTPGTSAPSTSGTSAPFTPGTSAPST PGTSAPSTPGTSAPSTPGTSAPSKPGTSAP STPGTSAPSKPGTSASSTPGTSAPSKPGTS APSTPGTSAPSKPGTSAPSTPGTSAPSKPG TSAPSTPGTSAPSTPG\QHPHHRGPQHPP SRGPQHPPHHRGPQHPPSRGPQHPPHLP QHPPSRGPQHPPHQGPQHPPSRGPQHPP/ PPGTSAPSKPGTSAPSTPGTSAPSKPGTSA PSTPGTSAPSKPGTSASSTPGTSAPSKPGT SAPSTPGTSAPSKPGTSAPSTPGTSAPSKP GTSAPSTPGTSAPSKPGTSAPSKPGTSAPS KPGTSAPSKPGTSAPADPGVL
1485	9536	A	2441	447	920	GWHWFLASQKSLKPLSRNPCVLVSCH MAQSWARTQEFLCPMCPTT/CAQSGTGT ESCFPNPN*VLGAGAPQPDQRCHKAGPF SSVPGFRLPSSRHGGPVLPGLTGPPGPPG RPPHKPSNEQRDAGQQLQLPPPACQPQK LPQLPFCLKFYSLPELPH
1486	9537	A	2442	1	374	LRKDDTQIREAFHIFVQSWRPALPSLPSL PLARALAEITLNQPFGLITPSGILLNSQ MLDFSWPNRTANHSAPS/TVVRPAEGLC GTYLALGANGAARGLSGLTQVLLNVLN *NRNLSDSLARGR
1487	9538	A	2443	1	315	
1488	9539	A	2444	3	2027	NSRVDDFVARARMAAENEASQESALGA YSPVDYMSITSFPRLPEDEPAPAAPLRGR KDEDAFLGDPDTDPDSFLKSARLQRLPS SSSEMGSDGSPRETRKDPFSAAAEC SCRQDGLTVIVTACLTFATGVTVALVMQ IYFGDPQIFQQGAVVTDAACTSLGIEVL SKQGSSVDAAVAAALCLGIVAPHSSGLG GGGVMLVHDIRRNESHIDFRESAPGAL REETLQRSWETKPGLLVGVPGMVKGLH EAHQLYGRLPWSQVLAFAAVAQDGFN VTHDLARALAEQLPPNMSERFRETFLPF GRPPLPGSLLHRPDLAEVLDVLGTSGPA AFYAGGNLTLEMVAEAQHAGGVITEED FSNYSALVEKPVCGVYRGHLVLSPPPPH TGPALISALNILEGFNLTSLSREQALHW VAETLKIALALASRLGDPVYDSTITESMD DMLSKVEAAAYLRGHINDSQAAPAPLRP VYELDGAPAAAQVLFMGPDFFIVPMVS SLNQPFGLITPSGILLNSQMLDFSWPN RTANLSAPLENSVQPGKRPLSFLPTVV RPAEGLCGTYLALGANGAARGLSGLTQ VRFTPWLAFSREPSCGLDCRCLS*QSNL LQVDSECAETSWGGHRDR*RKDSSQG CPWVHGSRRTNNFIIAVKDPRSPDAAGA TIL
1489	9540	A	2445	83	310	IFQCTKFTWDSQITPRLFHPAPPTWCRPL PVSG*RRVRGWTTTRQSGGGGRGPAPLS SQAPPKGPVPFQWHLRAEG
1490	9541	A	2446	1	1833	
1491	9542	A	2447	3355	3951	
1492	9543	A	2448	699	975	
1493	9544	A	2449	3	132	GRFSSESPRA\GPPAPHRGHVQRCCVS PTGLLIWKELERPF
1494	9545	A	245	1	293	FLRWSLALSPSLECSGAISAHRLN/RLPGS TNLPA\STSRVASTVGMATAPGLNFCIFS REG*VKHVGPGCLELP\TSSDPLPLVSPK LRDYRPEPLCLA

1495	9546	A	2450	2	1734	TDLKRCTYYETCATYGLNVERVFQDVGI IDSAVPCSAQKVVALRKKQQLAIGPASH CPNSPKHWAVSAASIPAVHNTQATNGG GKAFSDYSSSVPTSPISQRELRIETIAAS STPTPIRKQISKRRSNIFTSRKGADLDREK KAAECKVDSIGSGRAIPIKQGILLKRSKG SLNKEWKKKYVTLCDNGLLTYHPSLHD YMQNIHGKEIDLLRRTTVKVPKRLPRAT PATAPGTSPRANGLSVERSNTQLGGNR GRGVV*ICGWVSLTGADVGTGFEFNGR RERELGFSVQAQILASLQGLQCQGG DFDLGNQNAALAVQAVRTVRGNSFCID CDAPNPDWASNLGALMCIECSGIHRHL GAHLSRVRLDLDWWPELLAVMTAMG NALANSVWEGALGGYSKPGPDACREEK ERWIRAKYEQKLFAPLPSSDVPLRQQL LRVVEDDLRLVMLLAHGSKEEVNET YGDGDGRTALHLSSAMANVFTQLLI/W GESRASSLP*PRSS*PCSLKATSSFLPYNQ SLSSHVLPTVNMCFLLQYGV DVRSRDAR GLTPLAYARRAGSQECA
1496	9547	A	2451	329	3294	ESEELWGEQLAGGPPQQFALSNSAAIRA EIQRFSVHPNIIAYDLIERIEDLALQNI REHVISIEDSFVNSQEWTLRSVPELKIV GIVGNLSS\GKSALVHRYLTGGPIVQGG SPLKGGGLRSEIAADGHSYLLIRDEGGP GELQYAAWVDAMVF/VWSPCEDGITFS KTVYNYFLRLCSFRNASEVPMVLVGTQ DAISAA\NPRVIDDSRARKLSTDLKRCTY YETCATYGLQCGSVSFQ/DV
1497	9548	A	2452	493	955	TLCTYILISEVISLPGTAFIQRKGLGRPS QNNAYSLSQTSPLIIFLRVQKFDLNL LVLFSSGGTESRSIAQLECSGMTSAHCN LRFLGSSYSPASAS*VAGTTGACHHAQLI FLVFLVEKGFHRVSRDGLHLL/NLVIRPP QPPKALGLQA
1498	9549	A	2453	158	720	PPPCRAKQHQTCKKRPQQRATSNVFAM FD\QSQIQEFKEAFNMIDPDQDGFIDRE DLHDMLASLGKNPT*WSILDAMMMRA PGPPSNFTPWFPHHGFGE/RLNGHQIPE DVHRKMPFACFE*KKPLGTIR\EDYLRE LLTTHGGIGFTDEEVDELYREAPY*PKRG NFNY\SEFTRILKHGAKDKDD
1499	9550	A	2454	2332	3329	VAGATGTHHHAWLISFLRWSLTSPRL ECSGTFSAHCFNRLGSSNSPASAS*VAR ITGAHHHTRLIFVFLVETRFHHGGQVGL KLLTSGDPPASASQSTGITGVSHAWPY FKLFCRDGVLLCCPG*SQLGLKQSSCQ SFPK*LDYRCEPPRPTNL*RCLARDRVPYL TTSPVRSRGGTRM/EKEVPEQRLAGSRM GQELTQQPSTETSWSLGRRRTKSPLF*IFF MFLRRSL/NSVTQAGVQ*HNLGSLQPPPH GFKRLSCLSLSSWDHRCPTPCLDNF*IF GRDG/GFTMLARQVSNS*PQGPPTLASQ SSGNTGLSHCNQPVAPIFAPR
1500	9551	A	2455	566	1037	GSTLSPSLPGFCPENSCKCKFNTLLTAES LKLQDLSFDPSPQKPTQVRHL/ESPPGEG PP\SRAPQKNSHEIR\NCLMKCIFL*LGR MKAQTPTLFASPGLGMSPAARPRSFPGG LGEVGAGTISVPSTLTPSTSETLTPQPRY GMKLADADVGGKKKK
1501	9552	A	2456	349	679	ELGHWGNRVCLSEALGLAELHPCPGNE VGPQRQG*GLAVLILAILLQGTLAQSIK GNHLVKVYDWOEDGSVLLTCDAEAQN/ ISTWFKDGKMIGFLTEDKKK WESGEVM PRDPRGMYQC*RDHRNKSKTTSQVLFT GMCSTCI*/DLNAATISGFPLWKT VSL FVLAFGVYFIA\GQGWSSASPRASDKQT LLPNDPAPTQPLKDPKMTQYSHLQGN\

						QLRRN
1502	9553	A	2457	356	505	WTGGKKKAGWMPKKE/SVKLAQ*CMP VIPATQEAETGKLEPRSSRSAWET
1503	9554	A	2458	35	359	
1504	9555	B	2459	102	431	MIIYRDLISHDEMFSDIYKIREIADGLCLE VEGKMVSRTEGNIDDSLIGGNASAEGPE GEGTESTVITGVDIVMNHHLQETSFTKE AYKKYIKDYMKSIGKLEEQRPDR*
1505	9556	A	246	466	743	LNHAVQEMIVKIELTQHMYNFHGIKLEI NKGKKFGKLIHLWKLNNVLSLSDQ*VKA EIQKGNKEIVLRWNKKEGMMYQNT/W/ DVAKPVLRAW
1506	9557	A	2460	1	581	
1507	9558	A	2461	88	779	STWAVRGSRGWGVGWGGGGSHDEM FSDIYKVRGDRGRGLCLEGGRRVVSRT E/GNIDDSLIGGKCPPLKGPEGRVPERH QLITGV/DIVMNHHLPGNKFSSQKEASKK VHQRTMKSNKGL*RTDPEKSKTFL* QGAAEQIAHPLPNFQKLSFFGENMN PRWAWVLLLDYRE/DGWCPP*YDFLLRD GLEMEKMLTNVGNVFGSITLSSITGLLPC HPTQPPGT
1508	9559	A	2462	12	159	WSHLLRMLQL*WS/HPPKNAAAYSSCRV **ERRGLIRTYGLDMCSQSFCQYAKDIGF IKLD
1509	9560	A	2463	46	371	FVILGKRCRGALGCLKSQVEEATGGTRE HADWESLVPLQACTVAWESRDAGSSR LSAESCNFYDLQNRCLFSYSRVCSNRHG LIRKYGLNMCRQCFRQYAKYIGFI
1510	9561	A	2464	1	591	GLLQAECPWRSSGEAAFREITMEIWLLA WAISPVALSESTDPEWQSRCEDRHFLF KFLVIGSAGTGKSCLLHQFIENKFKQDSN HTIGVEFGSRVVNVGGKTVKLQIWDTA GQERFRSVTRSYRGAAG/ALLVYDITSR ETYNSLAAWLTARTLASPNIVVILCGN KKDLDPEREVTFLASRFAQENELMFLE T
1511	9562	A	2465	3	495	GRDRVMAETYDFLFKFLVIGSAGTGKSC LLHQFIENKFKQDSNHTIGVEFGSRIVAN LGGEPPVKLQIWDTAGQQTGFAGKTYT SLAAWLTARTLASPNIVVILCGNKKDL DPEREVTFLASRFAQENELMFLETSALT GENVEEAFKLCARTILNKIDSG
1512	9563	A	2466	1	2022	
1513	9564	A	2467	3	715	REQARPRRHIAALSGRDRVMAETYDFLF KFLVIGSAGTGKSCLLHQFIENKFKQDSN HTIGVEFGSRVVNVGGKTVKLQIWDTA GQERFRSVTRSYRGAAGALLVYDITSR ETYNSLAAWLTALTPVQPQKTGAFLC GNKK*PGPLEREVTFL/APSFAQENE LMFLETSAITGENVKAFLKLCARTILNK IDSGELDRERMGSIGQYGIASLRKLRQP RSAQAVAPQPCGC

1514	9565	A	2468	3	953	VKMALVASVRVPARVLLRAGARLPGAA FGRTERAAGGGDGAARPFGSQRVLVEPD AGAGVAVMKFKNPPVNSLSLEFLTELVI SLEKLENDKSFRDVLTSRPGVFSAGL DLTEMCGRSPAHYAVVLERPVQELWL RLYQSNLVLVSAINGA\CPAGGICLVALT CDYRILADNPRYCKGIQIRPKVGIICPFW G*KETLGKNLLGPGGESALQVGLLFP PAGRPKVGVVDQVWSPEKQVQSIGLS AIAQWMAIPKMAHKLTKAIMRKGQGP PAWSRKGADVQNFVFSISKDSIQKSLQ MYLERLKEEK
1515	9566	C	2469	1	774	MKEVVYWSPKKVADWLLNAMPEYCE PLEHFTGQDLINLTQEDFKKPLCRVSSD NGQRLDMIELTKMEHHLEAHKNGHAN GHLNIGVDIPTDGSFSIKIPNGMPNGY RKEMIKIPPELERSQYPMEWGKTFLAF LYALSCFVLTVMISVVHERVPPKEVQP PLPDTFFDHFNRVQWAFSICEINGMILVG LWLIQWLLKYSIISRRFFCIIGTLYLYR GITMYETTLTAPGMLCNCSPKLCGDCEA QLR*
1516	9567	A	247	243	935	IPVGELYPLLEDGIAAFIEWNPHEALWE PQEQQETQGPCKSKHGEAPVGASWPFR GFGEARPPPPVRPTLIHAWKSS*PICLFS RHCHQALPGGTLDKWSSPRG/GCSPRT PGVTQQAARLSPHRVAG*QSSSGACPW MSRSSAPFPFLTPSQSPRAAL*VRKTKSP GTGEHRLWTGLGAGGV SARPVVKHSAG PGGIHGGRAPGAEQRSGLWKAGCWGSV RASAPGP
1517	9568	A	2470	263	621	EVRLSRPWPHEHEHPWPLTIKWDFP DYRQWKIEGTPFRKTIQKKLGCKKGLR DWPWGRNEAWRYMGGFAK\SVSFS*CIL FKGFKWGDLLAFVAVRELEYLPGESP* IKDKKHH
1518	9569	A	2471	1	225	
1519	9570	A	2472	99	493	TASPAPPQAFRRSSSLKIRESIIRRGSEKL VSRLRGEAA/RTSRVSVDQVGKEP*HQ QNRQPTPPPPPFCSRTFHGSHLPCDTHRS NPVLERSLVEGGHSHWHSFPCCPLCRM KRDMSLNTLNVDAPRAG
1520	9571	A	2473	70	299	AVGSVHAGVQQWVSGGVGPPGSAGPP GRKPRL*RGPSDPARRNAPAIERLSRRR GRCSARGLRGRDQEEGQPGRT
1521	9572	C	2474	129	602	MFERIVXADEHVIDQGDGDNFYVIERG TYDILVTKDNQTRSVGQYDNRGSFGELA LMYNTPRAATIVATSEGLWGLDRVTFR RIIVKNNAKKRKFESFIESVPLLKALKD GQRFNPHLHFAFEGPFIRPLVKITPTQFLY LWFKTACLSNNLSA*
1522	9573	A	2475	38	1523	RRVARPGNAEPAKERRDVSRGRARRDL AGAERKAGVSEGRDGRRRPNPSIPSAA AGMSHIQIPGLTELLQGYTVEVLRQOPP DLVEFAVEYFTRLREARAPASVLPAAATP RQSLGHPPPEPGPDRVADAKGDSEED EDLEVPVPSRFNRVSVCAETYNPDEEE EDTDPRVIHPKTDEQRCRLQEAACKDILLF KNLDQEQLSQVLDAMFERIVKADEHVI* PKGDDGRQPFYCHRTGGTYDILVTLDN QTRSVGQYDNR\GSFWRLALMYNTPRIA ATIVATS\EGSLWGLDRVTFRRIVKNN KKRKMFEFIESVPLLKSLEVSERMKIVD VIGEKIIRDGER*ITQGEKADSFYIESGE VSILIRSRTKSNKDGGNQEVEIARCHKGQ YFGELALVTNKPRASAYAVGDVKCLV MDVQAFERLLGPCMDIMKRNISHYEEQL VKMFGSSVDLGNLRAVGVPHTSLLSVT PKPSGQPQNTYRKQT

1523	9574	A	2476	1	912	
1524	9575	A	2477	3	806	EEFAAVSERIHEQVRDRQLENEYVCRVE GEFPTTEVTCKEPILVVS YKVGVCVRVDP RGKPCETVFQRLSYNGQSSVVRCLRPLTG RTHQIRVHLQFLGHPILNDPIYNSVAWG\
						PSRGRGGYIPKTNE\ELLFVPG*AEHQAK QSLDVLDLCEGDLSPGT/LTDSTAPSEL GKDDL\EELATA\AQKMGGK*AEAAPQE LDTIALAS\EKAVETDVMNQETDPTLCK MPAGATGSLAPRPCDVPTCPNAIKGQAL STFHPMPAWAQDDWQKD
1525	9576	A	2478	184	793	DFLLVLTGLYIYRKS KIHKVLE*IEFINV TSYKVNIQKDIALRTSQKH*KTN*KYKA KYLEIN*TNQDFYNENYKTLRKVKDN LGKWTIIPYSSTGKLDIVKMSIILRLFYKT NAITGIVPK/HSFVKINPEIPKLI/YGNMGN REGKTILKNKKVGRLSLPDFQKYKAT*I KIVWY*CKKRQMNQEAETS AKRKPWS L
1526	9577	A	2479	69	403	SALRRGAGAKAGRPLAPATALGGQTQP EKGPAAP*NGWTGLGAGPPAWRARPRPS PPEFSQFSLSYNMS*AKVGG*EHGSTAPG EGG/P*RKGGGPPPPNPQRQGSPTSP
1527	9578	A	248	56	247	QEONPQISILTLNRNG/LNATLKRYRLN QIK/SFCKKDQTMCLQETYLTCKDTHR PKVKG*KNI
1528	9579	A	2480	502	834	RRLPTGILAGRVSAAVKPHTRTQNSLLQ QRITPRPWRGGSHL*SQHFGKPROADHL SPGV/PRVSPG*RGETPSLQRIQTLAQVLC CAPVVPATREVEVGGSPEPGRSRLQ
1529	9580	A	2482	1	220	VNMRDRFGQMIENLRRRQCELAGVETC KSLES\RIESLEFLDEM*/LLEQLM/RHYCL CWATKGGNELGLKEITY
1530	9581	A	2483	98	394	
1531	9582	A	2484	1	381	
1532	9583	A	2485	1	645	
1533	9584	A	2486	10	1228	AAPAEPGRALPSSVAFSLWLAPSPAARR PRFHVPGGAQLPGTVHARWPARQRIESSI VTSCCSTSSCDADDEGVRGT CEDASLCKR FAVSIG\YWHDPYIQDL\VRLSKQRKAP EINRGYFARVHGCSVQLIK\AFLR\KTEC HCSNCSNLGGQGMGSPPFWRKDEDLS SQVNIFEVDFFMIVTRKLHSIKWLAFPLS SPIELHSEDTLQMASDCIC\DGHILDSKR YAVIGADLRDLSEEEKLKKCNMNTQLA PTP*IAECVLVYMTPE\QSANLLKWAAN SFERAMFIYYQQVNMGDLFGQMIENLR GRPVC/DLAGVET\CKSLESQKERLLS\NG WENKHRPVRT*LEFVPPGLPSKLG*SRIE SLE\LDENWELLEQLMR\HYCLACWATQ RRK*SLGLKEITY
1534	9585	A	2487	3	247	
1535	9586	A	2488	1	922	MQLKPMENPEVSARCTATRRARGRGR GSRVADRFGFAFFFAFAQMLNKVLSR LG VAGQWRFVDVLGLEESLGSVPAPA CALLLLFPLTAQHENF\RKQIEELKGQE VSPKVYFMKQTIGNSLGPLGNSTQGPNI KDQLGFEDGSVLKQFLSETKKNVPLKD RAKCFEKNEAIQAAP*MPVGTGKAQCR VDDRVNFHFYSG*PTVDGPPSMNLDGP NAFSPWTHGPQLQEDTLK\ DAS\KVCRR NSPEREQRRSPASSARGFSCGSLNALW GGICWIFPSFPFKHGKYITPPCQSKMLQY L
1536	9587	A	2489	18	255	NWISFLPWHYSHFEVYERYDSVL*IPFSL LQ*PIENVYPKI*KKKSTSSNKIALVLSGT YKNSLEPRSGASSVLWFTPNL

1537	9588	A	249	1	372	RALAVSMLGAWPGPWALDWGPYSMTA RHGTFSL*APYPDPAGPPAPRQQGK APSGCGGRSICSGRLPSVWPLMPAWQR PS*/GGGLHSAPNARKAQAYPGCLPFYLP LPGLLSGWSAGFLC
1538	9589	A	2490	2	568	ERGRKMAVESRVTOEEIKKEPEKPIDRE KTCPLVLRVFTTNNGRVHHEMDEFSGWN VPSTELQIFPL/WMDATLKELTSLVKRVA YPEARKKGTHFNFAIVFTDVKRPGYR*F SFLQS*GGLASTMSGRKGTDDSHPELQ SQKFQIGDYLDIANYPNPGTHPPS\G RMRPILNFYLLFVEFIFPSVM
1539	9590	A	2491	3	506	FFFFLKTSTLSFITTHCLQIQREGPGAEG AAVAGGAPRGAEPAATSTETGGSAGD/ AAPSP/RLPSK*QEGPGFWGDPNARQ WPGGRGRREAWRGLRAGSGESHQVGP WPASRSTGGSGQVGGAGERLGEDSGL GQVKATRWGLSPPPAALEEAVANTGPSP PC
1540	9591	A	2492	3	639	APEFPGRHLLLTQLCSLASLIQTRMVHLT PEEKSAVTALWGKVNVDVGGKALGR LLVVLVPWDPKRSFEVLWGNLSQLPECC *WGKPLKVKGSMKEKVLGCPLSDGLA HLGQPSKGTFAHTEVSLHCDKLHRGSL KNFRLLGNVGLCLLAHHF\GKRISTPP VQAA*SRKLVGLVLAKCPWPHKYHLKL AFLAVQFLFKGFLWSLKTNY
1541	9592	C	2493	217	396	MSEETAKEVMRAYLQQLRQETGLRLCE KVFDPPQNDKPSKWWTCFVKRQFMNKS LXPGQ*
1542	9593	A	2494	79	778	NPGAAKMPAYHSSLMDPDTKLIGNM/A HLLPIRSQFKGPAPKRDTRIPDIVDEAIFL PSGPNVFFKNYEIKNEADRTL\IYITLYIS ECL\KKLQ\CQFPKAQGGGKEMFYAGE STNFSHFLGEPGFPL*PPFYAQTWPTTQ EDEVMRALFTTQLRQETGLRLCGESFS DP\QNG*TPAKW\WTCFVKRQFMNKS LXPGTVEGSPGQPTVFPEALGQHFSKML LHNLFAFIS
1543	9594	A	2495	1	471	
1544	9595	A	2496	1	1524	
1545	9596	A	2497	2	719	RPQRAGPVRRAGVMALLDLAEGMAVF GFVFLVLWLMHFMALYTRLHLNKKAT DKQPYSKLPGVSLKPLKGVDPNLINNL ETFFELDYKPLFFSVAPMKRIEKTQM** P*CSTY*YEVLLCVQDHDPAIDVCKKL LGKYPNVDAFLFIGGKKVGINPKINNL PGYEVAKYDLIWICDSGIRGTMEMPMSL EQSYDPNVRDPIYRNNGDADGQHLVLH DFYQQGSGPKCSLINA
1546	9597	A	2498	200	370	
1547	9598	A	2499	295	1546	CVLLDLAEGNVFVFGFVFLVLWLM HFMALYTRLHLNKRATDRQPYSKLPGV SLKPLKGVDPNLINNL\ETFFELDYK/ KFNLHTMLFD*YEVLLCVQDHDPAIDV CKLLGKIYPMVDA\RLFIGGKKVGINP KINNLMPGYEVAKYDPIWICDSGIRIFP DTLTDMVNQMTKEVGLVHGLPYVADR QGFAATLEQVYFGTSHPRYISANVTGF KCVTGMSCLMRK\DVLDQAGDFIAFAIQ YIAKDYFMAKAIADRGWRFAMSTQVA MQNSGSYSISQFKSRMIRWTKLRINMLP ATIICEPISRMPLLPSLINWDGQAHVFR WDIMVFFYG/CHCLAWFIFYIPTPGVS QGGTLCSKLGMLQSPWFIRESMITYIFL SALWDPTISWRTGRYRLRCGGTAEEILD V

1548	9599	B	25	922	2057	XTQTDSFWFMISEKQRNFNAESTIGSHIH GPRIVAGLHAPTLMEEDDALQETVRAS IRKEQRNSRHDGGDGIRKAHAAIPRESRS MKRSPRKEVKKKRWNRPKMSLAQKKD RVAQKKASFLRAQERAAES*
1549	9600	A	250	13	475	NGSSLRSPRLR*SRTIPQSS*VAGITGAHH HARLIFFFFFFFFETESCRVSQAGVQWRDL GSLQALLPGFTPFSCLTQSSWDYRHPPP RPANFLYF**RRGFTVLARMVLIS*FRDP PASASQSAGIIGVSHRARPRGRLLAPSYI CRNRGLEG
1550	9601	A	2500	3	331	GAILAHCNLRPL/GFKQFSCSLPRHS*TS Q*PLTSRLPMVRHG*VKKSEGILCSLPPC TT*VPTSSAPMPWPSRQWERSRTMTVIS SSQLMALGPSCPQRDGSPTSSP
1551	9602	A	2501	15	310	DRVSL/LSPRLECSGAILAHCNLRPL/GFK QFSCSLPSSWDYRRAPPHLANFLYF** RRFFRH/GCPGWSLLSSGN/PATLAF*KC* NYGHEPPHPARKIHI
1552	9603	A	2502	3	467	PAPQSLLSARHVSALPTPAS/R/CSGLPP MTPKTMPPRA/VGSPLCVPARRRSSEPRK NSAM/RALLVDIKLEPLAVTPDAA/SQPLI DLPLIDFCDTPEAHVAVGESRPLIDLMT NTPDMNKNVAKPSPVVGQLIDLSSPLIQL SPEADKENVDSPLK
1553	9604	A	2503	2	273	FASIPANSSRPLSNISKSGRMGHAMLRPA LPAGPVGASSWQAKR\SESSQLNKTRISIR RRHSCLNSKTKVMPTPTNQFKIPKFSIGD SPKA
1554	9605	A	2504	1	472	VGRVTVHSTPVRSSGPGPQSLLSARRV SALPTPASRRCSGLPPMTPKTMPPRAVGS PLCVPARRRSSEPRKNSAMRTEPTRESN RKTDSTLVDVSPDRGSPPSRVQALNFSP EESDSTFSKSTPLIDFCDTPEAHVAVGSE SKPLIDLMTNTPDMN
1555	9606	A	2505	759	1664	TAGCGLGCASGPQAGHPATAGPQTLLPS AGGRAWSSCPPRALHRWPAGWEGCG YRRWS/RAASYSPWKNKVLLIKPFSIRYK AQ\SNSYDKPTYQSPSRRSLAA*IPTHP* SLLSSRGCCERRCAPTMRQPGAADTEPMC YHSWPHHSLFLPSSCLWGAGVEDKEL VPLWRVFLPGRRSWFPSSQKSRCLSHSC LGGCQVSRGKFEQQNLSSVPDSPGKNK HHGKISGPTCLSGGPGESVPIVHRLSESS HWQMSLLQTRAAAPALSAAGFLKSPPLS SQPGPALCPASRSFQCQSAQGO
1556	9607	A	2506	1	377	ASRRCSGLPPMTPKRCPRGSPLCVPAR RRSSEPRKNSAMRTEPTRESNRKTD SRL VDVSPDRGSPPSRVQALNFSP EESDSTF SKSTATEVAREEAKPGGDAAPSEVGGLL EPRSSGPAWEMM

1557	9608	A	2507	3	2112	ILLLADEKFDLSSLSSSSANEDDEVFFG PFGHKERCIAASLELNNPVPEQPPLPTSES PFAWSPLAGEKFVEVYKEAHLALHIES SSRNQAAQAAKPEDPRSQGVVERFIQESK LKINLFEKEKEMKKSPSTSLKRETYYLSDS PLLGPP/VGESCTAHAASQAATQRKPGT KLLLPRAASVRGRSIPGAAEKRTARMPK GRRKRK*QVLF*G*GCCGG*GEG*GCGE AGSSRIA/PKKEIPASPSRTKIPAEKESHR DVLDPKPAPGAVNVPAAGSHLGQGKRA IPVPNKVNNEIFADSVFSHFAPVGLKKTLL LKAPGSTSNLARKSSSGPVWSGASSACT SPAVGKGLCCTPVCPARPARPLHSCCCK MTPSRPWLMMWQCREGLECP*GSGGTWV VRHSCDRRAGRGSQSPRPHFGSSEVLG* TWRPGERTGDSPTSSTPKLSRAQRPOSC TSVGSSRH*CCVC/RVTVHSTPVRSSGP APQSLLSAWRVSALPTASRRCSGLPPM TPKTMPRAVGSPLCVPARRRSSEPRKNS AMRTEPTRESNRKTD SRLVDVSPDRGSP PSRVPQAL/NFSPEESDSTFSKSTATEVAR EEAKPGGDAAPSEALLVDIKLEPLAVTP DAASQPLIDLPLIDFCDTPEAHVAVGSES RPLIDLMTNTPDMNKNVAKSPVVGQLI DLSSPLIQLSPEADKENVDSPLLK
1558	9609	A	2508	68	2331	LLTALSMEEGGGRDEPSASRAGDVNMD DPKKEDILILADENISTFDLSSLSSANED DEVFF*PFGHKERCIAASLELNNPVPEQP PLPTSESPFAWSPLAGEKFVEVYKEAHL LALHIESSRNQAAQAAKPEDPRSQGV RFIQESKF/KINLFEKEKEMKKSPSTSLKR ETYYLSDSPLLGPPVGEPRLLASSPALPS SGAQARLTRAPGPPHSAHALPRESCTAH AASQAATQRKPGTKLLLPRAASVRGRGI PGAAEKPKKEIPASPSRTKIPAEKESHRD VLPDKPAPGAVNVPAAGSHLGQGKRAIP VP/NKLGLKKTLLKAPGSYSNLQRKSSS GA/VWSGASSACTPQPVAKAKSSEFASIP AN*LPGLCPNISKSGRMGPAMLRPALP AGPVGAASSWQAKRVDVSELAAEQLTAP PASAPTQPTPEGGGQWLNSSCAWSES SQLNKTRSIKRRDSCLNSKTKVMPTPTN QFKIPKFSIGDS/PSDSTPKLSRAQRPOSC TSVGRVTVHSTPVRSSGPAPQSLLSARR VSALPTASRRCSGLPPMTPKTMPRAVG SPL/CVPARRRSSEPRKNSAMRTEPTRES SRKTD SRLVDVSPDRGSPSRVPQALNF SPEESDSTFSKSTATEVAREEAKPGGDA APSEALLVDIKLEPLAVTSDAASQPLIDL PLIDFCDTPEAHVAVGSESRLIDLMTNT PDMNKNVAKSPVVGQLIDLSSPLIQLS PEADKENVDSPLLK
1559	9610	A	2509	1	353	DVQLEGAKIGSTEITFTPEKIKGGIHTAY TKTAGSVCLLMQVSMPSVLFAASPSQLH LKGGT/FKVAQDMATAAVRCIKKEIRDL YVNIQPVQEPKDQAFNGNGNIIIAETSTG CLF
1560	9611	A	251	986	1401	LEQGCNLFHLKHS*LGEVFFVCFRRSFT LVAQAGVKWGDLSL/HKLPSLSLPSS WDYRHLPLRLA/NFFVFLVKMGFTVLA RMVSI*PRDPPTSASQSAGIGVSPRAGP VAGILMFCRWNISNPKGAVIEKKKKK

1561	9612	A	2510	29	1262	TKVSELLCGSQRLLFFLPLWRRLCRCGLG PRVSPMAGPRVEVDGSIMEGGGQILRVS TALSCLLGLPLRVQKIRAGRSTPGLSIMT *RPQHLSGLEMIRDLCDGQLEGAEIGSTE ITFTPEKIKGGIHTADTKTAGSVCLLMQV SMPCVLFAASPELHLKGGTNAEMAPQI DYTMVVFKEKFGFIFNCIDIKTRGYYP KGGGEVIVRMSPVKQLNPINLTERGCVT KIYGRAFVAGVLPFKVAKDMAAAAVR CIRKEIRDLYVNIQPVQEPKDQAFNGN GIIIAETSTGCLFAGSSLGKPGFNSDKVV IEAAEWLLANLRHGGTVDEYPARPSLI VFHGH*PNGVSRIKTGVPVTLHTQT/API HF AEQIAKG*ILL*RNPEDEEDAIAKDTYI IECQGIGMTNPNL
1562	9613	A	2512	900	1189	SQHFGRRADHLSSGVQDQPGQRGKTP SLLKIQKLAGRGSSLL*SQLPRRLRQREN RLNPGGGGCELSRSDCTPAWATEGNS VSKKNK*KKKKK
1563	9614	A	2513	1710	2221	SPLLDVYFKTRLLSRGRREPACTLRNTI GTLLSHCPLGIQGGPHPGPSGKTCGPFKPR GPGHSCPPDPKKQVPTVLPPLPAPLRWA QAGLPGYAGISGSPGRPLGAQAG*GSGV IGESNYFVHCMHPRGPGSPHL*PGG*GLQ PKPPRPRLPSSSGSTTGLGDRKPCSYSQ
1564	9615	A	2514	205	295	GCNGNKDSCGPIAPSSGDILLTVKRSLP R*NFSP\CA\PCSSSSKRAMCSRVCSPWGL *CGPIAPSSGDILLTVKRSLPR
1565	9616	A	2515	1	927	
1566	9617	A	2516	932	1688	KGFKNPTFPCEIPAGQTHKPHHHNHKSS PPVQKLKLQKMKKNEVYETFSYPESYS PTLPVSRRENNSPSNLPRPSFCMEEQR AEL\EDPI\LSARTPSPVHPSDFSEHNQC PYASVDG\ATYGSSSG\CLGNPRADSIH NTYSTDHASAAPPSVTRSPVENDGYIEE GSITKHPSTWSVEAVVFLKQTDPLALC PLVDLFRSHEIDGKALLLTHGVTVLPEAT WGVKLGTGL*SLCYLH*PDLKQGKCL
1567	9618	A	2517	3	179	
1568	9619	C	2518	140	490	MAWFHDMNPQSIALIPPA TEISADSQLP CIKDGSEGVKDVELVLPEXSMFEDASVS EGRGTQIEENPLEENILAGEXASQTGDSG NEXANRGDGS DVSSQTPQTSSDWLEXX XLX*
1569	9620	A	2519	194	405	KKILWKKIFWRGKQHLKLVTVTTAAN RGDGS DVSSQTPQTSSDWLEQVHLV*TA HIWGS KWYRYSVC
1570	9621	A	252	303	551	QEGIKSCKSDENSG LAPGQHGETPSLLK VSKLAGYGGAC*SQLRRRLRQENCLN RDLGGGGCSEPRSCHCTPAWTEQDSV

1571	9622	A	2520	1	2046	MRQNSGGNVHLPA AHLVLCGLVPNRPW TGKNKNKRHHLCIPQPPTLAKIAKAAK GSAGNFRYPLILGSFPANWVFMNFFQSK ATLDFNLICSLNVKDVAEVFQKWLKIEG KKCHCLSEKTKQNMGNNTTKFRKALIN GDENLACQIYENNPQLKESLDPNTSYGE PYQHNTPLHYAARHGMNKILGTFLGRD GNPNKRNHVHNETSMHLLCMGPQIMISEG ALHPRLARPTEDDFRRADCLQMILKWK GAKLDQGEYERAAIDAVDNKKNTPHY AAASGMKACVELLVKHGGDLFAENENK DTPCDCAEKQHHKDLALNLESQMVFSR DPEAEEIEA EYAALDKREPYEGLRPQDL RRLKDM LIVETADMLQAPLFTAEALLRA HDWDREK LLEAWMSNPENCCQRSGVQ MPTPPPSGYNAWDTLPSRTPRTTRSSVT SPDEISLSPGDLDTSLCDICMC SISVFEDP VDMPCGHDFCKGCWESFLNLKIQEGEA HNIFCPAYDCFLVPVDIIESVVSKEMDK RYLQFDIKAFVENNPAIKWCPTPGCDRA VRLTKQGSNTSGSDTSLFLLRAPAVDC GKGHLFCWECLGEAHEPCDCQ TWKNW LQKITEMKPEELVGVSEAYEDDRQ/CVC *VMN*TAKPCANCKSPIQKNEGCHMQ CAKCKYDFCWICLEEWEKT
1572	9623	A	2522	2	119	ESTVSCCEKPTGAMP*MHTACGRPCPSI WRLTKLSMRLR
1573	9624	A	2523	159	627	LGRMQDPQGGQMRWAYS LTFKDVQC LGLSHYFAGAASGGCAQARCGPGR* GPPAPVPSPPLALPPMGT RKLHPGMWT ALH/VRIP/VPGKEGCVQLIGEISCVLLQK ASWSEASTLCPAKGAIPNGAAFHQRCGR PEAHLGHRLSLAPPREPVE T
1574	9625	A	2524	3	307	
1575	9626	A	2525	1053	2813	RTWEKAPEQADLTGGALDRSELERSHL MLPLERGWRKQKEGAAAPQPKVRLRQE VVSTAGPRRGQRIAVPV RKLFAREKRPY GLGMVGRLTNRTYRK RIDSFVKRQIEDM DDHRPFFTYWLT FVHSLVTILAVCIYGIA PVGFSQHETVDSVLRNRGVYENVKYVQ QENFWIGPSSEDLIHLGA*ISPCMRQDPQ GLSFIRSAREKHSACCVRNDRSGCVQ TSEEECSSTLAVVWKWPIHPSAPELAGH KRQFGSVCHQDPRVCDEPSED PHEWPE DITKWPICTKNSAGNHTNHPHMDCVITG RPCCIGTKGRYVCVPASAAGLWAQSIAL GCEITSREYCDFMRGYFHEEATLCSQVH CMDDVCGLLPFLNPEVPDQFYRLWLSLF LHAGQVTLILHCLV SICFQMTVLRDLEK LAGWHRIAIIYLLSGVTGNLA\SAIFLPYR AEVGPAG\SQFGILACLFRGSSSRAGQIL GAALACLQACWLWVLFHLWGLLP WDLTTFAHIFGGSSVALFLSFAFLPYISFG KVRPVPETLPDHHLSGGLPRASWLAWW SSSTSILSAVSRVSSSPASPFTDKLL
1576	9627	A	2526	1	936	
1577	9628	A	2527	1	1023	
1578	9629	A	2528	157	512	LG*LQPPPPGFKRFSCLSLSSSWDYMRH HAWLIFVFLVEMGFTLISASRVAGITGM RHHAWLIFVF/CSRDGVSTCLGQAGSQT PDLKVICPLGPPKSAGITGVSHCSWPVIY VLSTLLHAVRNVLFKRTFPLKSSSFLSYD KEIFPILIGLKFYLVTLTSFVKGHILLK
1579	9630	C	2529	11	133	MFCSLQPTDLRKEXMNLQTLRLRSSNKH QRFPGLPRLCD*

1580	9631	A	253	3	401	STFGFQGTGWETRWGPT*PGVSAWSLVP SPVLETPDLERGKRAHLGVATAGGPAGP YRLSPHTLSSRKEGKGEAASKGTEAELM TIGIENSTCQSCLSFSFHYFWSPRGAGP KAMWLVGDRKGATKNDKRGY
1581	9632	A	2530	367	676	KVVTLIILILQRRKWGA/PGSDPKSPCCSD SKGQASFTAP*CSYLYTADGRLGLAWG* GLNRSAMTSNPDQTHLVAQTSKGPERK HKVSGFLVKVIPATAYDNG
1582	9633	C	2531	156	683	MKLRQRWRHPAHFSGTGKMIGEGTQVS VGTGVTVDGVCGLSTSSHYANRNADT FRCLCRKRCQRLLKSQRRGVKKSCISVP HRQLSQALQAMRDSSEPWALSISLRFRE DEALASKHYRRNAPRAALRQFLSDFHR DCLNVFKTKYHTLMYMGRTIMRCEPCA CGGEGKKNVLF*
1583	9634	A	2532	427	458	KNSQYTPLTLIQMMGF*FFVF/ERQSHSV VEAGVQSCSHGSLQPLPGSSNPPTSASR VAGTTGAHHHDLIFLFL*RRGFALLHRL VSNSWRSRDSA WPSAFPKWLGLWDVEA TTPRPGLFSHLVAG
1584	9635	A	2533	57	463	ARTPLQGAGGLVLSRLLSLPLGLSPLPT VSCARWPLCPRPWSSLPGFWDSWHCNH RTGHRTPGGGLDTQSA*VNKLIWGKGN HL*PQATAQLWPQLGGWQGWTRPS/RW WPLSSPHC*PGYRSLKDSFANTFLLF
1585	9636	A	2534	3	469	RKTTTATMTSLCRKVNGGHAG*ETLRRRL LVVYPWTQRFFDSFGNLSSASAIMGNPK VKAHGKKVLTSLGDAIKHLDDLKGTF QLSELHCDKLHVDPENFKLLGNVLETVL AIHFGKEITPEVQASW/QEDGDWSGQSP VLQIPLSSLAMMQSCQG
1586	9637	A	2535	41	676	APSPRRPWGHFTEEDQGLLSTSLWCKV NVEKCWKEKTPGKGSLLVYPWTQRFF D/SFGNLSSAFAHHGQTPKVAHGK/K VLTFLGRCQQSTLDDLKGTFQAQLSELHC DKLHVDPENFKLLGNVLTVLAIHFGK EFTP/ERLQASWQKMGDA*SGQCPVLQV PLSSLPMMQSFRRIRLLFLQAITNNKSIS AKRSHMIFSSFFIYFLNI
1587	9638	A	2536	107	331	
1588	9639	A	2537	386	1074	NNPEWRTLIYVDKENGEPTGRVVAKD LKLGS/SGPSIKALDGRSQVSTPRFGKTF D/APHPALPKAT*KGFGELSTGATEKSVK DPGDPLKQKNGPAFSGPKKMDLKKDCL KQKSISVSWPSGLMPNPRNKTFFPLQIL LDF*GVFD/LCPEEHPDLRHLPLSGVPL MIPLTREREL*KSWFQLGPPFHLWKDGP LPPWGIPICLQFSFQGISVRTWGVDLPPV CCDIDI
1589	9640	A	2538	1	359	
1590	9641	A	2539	1	483	FQLEVTPQNITLNPFGGPGVFSWRDQAV LRQDGVVVTINKKRNLVVSVDGDTFE VVLHRVWKGSVHQDFLGFYVLDSDHRM SARTHGLLGQFFHPIGFEVSDIHPGSDPT KPDATMVGVLQKDYSKDPWHGAEVSCW FIHNNAGLIDGAYTDYIVPDF
1591	9642	A	254	1833	2126	EKRKKRGFFKTKPLLKCPGPWGSESFW GPPKGKSQV*G/HI*MGPNLGERWKKGP KRPKKPKTKGPPPGVHPPKRNRPFLG/ WPGGPTLKKGKNNLFC
1592	9643	A	2540	3	310	EVANLSSQALRMWLDYGFVTPLTSMISI RGMADQDGLKPTIDKPSDSPLEMLGP RRTFVLSALQSPSTHSSNTQRLPDRVTG VDT*VVT*PYVLCWNLC
1593	9644	A	2541	1	1482	

1594	9645	A	2542	37	2885	SMDGAMGPRGLLLCMYLVSLILQAMP ALGSATGRKSSEKRQAVDTAVDGVFIR SLKVNCKVTSRFAHYVVTQVNTANE AREVAFDLEIPKTAISDFAVTADGNAFI GDIKDKVTAWKQYRKAAIS*EKA\GLVR ASGRTEQFTIHLTVNPQSKVTFQLTYE EVLKRNMQYEIVIKVKPKQLVHHFEID VDIFEPQGISKLDAQASFLPKELAAQTIK KSFSGKKTSSNGSHSRRFQGHVLFRTVS QQQ
1595	9646	A	2543	159	1222	NNSGVMPPEMPEDMEQEEVNP**GGFW VTGCHWGFLGRAVHKEFQNNL/WHA VGCGFRRARPKE*TG*ICWDSNAVHHII HDFQPHVIVHCAAERRPDVVENQPRCL PLQLNVDASGEF*AKGKAAACLGSI SPF YI*AQVVFV*WEPNPPYREEDIPAPLNL YGQTKLDGRKGCPWRNHLGAAVLRPI LYGEVEKLEKKCELLMFE*KCQFSQQS PAKQWIHWQARGSPPHMSKDVAPLCAR QLAEKRMLDP\SIKGTFWHWSGNEQMT KYEKGMCQLPDA\FNLPSSHL/RDPTDSP VLGAQRPRNAQLDCSKLETGIGQRTPF RIGIKESLWPFLIDKRWRQT VVFH
1596	9647	A	2544	211	463	
1597	9648	A	2545	188	366	SCQSACQKNGKIILRLQLLGP*DRLEDTL LNTHGLLQSQILCQFCFLCTCQKVLRI K
1598	9649	A	2546	1257	1441	
1599	9650	B	2547	74	733	MAWKSGGASHSELIHNLNRKNGIITDKV FEVMLATDRSHYAKCNPYMDSPQSIGR VQLVVGDRMGYAEAPYDAIHVGAA APVVPQALIDQLKPGGRLILPVGAGGN PNVGASIPGSRMASIQNEALWMGGDIRA L*
1600	9651	A	2548	45	972	TVQPHVSGSGGDGNSGSGDASGAV TVWEVVSLLGKLLGTVALKVVL YLLR VCLAMAWKSGGASTSELIHNLNRKNGI TDK\VFVMLATDRSHY/SQKCNPYMDS PQIK*GFQ\ATISCSTHCNAYALRNFLFWI QL\HIEGSLKLFVVGSGKWESLLACFAR MVGCTGK\VIG\DAH*RS**DDSVKLMF REGTIPTLLSFRGGVQLVCGGMGRMG\Y A\EEAPYDAIHVGAAAPVVPQ\ALIDQLK PGGRLILPVGAGGNQMLEQYDKLQDG SIKMKPLMGVIYVPLTDKEKQWSGGMI VKATSA
1601	9652	A	2549	2	478	
1602	9653	A	255	70	380	YSNNPKDRKGETGINEKTNNKMVDLSS YTSVITLNF*ML*/D/KIN*KFVKSP*KKPT LCCLLETYFKYGIGGLKVKRWRKI*HAH TIGKKTIVAILITKHTSELS
1603	9654	A	2550	392	1245	CTFTKVFLLLRIWYRNMLLKNSVTPLPS CHPSAQCLGTLMRALSQVFRDAW/WWV ASVDVVENEEASASIIVKMTDSFTEQAD QVTAEVGKLLGEEKVDA\ILCVAGGWA GGNAKSKSLFKN\CDLMWEAEHYWTS HLP SHL/ALTKHLKEGGLATLAGAKAA LDGTPGMIGYGMAKGAVHQLCQSLAGK NSGMPP\GAAAIAALPVTLDTMPNRKS\ MPEVADFSSWTPL*FLVETFDWITGKNR PSS\GSLIQVVTTEG\RTELTPAIFLGLISV PMRWPAQKSH
1604	9655	C	2551	60	266	MSWLSCLSNITVWNISPVLLSFFGGNSLI SHLXKIPEEEFPLTPLLSSSPSGFXPHVPR VLRQSATV*
1605	9656	A	2552	1	513	

1606	9657	A	2553	345	2343	LLGHEEQTRKGRKAKAAGMVLSQLL TFRD\EAIEFSQEEWKCLDPAQRTLYRDV MLENYRNVLVSLGIFSKCEIKELPPKESN/ KEYSRQ*CWKDMKSHRHTKIFCFRETQ KNVHDSQCLWKHD*RHYKRVRVITYKG KSH/CVEETMPG*KG*CHKSQPC*KSSLG LNPAVT/CLPRTCQPISKPEGKIYKYDHM EKSVNSSSLVSPQRISSTVKTHISHTYEC NFVDSLFTQKEKANIGTEHYKCSERGKA FHQGLHFTIHQIIHTKETQFKCDICGKIFN KKSNLASHQRIHTGEKPYKCNECGKV FH NMSHLAQHRIHTGEKPYKCNECGKV F NQISHLAQHRIHTGEKPYKCNECGKV F HQISHLAQHRTIHTGEKPYECNKCGKV F SRNSYL VQHIIHTGEKPYRCNVCGKV F HHISHLAQHRIHTGEKPYKCNECGKV F SHKSSLVNHWRHTGEKPYKCNECGKV F SHKSSLVNHWRHTGEKPYKCNECGKV F SRNSYLAQHIIHAGEKPYKCDECDKAF SRNSHLVQHRIHTGEKPYKCDECGKV FSQNSYLAYHWRIHTGEKAYRCNECGK VFGLSFLAHPKIHTGEKPFKCNECGK AFSMRSSLTNHQLRHTGEKHFKCNECG KLFRDNSYLVRHQRFHAGKKS
1607	9658	A	2554	3	517	STRTONVLGEKGRRIRELTAVVQKRFGF PAESLRYKLLGGLAVRRACYGVLR FIM ESGAK/GCEVVVSGKLRGQRAKSMKFV DGLMIHSGDPVNYVDTAVRHVLLRQG VLGIKVKIMLPWDPTGKIGPKPLPDHV SIVEPKDEILPTTPISEQKGGNAEPPAMPQ PVPTA
1608	9659	A	2555	3	495	
1609	9660	A	2556	24	861	INPPPPRLSFQSAARWPVQISKRRKF VANGILSKLNLNEFLATRELAEDGYSG/ VEVRVTPTRNRKSFIFSHQHRMVLGEK GRRIRIELPAVVQKSFVGFPRGA AVELY A*KRWPT*/RGLCAICPGQSLCVYKPS*G GLAVRRAL/CYGVLRGSFIGEVGPKGCE VCGCLGKLRGQRA*NP*SFVDGLMHNS GDPVNYVDT*VRHVLLRQGVVLGIK V KIMLAWDPATGKIGPKPLPDHVSIVEP/ RRDEILPTTPISEQKGGKPEPPAMPQVP TA
1610	9661	A	2557	116	718	IFLQAGCLKL VIRSKAGDISHVDTHCQTV HPKAVSISTMTENTPFLTSPALSPFN NL PFQCIK*YLILTLIFLIA YEVE SLCL*SVF LIYKIFL*PLSNFCCL*V/LLYILNLLFYY MYFPTPLFMKSNFIKVL*KVKGFTF*KCS QIYLFHGYWVLC LGWECLSYTFITIFFQ YFLLVIFNFHV*FILIFFIHD MK
1611	9662	A	2558	88	811	GSGGNHVS CCDTMEGGGGSGDKTTGVL AGFFGAGGAGYSHADLAGVPLTRMNPL CPYLNVDPRYL VQGYKMKFIFTLPELIK TRGQDLKLAFFTIGGCCMTGA AFGAMN GLARLGLKETQNM A WSKPRNVQILNNG *LGK GALWA\NTLGLWALLYSAFGVII EKTRGAEDDLNTVAAGTPAGLLYTCTG GLRGIAARGGLTGLTSLSLCTIYNTWG AHGKGS LASNSSLWKVFAQPP
1612	9663	A	2559	1	210	VIIRLPICKLFRCKPG*TWAPPGL*SGR PRSSSSPF*N*MHFLFERESSFHRCKWK AGITCVKSWYP
1613	9664	A	256	225	353	RWGFTQLRLRLRQENHLNRGVGGCSEP RLCTPAWATE*DSVL

1614	9665	A	2560	128	687	THVLWAFPGARVHLQTGSWRAGVAAA ALALGGQASLSYARGKES*GHSPPTHT HKAASGGREKAVSPSVAVVSHGPSPLLS EYTSSQVKGHSGPGDPVVTHL/WAPFP DQLPPSPCPPLSRKEPEPSPLSHPPQGVTP GQAQIGQLRTSGLWGHKRGGWARAEG APVSLLLRGPFDGPATVSEAQR
1615	9666	A	2561	246	410	
1616	9667	A	2562	1	414	AWHEETHKVDLGLPEKKKNKKVVKEPE TRYSVLNNDYFADVSPLRATSPSKSVA HGQAPEMPLVKKKKKKKKVSAALGKE VKRSQSKLRLRNTSP*VMTLRPPQKRK*S PKRR*SSQSSRSQL*KGRKRRRGKRG
1617	9668	A	2563	198	531	RNNPLLSLLALCLVHSSHLCWALPDEG GGQGKERALNSRKIATFFLSSQGTQFGQ WDTAGFENEDQKLKFLRLMGGFKNLSP SFSRPASTIARPVHMLGKKAADSLQONL
1618	9669	A	2564	190	510	
1619	9670	A	2565	1	1977	MEVDFKIRKVGQWTITLQEHVSVLLFIE ETHPENKPTSTAVEESHISRDVVMVNFQ CQLDWSKGYLEAYLTKINSICSHRFLD GSVTCHDETGSRRDARDTVGTGVRVND ESVEQLGLRRTMWLGICRGAAMAAVST VTAFAGRPRPGRSRNPRGWAGDSKWTS GSRRSWLSRGGGEISPTGMITKTHFVYL GLPEKKKKKRVVKEPETRYSVLNNDY FADVSPLRATSPS*ADVAHGQAPEMPLVK KKKKKKKGVSTLCEEHVEPETTLPARRT EKSPSLRKQVFGHLEFLRGKRKNKKSPL AMSHASGVKTSQDPRQGEETR VGKK\K SKKHKKKKGGPGPHSL/PVQDPWFCEA REARDVGDTCVGVKKDEEQAAALGQKRK RKSPREHNGKVKKKKKIHQEGDALPGH SKPSRSMESPRKGSKKKPVKVEAPEYIP ISDDPKASAKKKMKSKKKVEQPVIEPA LKRKKKKKRKESGVAGDPWKEVVPSE MDFAVGELRETDLEVVLEKKGNMDE AHIDQVRRKALQEEIDRESGKTEASETR KWTGTQFGQWDTAGFENEDQKLKFLRL MGGFKNLSPSFSRPASTIARPNMALGKK AADSLQONLQRDYDRAMSWKYSRGAG LGFSTAPNKIFYIDRNASKSVKLED
1620	9671	A	2566	1781	2148	VRRFAAAVATLPPGAAPSG/PAPGT/PGP QTRIPGFPWPPLCPLMSGSLGP*TRLLLV PPAPQGPAGSPGPIAGRGLAAPPQPLS PSRGPCAGSSWELRLEGLSDWGTCVPVC PCHYIHPPKN
1621	9672	A	2567	1	345	
1622	9673	A	2568	1	582	SGRALHASWAAGGVGAYSGRLRSDALE GESFALSFSASDAEFDAVVGYLEDIIM DDEFQLLQRNFMDKYYLEFEDTEENKLI YTPUFNEYISLVEKYIEEQLLQRUPEFNM AAF/TTTLQH/HIRDEVAWVTIFGNAGST FHKIFLGF*RKCFLDYRAEKESRGLDLS SGLVVVTSLCKSSSLPASQNNLRH
1623	9674	A	2569	2	705	GSVGAATVRPOPNALRCRLRSRAGRSPV LVFGVGKQPPCPSKKAKTTKTKRPQR ATSNVVFAMFDQSQIQGVQRGPFNMIDQ VNRDGFHSDK/EKVLHDMLASLGKNPH* WHYLDAMMNEGPKGPFKHQCSLTMF WLRKLNGVTRSPEDCHPETAFCFAFD*KK ATGTHFRKDYLRRSC*PTHGGIRFPD/ER EVDELYRGGTLLDQKKGNFQITFEHTA SWKHGSQRPKMT
1624	9675	A	257	238	512	HMYVPNLRTSKYMKRTLIELKGEIDSNTI LVGDFNTTLSTMGRTR*DISKETEDLHN TVDPMDLTD/SAELSTQQQNTLSSQAH GIFSRTE

1625	9676	A	2570	1006	1022	TRNSFLFFIYIYLFRLMGSCSVAQGWKCS GTILGVHCSLCLRLPGSSNSPTSASHVAG D/SHGMCRRHARLIFAFLVEMGVFPCWP GLGLELLTLRVIHPTLGLPKCWGL*AGG SAKIGRRAQIG
1626	9677	A	2571	668	863	TFCFFSDLKYSLASCENHLVCFLFVCFAP LV*T*NYFCL*TVNLIFSRRVTELCPFIFI VLIIT
1627	9678	A	2573	258	579	FKQICLFLLLFFEMESCSVTRLECSGTIS AHCNLHLP/GSSDSPASASPVGTGTCH HAQLIFLYFYMTGFRHVAQVGVVLLG/ *AIHLPWLPKVLGLQAPAPDL
1628	9679	A	2574	157	371	
1629	9680	A	2575	1	1431	MHKAGLLGLCARAWNSVRMASSGMTR RDPLANKVALVTASTDGIGFAIARRLAQ DGAHVVVSSRRKQONVDQAVATLQGEGL SVTGTVCHVGKAEDRERLVATAVKLHG GIDILVSNAAVNPFFGSIMDVTEEVWDK TLDINVKAPALMTKAVVPEMEKRGGGS VVIVSSIAAFSPSPGFSPYNVSKTALLGLN NTLAIELAPRNIRVNC/LAPGLIKTSFSRM VGEPEDCAGIVSFLCSEDASYITGETVVN LSVMFTGGGVCRAASWKEGGTGTPTP RESRQREPGETSSTDQENKVVWNLPA NPQRPAEAGPVRRTNKQKGIASAKD SINIRTKGDIHTKTPSIGHQHQRPKVDKT TKMERNQSKKAETSRNQNVSSLPKEYKS SPAREQNWENKFDDLTDVSFRRSVITN YTQLKEHVLTHCKEAKNLDKMLNEWLT RMKNLEKSLNDLMELITTVQELHEGYTS FNS
1630	9681	A	2576	201	398	
1631	9682	A	2577	195	434	
1632	9683	A	2578	150	284	
1633	9684	A	2579	1	625	MHKARLRGHCARAGKSVRLASSGMTRR DPLTNKVALVTASTDWIGFAVAQRLAQ DGAHVVVSSRRKQONVDQAVATLQGEGL LSMTGTVCHVGKMKDWERLVATGFSPY NVSKTALLGLAQTLPIELAPRNIRVNC APGLIKTSFSRMLWMDKEEESMKETL RIKKV*ASPEDCAGIVSFLCSEDASLHSL GKTVVVDG/GTPSRL
1634	9685	A	258	167	408	DRRITRSGVRDQPGQHGETPSLLKIEKL AGHG/GQAPVCGGRSYLRRLRQENRLNP GGRGCSEPLRHCTPA*VTVRDSVS
1635	9686	A	2580	84	1413	ARKSVRMASRMTRRDPLTNKVALETA STDGIGFAIARRLAQDRAHVVISRKQQ NVDQAVATLQGEGLSVTGTVCHVGKA EDRGAAWWPAAVKLHGGIDILVSNAAV NPFFGSIMDVTEEVWDKTLDRNVKGPK P*MTKAVVPEMEKRGGGSVVIVSSIAAF SPSPGFSPYNVSKTALLGLTKLAIKLAP RNIRVNC/LAPGLIKTSFSRMLWMDKEK EESMKETLRVRLGEPEDCAGIVSFLCSE DASYITGETVVNLSVMFTGGGVCRAAS WKEGGTGTPTPRESRQREPGENQARS SPRMLRPEFPPEASTSWMGPEPVGNR ERPCKPARKVGASPRALRLGSATRMLS RAALRAGVGARAPRGGGRGAHATATV WSGLASAAALTARALLKRSACAAAPQ RCGWRRLLCSSLGIRGSGWPCPPWSSI
1636	9687	A	2581	1	560	MVYRQNQLPSSCAPEMGREDGLRALHP AQPPPPRAQQSPPPLSA/PEPPPPRAQQ SPPPLLTPHRRHPQSFPAPSALSQRQ PGLYSAVTFSGSLGPRTSTCTPSPASSPS AHGLGHIHTDAGVCSLEAQEEAKAPGG RGPSCSAHGALGPTCTSGVAGDSGPVVG SQERALDPRRQGLQH

1637	9688	A	2582	775	1408	TIPVAYVWADPPLPPKGHSCPHPPGSD/D GTRTTGTA/PPCLGFQGDPPVHPAPAPP DW**FPNMGQPGPPPPFTWRAQLQLK SSVNMGRHWRNVPSGPHLEQISLSEL GHSHKPLFLRQNPNTVPWDVMLPFPLL NLLYGKMWNVVSLDLWGCHRNEEWRP TNIILLAPWRHGRLLQLKGAGARGRQLPQ LLLPAALLLVGYEMSF
1638	9689	A	2583	3	560	GVPPKSASKFLCTRNGKGRWAQSPPPST A/PPRAQQSPPPPLSAQK/KPPPPRAQQS PPPPLLTPHRRHPQSFPAPSAPSALSQRQ GLYSAVTFSGSLSGPRTSTCTPSPASSPSA HGLGHIHTDAGVCSLEAQEEAKAPGGR GPSCSAHGALGPTCTSGVAGDSGPVVG QERALDPRRQGLQH
1639	9690	A	2584	189	608	AFLT FNKLHRTDTCRGNKPHPPPPGSK VRKRTWGFAPPGPSWASLPHGLPPTA GRQGRGR/EGGGPRGGPGKSAQSSGT RAWRKPMGGCLTEDGPYGGPKGLWP*T TNG*K/PPGARWPPLPLGCPLEPRHPVL GP
1640	9691	A	2585	2	847	LKMAAEEPHQKQOEPLGSDSEGVNCLA YDEAIMAQDRIQOEIAVQNPLVSERL LSVLYKEYAEDDNIYQQIKDLHKKYSY IRKTRA/DGNCFYSGFRILPLGRHCWDDS KELQRFKAVS/WPRARVDLGCSQ/WGFT *ISQF*GIFHNKFHGT*LSRWRKQTSVAD LLASFNDQSTD\YLVVYLRLLATSGYLQ RESKFFEHFIEGGRTVKEFCQOEVEPMW KESDHIH\MALAQGLNGAIQGEDMDRG EGGTTNPHIFEGSEP KGYLLYRPGHYDI LYK
1641	9692	A	2586	468	1191	DVSRVGCLPPSRAMGWTLALLRRGSAV SALASGLVEEPM LGPPFHPTPRFKAVSA KSKEDLVSQGFTEFTIEDFHNTFMDLIEQ VEKQTSVADLLASFNDQSTDYLVGYLR LLTSGLL*GPRASSSTSSKGGRDCKPEF CQOELEPM*KESDHHSHHCAGPGPSAC PSRVGVHGTAAEGGNHQAHLSLRASEP KVYLLYRPGHYDILYKIGLGSSPLLPCCP PLPGARHVTEVFLWL
1642	9693	A	2587	1	326	HSVNRKRLNRNARRKAAAPRIE/CVRGLG FRVAVGLGRDGRDDGSAMSLFAGSSHI RHAWDHAKSVRQNLAEMLAVDPNRA VPLRKRKVL TWQGLGPCLLYSSPAILT
1643	9694	A	2588	879	1528	AAGAVVSAMPKAKGKTR*QKFGYSTL RKR\MSRNARRKAA/RAGLECSHIRHAW DHAKSVRQNLA*MGLA\VDPNRA\VPSR KRKVKAME\VDIEEEA*KNL YRKPYVLN DLEAEP SLPEKKGNTL\SRDLHLMYRY MV\ENHGE\DYKAIARD\EKNY\YQDTPK QISELSNVYKRFYPAEWQDFLDSLQK RKMEVKVPG LHHSCPSAEASGPSEAG
1644	9695	A	2589	1	310	
1645	9696	A	259	660	1200	LTVGKKNRQKQHQPKSPHGKPHLKGO QPSKVQIEDKFLGR*GKELKNPFTTQKG QSGFVYSKLIHNTSYRQGHSPGWRLRW MN*QK*ASEGG**QTSLS*RSTL*PNILER IPELKDWF SKIR/RQK*KRIKRKEENLQ*V WGYI*RPILQITGIPERRVEISMHWVRAC SFSSVKFVIP
1646	9697	A	2590	1	716	SALQRLEKKPKPRPPERSPRPRWVPEPQL EVGGACSA LAQSPSEKLDPA CLKPLS*S* IRRRRPTPAMLFRLEHSSPEEEASPHQR ASGEGHHLKSKRPNPCAYTPPSLKAVQR IAESHLQSY SAILNENQGFGRGREDELGE FWELGYPREDEEEEEDEEEEEEDSDQ AEVLKVIRQSAGQKTTCGQGLEGPWERP PPLDESERDGGSEDQVEDPALSEPGEFPQ

						RPSPSEPGT
1647	9698	A	2591	39	370	RGWSLVQTPNPRFKNVPGPPTPQVIAEC EESQCGGLGTLGGL*LSPGPAG*TDSRGPP MMPSEAQGGGAASKGPLGPPQAAGIHQ GTPLRMGEALEGQAGQTAGPRVQDGL
1648	9699	A	2592	229	358	
1649	9700	A	2593	257	386	
1650	9701	A	2594	217	398	KAWWNLLRKSEPKSCGS*GGLSTSRERL VECSSLGLGYCG**LCHLQEPHYGSLH RMSS
1651	9702	A	2595	1	3386	
1652	9703	A	2596	442	2093	CGFLQMGTVINHNIPGPEGYWHFHFNF KALLARAAVGAARGIHIHRCGLTKRPDA RRRRVAGAQQREPAILPGDRAAGARAT RTRGPGPAPKMPAIAVLAaaaaaWCFL QVESRHLDALAGGAGPNHGNFLDNDQ\ WLSTVSQYDRDKY\WNRFRDEVEDDYF RNWNPNKPFQDALDPSKDPCLKVKCSP HKVCVTQDYQTAL\CVSRKHLLPRQKE WGTWAQKHWGLDL*ILVKICKPCPVA QSAMVCGSRWATPNSIPCKLEFHACS TGQK/SFATLCDGAPCPCSSQSLEPPKHKG RKGVPTDKELRNLASRLKDWFGALHE DANRVIKPTSSNTAQGRFDTSLPICKDSL GWMFNKLDMNYDLLLLDPSEINAIYLDK YEPICKPLFNSCDSFKDGKPFNNNEWCLL PSQNPGLP/CAQNEMNRIQKLSKGKSL LGAFIPRCNEEGYYKATQCHGSTGCW CVDKYGNELAGSRKQGAVSCEEEQETS GDFGSGGSVVLDDLEYERELGPKDKEG KLRVHTRAVTEDDEDEDDKEDVGYI W
1653	9704	A	2597	1	844	LHQQAAVAWLPTSFLPSQEHCCSTEWR APQPAASGVHGICFA/RPFASSTVSTEVS GSFCYLPAP\WVYGFL*TERPLAWWCL GKYWLQELLGCHPVPLAML*DCLALLK SSLVPMGSPTHCKAIVTEEPLHLEPAAA AAHTSSPSSSCRCCKGCLGWVWPGGSAP GPLGPLSFDPTVSHQSGPSPAAPGPTS SS*RPSAPSHGMQGLADSQGHLCRHSRK GLRSFLLSHTHHSTCPPHLLQTGMPSPL ISIDADSSPPRIHRLRGQGHFSLAKGGQ R
1654	9705	A	26	238	446	GFVVSLDSR*GQWESSIIHAVTN*ASS SSSSSSSSFSR\VYPRFIEYLHKDIQSTG QKSPDAWVAGG
1655	9706	A	260	1	680	EQCRSPARARLQPPDPASTEAEERTYP GSIGAPAGEGKVPGLVIYLLWPWQNQDE ALSCLPSEAYSLSRQHGLPLAVNTMSAG GGRAFAWQVFPMPCTCRVYGTVAHQD GHLLVLGGCGRAGLPLDTAETLDMASH TWVALAPLPTARAGAAAVVLGKQVLVV GGVDEVQSPVAAVEAFLMDEGRWERR ATLPQAAMGVATVERDGMVYVSGGNG P*HGPPPGT
1656	9707	A	2602	144	520	IGKEEIKLLLFPDNLMEYTVNF*MYKPLE LIS*FSKVTEYQVNTK/SNCIYT*QLQIE NEIAKTI*FMIAKSIKYLEISLTKCNKW RDILCICIGRLSIHKVLVLPKLMCGGEKIF NPNPTGFW

1657	9708	A	2603	105	440	RSTPDPVCLGRSSGCRTADFREP*MLLS DRSSGSFVSEYPAV*SVSLPLLGECLPV RLLRDGHWS*HDSOSS*VFKMADNFPA GFHRLGRSGDGRAEHRRCLASQRCC
1658	9709	A	2604	1	1047	
1659	9710	A	2605	1	690	
1660	9711	A	2606	210	424	
1661	9712	A	2607	651	835	PRWSRFPDLVICPPRPPKVLGLQA*AIVC ASISITKMWLRNAGLTSSMNWPRRSARV LSVS
1662	9713	A	2608	198	755	
1663	9714	A	2609	1	1305	MMRAHAPPTAVPACTAPRAPPPRDHRA GIAREALGRTGRSGFRDCLGTREVALQA REKAQAAAQWQGEAGCSAHWVRHTRGA APEGRPRVPRAAGVLTGCTVFRRTWIQR DAQIQARQERWAKGESGPWGELRGLAT QPAVRASGRRGRRLERQDILEVFRCLAA SWNGGFGAVKPPEVADARSGLSGGDSF CLVSVSLTKTAKKGLELKQNLIEELRKC VDITYKYLFISSVANMRNSKLKDIRNAW KHSRMFFGKNKVMVALGRSP\SDEYK DNLHQVSKRLARGEVGLLFTNRTKEEVN EWFTKYTEM DYARAGNKEGFHC*AWD PGPLEQ\FPHSMEPQLRQLGLPTALKRG VVVTLSD\YEVCKEGDVADPRARASRS* KLFQVMRWLNFKVITIPNYMWDSQSGRF QQIGKTD\LPESA\SEFPESDSEDDDD
1664	9715	A	261	1	403	RTRGQLNRGVYGP RRSLSPSTLAGAPL AGRLDETS GEEQTLTLCGGKMSGPTQPP AEGTEGTAPCGGAPVPPFNMTSNRRLOQ TKAQVEEEVDIIPVNGDNVLRDHLKRE LDDRS\DALQARA*PFESSAAS
1665	9716	A	2610	319	632	GEPNIGMSLPWGGPSGSTGMPAPAMPL PAMTPQC/C*GQGPV/GPCAS/CASA/CFR CGL*AGRFC/G/PCPGHC*CFYFNSVFPN VECMGLREPAVLPAFHLGEEAGRISGQ GRSQNLPA
1666	9717	A	2611	156	621	LHVPMELQSHSKDEVSPTYLGMSLPGVA PLGSTGDASPCHAPRPWTPQCSKGQGP CCAP/WCP/CCP/CPPCPWSHGCL*LLCDP CPPPALPAAEQQPLCKLASAVSGVVSR LGNFATCPWPLLMRPASSPRWKAGRTA GSLRPIHSTLGNTEFEK
1667	9718	A	2612	1	585	
1668	9719	A	2613	1	1047	
1669	9720	A	2614	1	1674	MRSQGEVRRYLKRQSCRFGLSREKDM VTPSASSVCLIDEQIPAAAGESYDIIDPRSK HKFKIHTYGSPTFCDHCGSLLYGLIHQG MKCDTCDMNVHKQCVINVPSLCGMDH TEKRGRIYLKAEVADEKLHVTGKACSSR SSIVGRHLDEGYTDIKAGPQLDAFLCISS QPPFGKNAIHTSSSSSIITLLKHGPRRFYSF ASCSCMSSTVSVTNPKILGKGFIDSVWV TCHPGPMDCDWRADMGWGPVRLCIWF S

1670	9721	A	2615	3	2089	RPQLPGGGKRWLGGMADVFPNDSTA SQDVANRFARKGALRQKNVHEVKDHKF IARFFKQPTFCSHCTDFIWGFGKQGFQCC VCCFVVHK\RCHEFVTFSCPGCG*GDPTL DDPRRQATRFKIHTYGSPTF\CDH\CVGS LLYGLIHQGMKCDTCDMNVHKQCVLN VPSLCGMVHTEKRGRIYLKAEVADEKL HVTVRDAKNLIPMDPNGLSDPYVKLLI PDPKNESKQKTKTIRSTLNPQWNESTF KLKPSDKDRRLSVEIWDWDRTTRNDFM GSLFSGVSELMKMPASGWYKLLNQEEG EYYNVPIPEGDEEGNMELRQKFEKAKLG PAGNKVISPSEDRKQPSNNLDRVKLTDF NFLMVLGKGSFGKVMLADRGTEELYA IKILKKDVVIQDDDVECTMVEKRVALL DKPPFLTQLHSCFQTVDRLYFVMEYVNG GD\LMYHIQQVGKFKEPQAVFYAAEISIG LFFLHKRGIIYRDLKLDTVML\DEG\HIK IADFGDVQGN*WDGSHGPGTFCGTPD YIAPEIIAYQPYGKSVDWWAYGVLLYE MLAGQPPFDGEDEDELFSIMEHNVSY KSLSKEA VSICKGLMTKHPAKRMGCGPE GERDVREHAFFRRIDWEKLENREIQPPFK PKVCGKGAENFDKFFTRGQPVLTTPDQL VIANIDQSDFEFGFSYVNPQFVHPILQSAV
1671	9722	A	2616	1	1136	MTQISNIKQPFAMQHRFFISLLHWTQIV YPALFLGLCERGRNGRCDQVPEGSVLSL LVWVVPGLAFPEVAPGTCGTSYVPDAG LHGPEVESKLGLDPGSMGTGTQPTRPAQ PAAAEPPALTGPGRVHQEQAVLACGFLG IYHLGAASALCRHGKLVKDVKAFA SAGSLVASVLLTAPEKIEECNQFTYKFAE EIRRSFGAVTPGYDFMARLRSGMESILP PSAHELAQNRLHVSITNAKTRENHLVST FSSREDLIKVLLASSFVPIYAGLKLVEYK GQKWVDGGLTNALPILPVGRTVTISPF GRDISPQDKGQLDLYVNIQDIMLSL ANLVRLNQALFPPSKRKMESLYQCGFD DTVKFLLENWFE
1672	9723	A	2617	118	1018	VTARPRASRLKGLVQHGSVPGLHCATA RMKHINLSFAACGFLGIYHLGAASALCR HGKLVKDVKAFAAGASAGSLVASVLLT AP/EKKLEECNQFTYKFS\EEIRRSFGA VTPGYDFMA\RLRSGMESVLP\nPSAHELA QNRLHVSITNAKTRENHLVSHFFSSRED PQLRSLSPASFVPPIYART*SLVEYK\GQ KWVDGGLTNALPHPCPVGRTVTISPFSG RLDISPQDKGQLRSVCLISAKQDIMLSL ANLVRLNQALFPPSKRKMESLYQCGFD DTVKFLLENWFGIKCIKVL
1673	9724	A	2618	60	388	GLDSFSATETRRTHNTPEHSQSQEPSNG EPQKEEPAAESRDPTPGQTEEDQDTAEI PVRDMEGDLQELASVKHRG*ILDLS\SV KVKIIPKEEHCKMPEAGEEQPV
1674	9725	A	2619	1	4123	
1675	9726	A	262	72	276	AIQFSVYICVPGICISPDREKRDRGKDG GRHRTRWRQGE*KGEVGRERRRGRER\ DRQRDRDRIYSPD
1676	9727	A	2620	71	547	KQIPSLPISRPSVLAVMVTMTLKVGAPP MLFIQRSVVNSPSCSSESTTVYFWPPSV SPFMTKLDQSLPTRTPTSAGVMLRKVFP PTSREKPTCFSSNA*KELP*GWQESGCSR QCPLSSRETCRASCINESANARGEAVCV LGARVVFLFTSETGNS
1677	9728	A	2621	241	452	ENVMLCIIRAKEKNHMITLSYTVKAFGK LKTFFMIYKNKPQKTLMSIRREGNTFNPI KGRFEKNS/AGNIILNGIGLNAF/PIKSEKK VEYLLFFQFSIILEI*INAIK*EK*IKGRFE KNSEVTLY

1678	9729	A	2622	1014	1432	SARLSLPKCWBYRREPPCPASFLYLKNI LYIIRAKEKNRMITLSYTVKAFGKIENFF MIYNNKPQKMLYMMRTEGNTSNPIKGR FEEPTGNIILNRHKIGCFSIKSEKKVEYLL LLF*FSIILEL*VNAIK*EKLIK
1679	9730	A	2623	55	316	NFWGGGAPKAPPPKKGFFPKIPRGVLNR PPQKEKKLFFPPPVKLGPPKDFLKRAPP* TPKKFFFFPKP/YKFLGGGGPKSPPPKR VFSQNPGRGFKSPPPKRKKIIFPPPRKIGPP QGFFKKGPPPLFIFFCLFPAFMETTCPSK SLSKKFTKTK
1680	9731	A	2625	1	963	PTRPNFHSPHPTSPAAGVSAALRCSGRR RSLEVATSLPHSPGPRPAADVMSSEE VSWISWFCGLRGNEFFCEVDÆDYHPGT NFNLTDLNKQVP/HYRTSSKP*SLDPEPD EELÆEDNPNQSDLÆEQAAEMLLWDLIH ARYIPLPTRRHRPRCLGKVPKGDGFGYC PRVYCENPANCPIGLSDIPGEAHGESS YCPQ/CAMDV*HTPSQSRQPSTRMGA*L RATGFPSHGFMVAIPELPGPKRPAQPSF VA/RGFLRGFKIHPMAYPAGSFQGRPAT FKKPQFKTDSLIPSPTCPAVFCLFLSFLPT LSGTLYGF
1681	9732	B	2626	44	403	MKALILVGGYGTRLRPLTLSTPKPLVDF CNKPILLHQVEALAAAGVDHVLAVSYM SQVLEKEMKAEQRLGIRISMSHEEEPL GTAGPLALARDLLSETADPFFVLNSDVIC EFPFOAM*
1682	9733	A	2627	159	309	IGPSLALGSKVFLQKKQSLLFIRCWLQA LQDLWPQGWNATAEMGWA*QMG
1683	9734	A	2628	545	2302	AACAPSPRTESSTVSSLPLQECLLGAMK ALILVGGYGTRLRS/LTLSTPKPLVDFCN KPILLHQVEALAAAGVDHVLAVSYMSQ VLEKEMKAEQRLGIRISMSHEEEPLGT AGPLALARDLLSETADPFFVLNSDVICDF PFQAMVQFHRHHGQEGSILVTKVEEPSK YGVVVCEADTGRIHRFVEKPVFVSNKI NAGMYILSPAVLQRIQLQPTSIEKEVFPI MAKEGQLYAMELQGFWM DIGQPKDFLT GMCLFLQSLRQKQPERLCSGPGIVGNVL VDPSARIGQNC SIGPNVSLGPGVVVEDG VCIRRCTVLRDARIRSHSWQESCIGSGG SWKLLTIDQDLMVAQFSTPSLPPTLKVG FLPSAGKEQSVLWVSLEEAEPIDHWGI RVLQPPPRARECAEVRMENVTVLGEDVI VNDEL YLNGASVLPKHSIGESVPEPRIIH DGGFAEEAVLVVHQVLVDGTGTTGEGM RTALHVPTALPTTKLWGPLLADLWAQG WDTAEMGGGSCCLGRCRGQVRQDLFQ LGQLIGTDIIRIWGVVGSVKSEVAEDVMP LEYSQPTTLLFLRLLTRPSRPF
1684	9735	A	2629	124	1315	RARGRARRWECAAGTGQAGCRHLRAR DTPSTSAGAMKALILVGGYGTRLRPLTL STPKPLVDFCNKPILLHQVEALAAAGVD HVILAVSYMSQVLEKEMKAEQRL*IRIS MSHEEEPLGTGVLPLARDLLSETADPF FVLNSDVICDFPFQAMVQFHRHHGQEGS ILVTKVEEPSKYGVVVCEADTGRIHRFV EKPQVFVSNKINAGMYILSPAVLRIQLQ PTSIEKEDLPIMGKEGQLYAMELQGFWM DIGQPKDFLTGMCLFLQSLRQKQPERLC SGPGIVGNVLVDPSARIGQNC SIGPNVSL GPGVVVEDGVCIRRCTVLRDARIRSHSW LESCIVGWRCRVGQWVRMENVTVLGE DVIVNDEL YLNGASVLPKHSIGESVPEP RIIM
1685	9736	A	263	166	396	PQIPPPPGIPRKRENLSREPGG/PNPWGG* A*FPLLEKFLGKKNLGPPPGGGPTFPFPF NPNNLLGGPKGGDQKAGKKP

1686	9737	B	2630	162	276	MGRANESNLVIVYHFLQKGVQCRL QLVQVVLQHLLX*
1687	9738	A	2631	2	292	
1688	9739	A	2632	3	2111	SSCGLGGQHGLGAARVRSLFKEARARA PCIVYIDEIDAAGKKRSTTMFGFSNTEEE QTLNQLLVEMDVFYAKIEELKLVNRRAE TGVSLSRCSTQK*KS*NCWILITVFYAAIE ELKLMYPYHGVLCSSRRKLSSCSNKEMT QSEKSQA*YRMTPLGMGTTDHVIVLAST NRADILDGALMRPGRDRHVFDLPTLQ RKGVALSPRLECSAAITHCGLNLQGSS* GARTTMGVRRRAG*FLTESRCVAKAGV QAAISAHCNHHLPGA/RKIFEQHLKSLK LTQSSTFYSQRLAELTPGFSGADIANICN EAALHAAREGHTSVHTLNFEYAVERV AGPHGFQLWESSGFLPEEWGQLLCQTLQ NTPGFSPTALRGREDWRCLCLTENLFSC NHLLLCGNRKAFYNSSKAGRTWEWQA S*KKIHDVLECSGPRADSSCTEWLTDV WKI*DRK*SLTRAKKSKILSKKEEQKVVA FHESGHALEGWMLH/TEAVMKVSITPR TNAALGFGQMLPKDQHLFTQ/ESSFERR FIALGGRAS\EHFSLNEVTS\GAQDDLK VTPIAYSMVKQVGMAGPISFPEAQEG LMGIGRRPFNQGLQMMMDHEARLLVA KAYRHTKVLQDNLDKLQALANALLEK EVINYEDIEALIGPPPHGPKKMIAPQRWI DAQEEKQDLGEEETEETQPPPLGGEEPT WPK
1689	9740	A	2633	2	2416	FQANMAVLLLLLRALRRGPGRPLW GPGPAWSPGFPPARPGRPYMASRPPGD LAEAGGRALQSLQLRLTPTFEGINGLLL KQHLVONPVRLWQLLGGTFYFNTSRLK QKNKEKDKSKGKAPEDEEERRRRERD DQMYRERLRTLLVIAVMSLLNALSTS GGISWNDVHEMLAKGEVQRVQVVPE SDVVEVYLHPGAVVFGPRALMYRMQ VANIDKFEEKLRAAEDELNIEAKDRIPVS YKRTGFFGNALYSVGMTAVGLAILWYV FRLAGMTGREGGSAFNQLKMARFTIVD GKMKGVSFKDVAGMHEAKLEVREFV DYLKSPERFLQLGAKVPKGALLGPPGC GKTLLAKAVATEAQVPFLAMAGPEFVE VIGGLGAARVRSLFKEARARAPCIVYIDE IDAVGKKRSTTMGFSNTEEEQTLNQLL VEMDGMGTTDHVIVLASTNRADILDGA LMRPGRDRHVFDLPTLQERREIFEQHL KSLKLTQSSTFY\SQRLAELTPRFSVADIA N\N\NEAALHAAREGHTSVHTLNFEYAV ERVLAGTAKKSKILSKKEEQKVVAFHES GVHPLVGWMLHTEAVMKVSITPRTNAA LGFAQMLPRDQHLFTKEQLFERMCMAL GGRASEALSFNEVTSQAQDDLKVTRIA YSMVKQFGMAPGIGPISFPEAQEGLMGI GRRPFSQGLQMMMDHEARLLVAKAYR HTEKVLQDNLDKLQALANALLEKEVIN Y*/EDIEALIGPPPHGPKKMIAPQRW/V DAQREKQYLGEEETEETQPPSLGGEEPT WPK
1690	9741	A	2636	350	1256	LCLFPLPARKMATNFLAHEKNLVDFK YDDAERRFYEQMNGPVAGC/ASRQENG A\TVILRDIARARENIHKS\LAGSSGPGASS GTSGDHGELVVRIASLEVENQSLRG\VV QELQQAISSEARLNVLEK\TWPG\HRAT GPQ\TQHVSPMRQ\VEPPSPRSPPTPAEG/ DARDDIALF\GSDNEEEDKGGGTSLRE E/RGFREFPGEKRPKPRLV\AQLSFLLG* NPWDR*KDMAQLEACVRSIQ/LGTGRS WGASKLGAPWATGIRK\LIQCVVEDDK

						VGTDLLEEEITKFEHVQSVDAIAFNKI
1691	9742	A	2637	1	304	GKTFDTFCPLGPALVTKDSVADPHLKI CCRVNGKVQSGNTNQMVFKTEDLIAW VSQDVILTGTTPPGVGVRKPPVFLKKGD EVQCEIEELGVIINKVV
1692	9743	A	2638	1	927	
1693	9744	A	2639	3	847	PSGSDFAAAVVPRLDAVTGASAPAA LDLPPREP*LSAGGPVAAAAARALAAQ LPVLPREVTFLAPVTWPDKVVCVGMN YVDHCKEQNVVPKEPIIFSKFASSIVGP YDEVVLPPQSQEVDWEVELAVVIWKRK ASTSR*SGKGGLPVQSAEAPAPASPSD LTHQHTVPAVPDTRKQSASLLPDTAFPF THLWLALATNMG*QLRDPL*VLVSPMI *PPVWPNPPLPP*ATDAMAHVAGFTVAH DVSARDWQMRRNGKQWLL*KTFTDFCP LGPA
1694	9745	A	264	3	413	SSYRWPSFPILKTCRGPMAPSLSFPGSFLS GLSVPLPLHPPCPT*LKAAYPNCQLWP FLASVAPDTAPPECPSCFLLQRAQA/PPF LLDLFPYDC*GLCCT*PHQPRGNPLTPRQ GLWLGLKTHCMGTAGPGIPR
1695	9746	A	2640	2	562	ITPRFHLCSDPHNLKICCRVNGEVVQSS NTNQMVFKTEDLIAWVSQ*VTRAVLSAP LHLPHMWRLT*ALHLWLWPLSQPLVSL GPFALLQFVTFYPGDVILTGTTPPGVGVF RKPPVFPQGRFSEKQREQGPPKPLAGLPS DLRSTGLCMCV*RKGLTLSWPALLQKG DEVQCEIEELGVIINKVV
1696	9747	A	2641	867	1476	LVPVLRRLPLPLTSRPASPNSAQEDRLPPV RRQEVNWEGLAGVIGKKGKPIKATDA MAHVGGFTVAHDVSARDWQMRRNGK QWLLGKTFDTFCPLGPALCDQVTGVAD PHNLKICCRVINGEMVPERQTPNQMVIS RQRT*IALGLPSLVTLPPGDVIPNLGPPH LHPGVGVFRKPPVFLAKKGDEVQCEIEEL GVIINKVV
1697	9748	A	265	646	1333	EPGMWQSPPSIGCPHRTGQASCA/SPPS TGLS*IPAFPGWRPAIWHLHPLLTSPCTC* L*SLGVFPVPPQPWSTPSQDLNDIFPV PPSYRWPSFPILKTCRGPMAPSLSFPGSFL SGLSVPLPLHPPCPT*LKAAYPNCQLW PSSASVAPDTAPPECPLLCFRGPGSPILL TSPICLLRTLQLSSPASGESHYPPQGRAV GWA EKPSAWSTRSLALGFPMNNEN
1698	9749	A	2651	28	352	VRVWVGNAGCRLCFRADGVASGVGCA WDGDRMCLPESFIRAPVLSVSTAGPQSS QGSSGRSATPGEGAQGINRTLPSALPSP PMAPPSYLVTSPAPHSDDGCWP
1699	9750	A	2652	1198	1889	LKLPIFRDLKVQCGWVELENRLTKMLLS TSVLSCFSSRPNMSEVSCNKRYDYLEWP EYFMAVAFLSAQRSKDPYSQVGACIVNS ENKIVGIGYNGKPNGVHNSLFP*RRTPK NKLDTKYPYVCHAEALNAVLNKKFRPDV KRPEVCMFALVPPGK*NGGLSLII/LQAGI KRKLIFHVLINYPG*LTGATAARLLF*YG PGVTFARKFIPKCSKIVIDFDSINSRPSRKL Q

1700	9751	A	2655	1099	1712	CALGEGNSGHRAFSKDRARLRPGWWSG RAKDELGKPKPLGPS*RRADRR*GQSAC DSSPPSGPGP/TGDGARGRC*AARPGPRA RRRRLGPSGEDRSCQMGTGEEHHGRLW GLSVGPAPKPESAPSSLTCPREETPGRGR PPAPQFQSLARSHGIRGAGDKPTEEKSL PQQRHRGGASSVGRGPLGFFPLEEAPLP YPWPPNLQ
1701	9752	A	2656	1	900	
1702	9753	A	2657	465	1269	TSSSCSCHPPPNACCRGTSSVLSQKAGQ APHLPGPTGKPLRSSGSLRAVRAPGPIGG GQAPWSDPPVLQAPPRPPQAPRGSWRG AGPRQGRDAAPRMLLPFQPRYRTLQPP RLMPKKNRIATYELLFKVEGVMVPKKVD VPIPKHPELADKNAPNLRVMKPMQVSQ GRGGYVKGQFAWRHFYWYLT*GSK COLHTEAARLGQP/DIPT*TRAL*PATG HLSMRARSLEVQRPTAAPSGPSWLSLLQ KGMWTGKNEDLHFRRCR
1703	9754	A	2658	1	433	
1704	9755	B	2659	140	480	MVFEFLYKMCVMAAYFGKISEENIKN NFVLIYELLDEILDFGYPQNSSETGALKTFI TQQGIKSQHQTKEEQSQITSQVTGQIGW RREGIKYRRNELFLDVLEKVNLLMSPQG S*
1705	9756	A	266	268	926	ASCTPFPTLPVRGRLGYNPDSPGTSNAH WAGDNEMSLVGLGPVTKPYPHGALPQG WGSWWVRGLSRTPAVTLSQLCSCVLE TCWGPGEAWFLSPQSVCDLESRSPA DPQDGLGVYGLASSWTNVQPTWNTSR IGSACQA/RSEFNKSHLFIFLEGET*GPQK GGGVPPKPHYKAPMQSPGPILWTQPRAP PTGAIYFFLQMGGPPWRFSLFGVGG
1706	9757	A	2660	100	1674	SAAMIGGLFIYNHKGVELISRVYRDDIGR NAVDAFRVNVIHARQQVRSPTNIARTS FFHVKRANIWLAAVTKQNVNAAMVFEF LYKMSDEMAAYFGKISEENIKNNFVVH YMELLDEILEFGYPQEFRD/SGALKTFITP AGHSRSSGFRQKEGSSQFTSQVTGQIGW RREGIKYRRNELFLDVLESVNLLMSPQG QVLSAHVSGP/VWVMKNYLSGMPECKF GMNDKIVIEKQKGTADETKQEPGSNQL LIDDCTF/HTQCVRLSKFDSERSISFIPPD GEFELMRYRTTKDILPFRVIPLVREVGR TKLEVKVVIKSNFKPSLALQKIEVRIQPP LNTSGVQVICMKGKAKYKAGENSFVW KIKRMAGMKESQIQRGFELLTNDKK KWGC/RPPFPMNFEVPPFAPSGLKVG/YL KVLNPKLNYSDDVIKWVR*IGR/SGIY ENSACKATRQLAQLPQPPFQQVQVPLL PQTHQVSPSLPALLPSPLHQARSLRSGP KQHYKVGVPPEPALGLPQGGEF
1707	9758	A	2661	1	356	
1708	9759	A	2662	303	774	DPKSCGRWRRGRNGELADLQAESHR ARAAGRLPGALARVQPEAAAAEVGAR CGRGAIAENSIDFVSRELCAHSIRKLQAH VLLIKAVHGYFDPRENYSDKESLSFMIDT MKSTLKERFQFVEVPGNHCVMSEPQH VASIISFLOCTHTLPAQL
1709	9760	A	2663	572	902	GALARA*PPQQRWVSCPR/GVP/GAL*RE FTMFLSLQAENSIDFISRELCAHSIRKLQA HVLLIK*VAQAGAQRSQLTGYGSLTWA CPPLTTVKSHGTAPPHLLHEPSFTSDLPP SMTLLPGGLPKKDLES
1710	9761	A	2664	1	398	PNPLSTQMGTSGGKGHQUELLEYSPPGGP PPGPRKQFHCSPPPNPASGKKGH/SPPL /SPHSFSKVKFNQAPPPPTPTPKQERKS* LKMLFNFSAPVDPTPAQMAPPGLFVPSP SPPLHRLPPQAWGQRHSQQ

1711	9762	A	2665	119	496	TGAVSFQMPEETQTQDQPMEEEEVETFA FQAEIAQLMSLIINTFYNSKEIFLRELISNS SD/GEPMGRGTKVILHLKEDQTEYLEERR IKEIVKKHSQFIGYPITLFVEKERDKEVSD DEAEKEDN
1712	9763	A	2666	1	235	
1713	9764	A	2667	1	2424	RKVREASGKSAARWAGPSLYKAGAGV ARQLLQRPVAVPLVLCGHLAKMPEET QTQDQPMEEEEVETFAFQAEIAQWISLI NTF*LETKRSFLRELISNSSDALDKIPVLN A*HDPHSIRPLGKELAHITLLPDQTKIRTL TIVDTWNLE*PKADLINNLGTIA/RSLGT KAFMEALQAGADISMIG\QFGVGFYPA\ YLVAEKVTVITKHNDDEQYAWESSAGG SFTVRTDTG*TYGSVGTKVILHLKEDQT EYLEERRIKEIVKKHSQFIGYPITLFVEKE R\DKVETDDAPQEKEDKEEEKKEEEKES EDKPEIEDVGSDEEEKKDGDKKKKKKKI KEYIDQEELNKT\PIWTRNPD\LTNE EYGEFYKSLTNDWEDHLAVK/HFFQFEG QLEFRALLFVPPTVLPFD\LFENKKKKKN NIKLYVRRVFAMDNC\ELIPEYLN\AIRG VG\SED\PLANISREMLQ\QKPKF*KFSRK NFGPKKCLELFT\ELAE\DKENY\KKFYEQ FSKNIKLGIH\EDSQNRKKLSELLRY\TS\ ASGDEMVS\KDFCPR\MKENQKHIYYIT GETKDQVANS\AFVERLRKHGLEVIY\IE PIDEYCV\QL\KEFEGKTLVSVTKEGLE LPEDEEEKK\KQEEKKTKFENLCKIMKDI K\EEKVEKVVVSNRLVTS\PC\IVTSTYG WTANMERIMKAQALRDNSTMGYMAAK KHLEINPDHSIIEPLGPKA\EADKNDKSV EGILVIWLKETAPPS\AFSL\ENPRTHAT R\IYRMIP\GLG\DEDDPTADDYQWLLV TEENPPLE\GDD\TSRMEEVD
1714	9765	A	2668	524	797	AVSPSEGEQERGEKRA\GCGSRL*SQHF VRPRWADHLRSGV*DQPGQHGETPVST KNTKISWAWW*ASVIPATREAEAGEWL EPRRRRLQ
1715	9766	C	2669	102	323	
1716	9767	A	267	599	1420	SHLPSLSLLPRIPPEVIVGSE\RGPVV\FPCP WGSCWGLSRTPAVTL\SQLCSCVLETC WGPGE\AWFLSPQSV\MC\LES\PRSPADP /RGWKFRVYGLASSGQMCNHLEYSRML VLARHSELISPTY\SF\EGETE\AQRG*GIPP KPHSR\NAEPGPYTGHTWPLHTGTFTF SSQMRG\PSGLLD\SGGWIKTEGDKEKAPG LMGLKDRDTGTCYGCVC\SKCPGQGLQA GGVLYLAQPPALIRLPNGPRPARARERR DWHHREETGFL\DEATLLKARP
1717	9768	A	2670	146	804	TETRFSDSVAQQAGPGTFGLLLLALPRL TFSPLLSFPTVGTCKGNPLWAPKPCPALA APSGCRMTWKEQGRKMGVNC/PRPVAA CMCV*TGKRPPSPMFLSPRFSSETRRAA RGSS\ELPWVAGAWSASSSDSPLRSTAP RRSVCTHCGLTQPTRHACQKGAGVCVR GPRSEAKGGWRGRALLLLAATPCPLSCP NLGLPAKVTP\EQGLVRRGGRPAGP
1718	9769	A	2671	1	787	LNSRVEPRVRSRTMETKPVITCLKTLLIY SFVFWITGAILLAVGVWGKLT\LGTYISLI AENSTNAPYV\LGTTIVV\GFLGCFAT CRGSPWMLKLYAMFLSLVFLAELVAGIS GVVLRHEIKDTFLRTYTDAMQTYNGND EVRSAVDHVQRSLE/SCCGVQD\YT\NW STSPYFLEHGIPPSCCMNE\TDCNPQDLH NLTVAATKV\NQKGCYDLVT*FSWETN MGVIAGSGRLGI\AFSQLIGHAGWACCL SRFHHGPIQY

1719	9770	A	2672	1	670	YKVLIFT/SPCS/VQQLCSALCSCFRPKDT ER/LRG/APEGFSRTDLHLA/VVPVLTALI SYHNYLDKTKQREM VYRLEQGLIHRCP/ RQCVVALSICSVEMPDIIIKALPVLVVKL THISATASMAVPLLEFLSTLARLPHLYRN FAAEQYASVFAISLPYTNPSKFNQYIVCL AHHVIAKPLHRLQPSPHLAMRWASGSAS SPRWRTSPSLCEAGALPPALALDGIACQ
1720	9771	A	2673	1	154	
1721	9772	A	2674	237	410	
1722	9773	A	2675	1	414	
1723	9774	A	2676	1	6371	MPDSCGLHIPAAHAAPSRDARIAGLSAR GRHRTTTPSKLPRRPSAQCRYRKCGSRF RRRPGARGVRLSPRRGGPERGGAAREGF SGASWSTMAKPTSKDSGLKEKFKILLGL GTPRPNRPSAEGKQTEFIITAEILRELSME CGLNNRIRMIGQICEVAKTKFEEHAVE ALWKAVADLLQPERPLEARHAVLALLK AIVQQGERLGVLRALFFKVIKDYPSENE DLHERLEVFKALTDNGRHITYLEEELAD FV
1724	9775	A	2677	1	5405	MAKPTSKDSGLKEKFKILLGLGTPRPNP RSAEGKQTEFIITAEILRELSMECGLNNRI RMIGQICEVAKTKFEEHAVEALWKAV ADLLQPERTLEARHAVLALLKAIVQQG ERLGVLRALFFKVIQGDYPSNEDLHEIR LEVFKALTDNGRHITYLEEELADFLQW MDVGLSSEFLLVLVNLVKFNKLVTLDE VQSQRNGFKMICLLACVRTASSVDIEVS LARLLDAVGLANNCLPAESLPLFIV
1725	9776	A	2678	1	5469	GASWSTMAKPTSKDSGLKEKFKILLGLG TPRPNRPSAEGKQTEFIITAEILRELSMEC GLNNRIRMIGQICEVAKTKFEEHAVEA LWKAVADLLQPERTLEARHAVLALLKA VQQGERLGVLRALFFKVIKDYPSENE HERLEVFKALTDNGRHITYLEEELADFLV LQWMDVGLSSEFLLVLVNLVKFNKSCYL DEYIARMVQMICLLCVRTASSVDIEVSL QVLDAVVCYNCLPAESLPLFIVTLCRTIN V
1726	9777	A	2679	35	239	SPSSQPPPVIPH*PVCKQPTSCRSPRKR V LNLVGGGEGAASY
1727	9778	A	268	1755	2524	VPWGNPGSES VGLPGGRGLVTAPAVFLP PKPAPGFGAQHVRSRK/PSRRGQLIRAA WLTGSPVRPGQEMLGAGRGGASGRAG* GPAPYRKLSSASARGAGHPESGNCSSSG SGSTWSSSWGSGSSWGSRGLSQEMV EEVL/HFIQGGAG*AGGTLQWALVSNLG FGVRQGDIVVVTLIGLHGSIEDGAGVQ GRSEAMEPRQAG/RGTEGWLGHSSETP HPPAGTSFCNL RPTVSREAAPAGRRGAE SQTSLPSTSA
1728	9779	A	2680	118	359	AVCKQPTSCRSPCCPSPGCQASPC*AFRR LEI/CRAGF*A*ALGPGKSQGNCPRSSPP PSP/CPLLKYGQNCG*KCPQRLH
1729	9780	A	2681	229	455	TMQGSNLKPLPSP*PRAATKIPNP/SPSP PQPAPQTTPHSILSTKAMTPVTIQALFSRI VRYLDCRRDSLTSQSF
1730	9781	A	2682	1	373	

1731	9782	A	2683	72	1031	GCPRLILLRGRSGLEPGTFRKMAAARPSL GRVLPADSSVLFCDMQUEFRHNIAFYFQ IVSVGSRMLKVARLLEVPMLEQYYPQ GLGPTVPEAGD*GPSAAWQKTCFSM/CC LPLQQELDSRPQLRSVLLCGIEAQACILD PRSYPLALTSLYPQNTTWDLDRGLQ VHVVDACSSRSQVDRVALARMRQSG AFLSTSEGLILKLVGDAVHPQFKENQKLI KEPAPDSGLLGLFQQNSLPPLNSNPALR EDHPPVHPGPQWEARFPPSLGFPRVGAIP PGSCRPLVGGGQWCCLPIGQLLPEMQM RLLETGWEMG
1732	9783	B	2684	1	792	MGVLPYSYFWDEEAEAEQEGICLSLKQRM PVGRAGHSGHFLADATSRALARREEV GKQEERG VKESSESTNTTSRMKTPKEDV RPGMTAFEPEALGNLVEGRTSIDSILKTV SNSFSLGACCLLSFHVLLDGTAGRGSDR DEQNAHSVVPQQARAHHPESHILM GDESACIAYIRTRSTWTLAASHAPPSRRD PCLAPPGWQMADRPLHRSGAPSVLPHSQ DTDTEMNQERYMNASISFPKPPHSTSQQ VLFIQPGEEIEI*
1733	9784	C	2685	10	126	
1734	9785	A	2686	2	370	HCIQQILEAVLHCHQ/MGVVHRDLKIPGE KKNQTLGRAVLLSFT*RRQLSLGLHQLH SLAPSAGTSWISLLILMVS VAGFAGT/PG YLSPEVLRKDPYGP/VDLWACGG*RFS GPLPGVILYILLV
1735	9786	A	2687	1	1593	
1736	9787	A	2688	3	1607	IPGSTISCSSVKPVLCLHSAARACKWSLG SGAEQQRLSPGPPVPSLTCLPSARMATIT CTRFTTEYQLFEELGKGAFSVVRRVCVKV LAGQEYAAKIINTKKLSARDHQKLEREA RRCRLKHPNIVRLHDSISEEGHHYLIFD LVTGGELVEDIVAREYYSEADASHCIQHI LEAVLHCHQMGMVVHRDLKPENLLASK LKGA AVKLADFGLAIEVEGEQQACVGF AGTPGYLSPEVLRKDPYGPVDLWACG VILYILLVGYPPFWDEDQHRLYQQIKAG AYDFPSPEWDTVTPEAKDLINKMLTNPS KRITAAEALKHPWISHRSTVASC MHRQE ARGPA*KKFNARRK\K GAILSTMLAT RNFSGGKSGGNKKSDGVKESSESANTTI EDEATKVRNQEIKVTEQLIEAISNGDFES YTKMCDPGMTAFEPEALGNLVEGLDFH RFYFENLWYRNSKPVHTTILNPHIHLMG DESACIAYIRITQYLDAGGIPRTAQSEET RVWHRRDGKWQIVHFHRSGAPSVLPH
1737	9788	C	2689	6	167	MXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXXIS KH*
1738	9789	A	269	3	389	GVSPCWPGWS*TPDLK*STRLGFPRCWD YRLLEVDPCTGHSLYL*KDPPVLPLPAEG CDYQGKEYALSSCCDKSYLLPDYRTKFL CCHPERGTWKLGTVGGCYAPIQSFGIAD EQAWLQHGSGAVYLC
1739	9790	A	2690	310	593	LQVISEYLFWRINFFLFLF*TVSLSVAQA RVQWRDPGSLQPLLPGFKRFLASASRV ARVTGAHHLHAQL/ILYF*VETGFHHVG QAGLELLTSGK
1740	9791	A	2691	58	481	LQVISEYLFWRINFFLFLF*TVSLSVAQA RVQWRDPGSLQPLPGSRDS*ASASRVA RVTGAHHLHAQLFCIFK*RQGFHPGWSG WSSNLPDLQANPAASALPKVPGITGTSP LHPPWSINFKNIKIWNQETSILVFFRL
1741	9792	A	2692	1	398	

1742	9793	A	2693	3	267	AMVGGGGVGGGLENANPLIYQRSGER PVTAGEEDEQVPDSIDAREIFDLIRS*AW PLTPQPAYWYPGPSSCQGCYRCFLESLT MRN
1743	9794	A	2694	1	942	
1744	9795	A	2695	3	707	AMVGGGGVGGGLENANPLIYQRSGER PVTAGEEDEQVPDSIDAREIFDIRRCWAR AGSGGLRWGEQ*YRAAGGAASQQGVP GRGF*VGKGAESLFLHFPQLIRFLNDPVE HSLTLEELNVVEQVRVQVSDPESTVAVA FTPTIPHCSMATLIGLSIKVKLLRSLPQRF KMDVHITPGTHASEHAGKCGLVVRVLA RAPPKQSEASPLHRSLWARLEMGNVCVSE IARDSSVWVIA
1745	9796	A	2696	2	604	ARSHRISGGGSAMVGGGGVGGGLENAN NPLIYQRFGE\RPVTAGEEDEQVPDSIDA REVFDLIRSHQMTPEHP\LTLEELNVVE QVR\VQVSDPESTVAVGF\PKPTHSGTCR HGPPLIGLS\IKVKLLRSLPSAFSRWDVA HLLPGDPLPQEHAVEQATLQIKEAGWAT ALGRTPHLLVV\NQCLSSPAGTWAFV PLSLA
1746	9797	A	2697	79	690	KVSKAIAGCLRNYGVCLAHLRTWAIPEP PKMNPVVEPLSWMLGTWSDPPGAGT YPTLQPFQYL\EEVHIS\HVQAMLNFSF NSFHPDTRKSMHREC\GFHASKPDTNK VGLCQAPQNTGLGWNWKEGEVKRARS LCIRIPLPFARISFRQ\KPHVEQIT/RGKFR LNSEGKL*ADGSPMGNPRHSPMTQHH HDTYQEGEHRKP
1747	9798	A	2698	1	405	
1748	9799	A	2699	1	1437	
1749	9800	A	27	244	309	NPKGQKDREAPLSRSVFVKIKIKRAFAL LLHGRF*PSTPAASAPASKSPRGSGKAL ASALFYIVQLTK
1750	9801	A	270	555	1181	RGPMERPKQMTAVHCQGHQRGDSEIRN FRCHGPNSTRWGSPPHASAFSTCL*N KPKYFPWGISFLSFLSRRSL/DSVAQAR VQWCNLGSLQPLPPRF*QFSCIRLLSS*D YRCMPPCPA/NYL*F**RQGFTI*ARLVLN S*PRDPPVLASQSAGITGVSHQARTFFLF FETTFHSVAHAGVQWHDLSLPPPPPRF KRLSCLSLSSS
1751	9802	A	2700	78	399	FIHRPSDSGPPAERSPCRGRVCISGKKHS YPSCWYPLPKHTASCPISTSILTPL\DL RIPLMWKDTEYFKNKGDLHRWAVFLL QLGEHIQDTEMIIVDRTLTYCI
1752	9803	A	2701	2	368	VVAGALGCSWLIGAGFLSGREGACRR ERGQQQTGTPLPSSLPLPSLEKRAGRTA ATKARLDTLCLEPPLQLAFPPGDPTYP/T SLSFSSLPG/LPA/WPPEQQWGEENLSQQP EGV*QELQRDKGSFCPLPKSWPPL*RG GARLQLARNRGWFPVWKGRGLQKGAG TAADRHTPAFLSPSPFSGKASWENSCH QSETGHSVPRAPSAAGLSSWGPHLSSLR FLFLPCLGSRQAPGAAVGRGKFVTAARG GLTGVAEG
1753	9804	A	2702	1	588	VRAGELDQALGRPFTLSISNQYGDDEVT HTLQTESREALQSWMEALWQLFFDMSK REGGWVEPLGRTGVCHF*YRPLFQDYV EGNVAGERAAWLSLLISALLPGQWKQC CDEIMKIETPAPRKPQALAKQGSLYHE MAIEPLDDIAAETDILTQREGARLET PPWLAMFTDQPALPNPCSPASVAPADWT HPL

1754	9805	A	2703	46	1825	AAAGSETGLGSCLEGKGAEGSGDSSRQ AHPCLPLSLSSLLWKSEDTLQRKLDHEI RRLRKGPC\KLLANLLPSEKQALEA\TKSL LVCNSRIL\SYMGE\LR\KEA\QLLGKT SRRPSDSGPPAER\SPCRGRVCISDLRIPL MWKDTEYFKNKGDLHR\WAVFLLQL G\EH\QDTEMILVD\RTLTDISFQSNVLF AEAGPDF*TCGLELYGACVEEEGALTGG PKRLATKLASSSLGRSSGRVRASLNSAG GSR/GAIPFMLPTPEVGGPRYHLLAHTTL TLAAVQDGFRTDHLTLASHEENPAWLPL YGSVCCRLAAQPLCMTQPTASGTLRVQ QAGEMQNWAQVHGVKGTNLFQYRQP EDADTGEEPLLTI\AVNKVMGPLVETRVR AGELDQALGRPFTLSISNQYGDDEVTHT LQTESRGSTCRAWMEAL\WQLFFDMSQ WKQCCDEIMKIETPA\PRKPPQAL\AKQG SL\YHEM\ALFEPLDDIAAVTDILTQREG ARLETPPPWLAMFTDQPALPNPCSPASV APAPDWITHPLPWGRPRTFSLADAVPPDH SPRASLRFAPLPTFSESPTTRGLLQAKGQ PRTWLQSPV
1755	9806	A	2704	1	370	
1756	9807	A	2705	1	363	
1757	9808	A	2706	158	301	IIMTLAEDLLCSAAQNSRLSAQRTQAGW LLISALMTLGNSL*KVYIP
1758	9809	A	2707	182	395	
1759	9810	A	2708	1	434	SSYIPFSIQQLFPTHTFTL*HPVSWKNC RK*TRENK\ITAELIFQEGIKVLETLVT VAEEHRAQLVACLLPILISFLLDENSLG SATSIMRNLHDFALQNL\MQIGPYSSVF KSLVASSPALKARLEAAIKGNQESVKVK I
1760	9811	A	2709	112	501	
1761	9812	A	271	80	599	SIQEKRLSGGEQSPTFLKELQEGTSWLLM AKLYEAVTFKDVAVIFTEELGLLDPAQ RKLYRDVMLENFRNLL\SQWGINHAMEI LSTS*GKEKLWVMGTSSQ*ERNLGGKIQ TEMETVPEAGTHEEFSCQIWEQIASDL TRSQDITISNSQLFEQDDNPSQIKARLST VHTR
1762	9813	A	2710	1298	8400	FPTNTTFPLLKVCYRFHYAEPVPGHCR AGVRREGADWGTGSADKQRGPFLLDY GKVWLPCAQQNDVREKQKTLVEQLLSL LNSSPGPPTRKLLAKNLAILYSIGDTFSV HEAIDKCNDLIRSKDDSPSYLPTKLAHV VCLGSLYKKLGRILGNTFTDVTGNILKA MKSAESQGRYEIMLSLQNILNGLGAAAA PCHRDVYKAARSCLTDRSMAVRCAAAK CLLELQNEAIFMWSTDLDVATLCFKSF EGSN
1763	9814	A	2711	2107	2424	TTRYLKKTSTTGQRKKRGRNGSFPTEN LVPSGTVTGSQQLGPPFR*N/HTEECWGP PTADGRAGKGPRQPGRAQRIYRWDP DGTTWHHRPCGSRGTDQPETK
1764	9815	A	2712	1	368	FRREGRPAGAGAGFADSGGAPSSCCGPT VRPVAATAENVLHV\RGAFQEFVPCQAG VQWRNHGSLRPPP\GSSHPISAS*VVET TGMCHHVWLIF**NFFVETGSPYVAQAL ILLMLGIKTL
1765	9816	A	2713	1	278	
1766	9817	A	2714	188	406	

1767	9818	A	2715	123	914	PRAGGCGGSGRVTACLCACATLVWPPR FQEVLLVLSGLVHARGCTYSQLWSRSH FCCSRGPLAMAGILFEDIFDEGY*PEGQ EVWTECSRLHCESESFRMDLILDVNIQIY PVDLQDKFRLVIASTLYEDGTLDDGEYN PTDDRPSRADQFEYVMYGVYVRIEGDAE TSTEAAATRLASAYVSYGGLLMRLQGDA\N NNLHGFEVGLPRVYLLMKKLSLLNLAL NQPSLPSHSGRGHCSSLGQPLFAHLLRK GWLTVHRWRHL
1768	9819	A	2716	1	2415	
1769	9820	A	2717	2	964	
1770	9821	A	2718	276	482	
1771	9822	A	2719	329	3354	PVRQFIFPKLPIRHCLEAEVGGRGQTCA PRKWAVPIGLHSRSATSQSGCGGGRSWL CSSLKMAAQPPRGIRLSALCPKFLHTNST SHTWGHSVQLELIG*CLWIPDVNAKQI WGLTKQWINDHICLTFTDNGNGMTSDK LHKMLSFGFSDKVTMNGHVPVGLYGNG FKSGSMRLGKDAIVFTKNGESMSVGLL SQTYLAEVIKAEHVVPVIVAFNKHQMIN LAESKASLAAILHSLFSTEQKLLAELDA
1772	9823	A	272	1321	1913	VEMRRNQCKNSSNSNGLCVICPSNNHTS SPTRVLATWMNCLELHKYNV*IWIGKKII *TQENGKTQSEENKNNIKVLQELKDKVA GIIKKNLTDLNAPKNTLLEFHNAFTSINS RK/DKSDERISELEDWVSNIRWTKVN*NE QILHGGWDDIMRPILQITGISEREVEKSN NLENVVQDIIFESFPNLARKANSQIQE
1773	9824	A	2720	1135	1476	HGVSLLLPRLECTGH/VISAHCDPRLPGF EVRFSCLSLPSSWDYRHAPTHAQAKFCI FKWRRGFSHVQGAG*HFYFPSQVLGTN MEDFFLTGLILHGLFQEDSNAPYSFKWG SLR
1774	9825	A	2721	670	1253	ACYALNLFPKHTDIFYFFFIYFFCRDRGP RYITQAGLKFVDFK*ILPPWPYQSVGIISV SHPPGPH*CILNAINKNYRYRN*LLY/IQ YPMLFGVFLRQGFAVT/SAAVQWYDHG SMQPQLPGLRWFSHLSLLSGWEHRRTPP RLG*FCIFSRESFVMLPRLVLNSWGSNDT PALASQSVVITGMSHAPAFPMFLF
1775	9826	C	2725	95	310	MREYNLVVLGSGGVGKSALTQFVQGI FVEKYDPTIEDSYRKQVEVDCQQCMLEI LDTAGTLPRLTTYRT*
1776	9827	A	2726	1	1101	
1777	9828	A	2727	53	772	IPRSGITGSEGDYPVYKSMCLTAPSMALS RSSVFKQITSLREYKLVVLGS*GVGKSAL TVQFVHGIFVEKYDPSIEDSYRKQVEVD CQQCMLEILDAGTEQFTAMRDLYMKN GQGFALSIFYLQLQSTFNGLYRDLEGNQ ILRV*GTRE/VMFPMILVGNKCDLEDERV VGKEQQGNLARQWCTLALLESA/RRSE IQVNEVLAYDPVRQINREY/TPVEKKKP*K NSMSTLLGPIVRRQL
1778	9829	A	2728	377	615	VPAQCSF*DTASCLLVKRKMRLDAVAH AYNPSTLGGRGGW/IRGQEFKTSANM VKPVSTKNKKISRVVWHNRNPSYSGG

1779	9830	B	2729	1	1224	MPTVGKAQARRRTRDITLLDITQVLIDQ SPRKDTGLAQQTGIVVPSKGVKYWRAQ LKGDMKYASPAFELFYFSVRAQSTDGIV TLLDPTTREDCDISSAPNPEVRTQRQAEV AGVGLLAVKVPRDEEGVLGGAPGPQKR SRVCGEPTLQRRSGPLPARPGSRCPPT SVSSPVPEDEYGRVVMIRLDNPGISGRT IENNPPELEKQLPGEPSSENSPYLGPPQVLF LLRDPREDVMLLLNQTPPTAEKQAVLQ AAEIFRNEQQISYNTSKGKGDRECEEIA ETPFQIGSEAVPLDNPWNSSSSAGEWK RRHFLICILEGLERTKAKFLNCSKLSMVD QKPDENPAAFMERLREALIEQTSLSPDSV EKQLILKDKFVTQSASNIRRLKQKAIGP ISTLKNLLK*
1780	9831	A	273	193	310	
1781	9832	A	2730	877	1536	TNFLFALSPSCLAGLLPPKFKQFSCLSLLS SWDYRNFYIFW*RWGFTMLARLVSN*P Q/CDPHTSASHSAGITGMSHCAWS*TLNF FSYELFFSFTSALS*KDHCKGGHNMGCQ FT*MHQ*L*EKPP*LLFETESRVA/QAG VQWRNLGSLQPPSPGKFRFSCSLPSSW DYLRTPPRANCCIFSRDGVSPCWPGW SQSLDLVICPPWPPKVLGLQA
1782	9833	A	2731	3	643	RLEEDLGRRQSLAPVGVVRVETVTVVL WTITMGIQGSVLFGLLVAVLCVHS GH*PCQC/YNGFLPQTADCQKQPFNCSS GFWMRVFITQKLGQVYNKICWKFEHC NFNDRHNPA*RKMGLTILLCKKG/LRCN FTEARLENGGTSLASEKTVLLLGEHLFWA AAWEPSIPKSNTRCFLTKLPRSLRSSVF PLGWPHSKGLDIFQMGSWLGKE
1783	9834	A	2732	11	431	RHLLAAPPAPAAAAAALSHCLRSSG RLAPHTSRRLPRVVKRRVNALKNLQVK CAQIEAKFYEEVHDLERKYAVLYQPLFD KRFEIINAIYEPTEECEWKPDEEDEISEE LKEKAKIVDEKKDEEKEDPKGIPEFW
1784	9835	C	2733	257	358	MILLVFLPXHQVFLERXQESEILHHLNTL ADVL*
1785	9836	A	2734	2	387	
1786	9837	A	2735	64	467	PAAWLPILVAARQLTVQMMQNPQILAA LQERLDGLVETPTGYIESLPRVVKRRVN ALKNLQVKCAQIEAKFYEEVHDLQRKY AVLYQPLFDKRFEIINAIYEPTEECEWK PDEEDEISEELKEKAKIEDEKDD
1787	9838	A	2736	1	795	
1788	9839	A	2737	1	982	
1789	9840	A	2738	2	138	SARGAASCSSRCCRCRPESLPAQLRAA WLPILVADIWSSYNMADIDNKEQSELDQ DLDDVEEVEEETGEETKLKARSA*LFR MMQNPQILA/ALQERLDG/LWVETPTG YIESLPRVVKRRVNALKNLQVKCAQKE TQFYEEVHDLERKYAVLYQPLFDKRFE IINAIYEPT/EKECEWETR*RKDEDFGGN WKEKGQIEDEKKDEEKEDPKG/IFPEFW LTVFKNVDLLSDMVQEHDEPILKHLKDI KVKFSDAGQPMFVLEHFHFEPEYFTNE VLTKTYRMRSEPDADSDPFSFDGPEIMGC TRVPR*DWKKGKNVTLKTIKKQKHKG RGTVPYCDLKPVSNDSFFNFFGPLPESSL RSGDLDDAEANLAADFIEIGHFYRERIIP RSVVNFTGEAIEDDDDDYDEEGR*RS* GRLAPHTSRRYLEFLQHGRH

1790	9841	A	2739	1	435	PRARAERPAPASCSSPTSTRITPDTEVC IVERLFSSSLVAIVSLKAPRKLKVCHFKK GTEICNYSYSNTILAVKLNQRQLIVCLEE SLYIHNIRDMKVLHTIRETPPNPAGLCAL SINNDNCYLAYPGS*SGEAGAGQLLFAN FNQDNTDTEVCIVERLFSSSLVAIVSLK APRKLKVCHFKKGTEICNYSYSNTILAV KLNQRQLIVCLEESLYIHNIRDMKVLHTI RETPPNPAGLCALSINNDNCYLAYPGSA TIGEVQVFDITNLR
1791	9842	A	274	831	1102	HFGRPRQVDCLSSGVQDQPGQHGEVQS VLKLAKKLAGHGG AHL*SQLLWRLRHEN HLNLGGRGCSEPRWCHFTPAWTEQDS V*NNNNNNK
1792	9843	A	2740	3	438	
1793	9844	A	2741	1	1336	MLLRLQRIKTLRPPGCPHMTTCSAGTLS AVPCVSPRQVVFERRFCLWHSVEMFT HVLFPVISADTEVCIVERLFSSSLVAIVS LKAPRKLKVCHFKKGTEICNYSYSNTI LAVKFNRQRQLIVCLEESLYIHNIRDMKVL HTIRETPPNPAGLCALSINNDNCYLAYPG SATIGEVQVFDITNLRANMIPAHDSPA ALAFDASGTLATASEKGTVIRVFSIPEG QKLFEFRRGVKRCVCSICPLAFSMDGMF LSASSNTEDTVHIFKLETVKEKPPEEPTT WTGYFGKVLMASTSYLPSQVTNMFNQ GRAFATVRLPFCGHKNILLG*PTIQKIPR LLVGAAIDGYLYMYNLDPEGAGECAL MKQHRLDGSLETTNEILDSASHDCPLVT QTYGAAAGKAYTDDLGA VGGACLEDE ASALRLDEDEHPPMIRTD
1794	9845	A	2742	152	1616	VQDPSSRARPPRGPLAARFAMNLSAQ SGEAGAGQLLFANFNQDTEVKGASRA AGLGRRVWVSLAVGSKSGYKFFSLSS VDKLEQIYECTDTEVCIVERLFSSSLVAI VSLKAPRKLKVCHFKKGTEICNYSYS NTILAVKLNQRQLIVCLEESLYIHNIRDM KVLHTIRETPPNPAGLCALSINNDNCY LAYPGSATIGEVQVFDITNLRANMI PAHDSPAALAFDASGT*LATASEKGT VIRVFSIPEGQKLFEFRRGVKRCVCSICSL AFSMDGMFLSASSNTETVHIFKLETVKE KPPEEPTTWTGYFGKVLMASTSYLPSQV TEMFNQGRAFATVRLPFCGHKNICSLATI QKIPRLVGAAIDGYLYMYNLDPEGGE CALMKQHRLDGS LGKRPNEILDSAISH DCPLVTS DITAQLAGKGTYPSSPTETCP TRDDLGA VGGACLEDEGPALRLDEDS EHPPMILRTD
1795	9846	A	2743	122	1162	LGLEGDGGASQWVGGRQRLQDCNRSL QGSPETLIPP/SLQITVPSRTCFF/SLQVGL T/FPPRAVPSAAAA LGRNRL*RGWHRR IPPVWASISRAASSWG/TKPPLFKVPSQPE TLGETWVIK MAGTYGGSRTLPSPGG NFRSTVPR*VQTTPRQPGAGLPKPVVVA TSSD*QASRSSPGRSRKDGPDSPALPVS/ RGEPEPSLQPPPPSTR*PSRLRGPRP PSA LSGPLRAPEHAQSSTSPSRWTTSPRMLR APARAPPCPSPTLVVSTPSPFP*RSQ* SGHTPGRFFPCSPPRIRASACASLGGTTD GSTAYQIAHAPHHVFLTSRAFLRLAGS CTNHG
1796	9847	A	2748	54	188	NMTKLQVVS KNLLLKMLIKERETQRK GGSS*KSTQGA KGGAPR
1797	9848	A	2749	572	857	GQKKGFSMGG*GEKGS LGNPSWG TAGG QAPVPPQGLTGTRFTQGSSGTAGPPAST FCLGGHGAVVGTYGRQMYMYEFVFC VGVAQKKDLCPRE

1798	9849	B	275	53	403	ALVTEFQETHSQDAIEHVLNLANFAYD PSNYQYLRQLQVLHLFLDSLSEENETLV EFAIGGLCNLCPDRANKEHILHAGGVPLI INCLSSPNEETVLSVITTLMLHLSPPGRSFL P*
1799	9850	A	2750	3	127	
1800	9851	A	2751	1	359	LILVKAALDGTGHLSPWFGVRCFAQNP GRRGCS/PEGKQLQSRVI*G*EFQSTAAC EEHYMASIRRSVSPSLSVCTSPPLSVLDIL PPTDLYFEQHSPIL*LKVKGSLH*RSSPLR KES
1801	9852	A	2752	1	1270	MGATTMDQKSLWAGVVVLLLLQGEMG FCYVARAGLELLGSRSPASASQSAGITG SAYKLVICYFTNWSQDRQEPGKFTPENID PFLCSHLIYSFASIENNKVIKDKSEVMY QTINSLKTKNPKLKILLSIGGYLFGSKGF HPMVDSSSRLEFINSIILFLRNHNFDFGLD VSWIYPDQKENTHFTVLIHELAEAFQKD FTKSTKERLLLTAGVSAGRQ MIDNSYQV EKLAKDLDFINLLSFDFHGSWEKPLITGH NSPLSKGWQDRGPSSYYNVEYAVGYWI HKGMPSEKVVMIPTYGHSFTLASAETT VGAPASGPGAAGPITESSGFLAYYEICQF LKGAK/TRGSRDQQVPYAVKGNQWVG YDDVKSMGDQGSVL*RFKTWGGAMIW SIDMDDFTGKSCNQGPYPLVQAVKRSLG SL
1802	9853	A	2753	385	570	KLGTEDKGGRIILLVWAKLHQLSY*HI RVLSIGGN*GPGE*MGMPGVHLLFFRT KIRIQI
1803	9854	A	2754	1	1022	MTLAPSDQDLFVFRSGPPAAAGMPCLF PEVPFCTRVHQPTGRDGSKNLLNELFIAC PGGLMAQGPLDPTESSVPNTKALCGIFS DVAATAENRQTFMQSAIQFLRKYNFDG LDIDWEYPGNRGSPADTQQLFTILLKEM YEAFAQESTRSHKPRLLMSAAVSAGKGT IETACQIPEMSSSTPSRKEPPRVWNA PWEVPYVYKGNQWIRYDNSKSFTLK/AVLPH SKDKV*TTEFFALLCLSPA HGKFTQAEPK SGGDRASGLLQSTHLYPGHQLAPIITAA PGGGSTGGSGFCTGKSKGLYPVPHSKH AFYNCVDEHTYEEACQEGLVFDTSCASC CNWA
1804	9855	B	2755	143	867	XVVVLLLLQGGSAYKLVICYFTNWSQDR QEPGKFTPENIDPFLCSHLIYSFASIENNK VIKDKSEVMYQTINSLKTKNPKLKILL SIGGYLFGSKGFHPMVDSSSRLEFINSII LFLRNHNFDFGLDVSWIYPDQKENTHFTV LIHELAEAFQKDFTKSTKERLLLTAGVSA GRQMIDNSYQVEKLAKDLDFINLLSFDF HGSWEKPLITGDNPSPLSKGWQDRGPSSY YNCEICCGVLD*
1805	9856	A	2756	2	394	CSAHSTALRVVRNHFYFTITATQVHKGS SSHPCTDRGNEMMASSQPSAFGIPGWG AR*PAPAPLPHRRGLPGSVTG*WRPIVGQ */PSPHCHCKASTKAQPEGPGTPPPGKPS WKELPESHKKSLAPSFP
1806	9857	A	2757	499	1592	QPSQFLSAGLNQTVPWGTCLHRAELSP STENSSQLDFEDVWNSSYGVNDSFPDG DYDANLAEAAAPCHSCNLLDSDALAFFIL NQCSWGILASRTGLFMPFRPFRWQLCP GWPVLGTAGCGAVAFFQHLWVPVFGP QGYGSTRSSALL*LGATGVWYGSAFAQ ALL\GCHASLGHRLGAGQVQGLTLGL TVGIWGVAAALLTPVTLASGASGGLCTL IYSTEKALQATHTVACLAIFVLLPLGL FGAKGLKEGIGLMGPGPLDEISLW\WF IFWWPHGVVGLDFLVR\SKRLLSTCL AQQALDLLNLAEALAILHCVGTPLLLA

						LFCHQATRLLPSLPLEGWFFHLDLGS KS
1807	9858	A	2758	1541	1830	KRFLHLHQHTSGKGSRGFHLCCCGFSS KSP/GS*PGAGGASSSSQSKSPGPRPARV RRRLWVRAPPATSQEEASAGRRVRPPSS VHVNIPPSVRPA
1808	9859	B	2759	4	1698	MGDFNTPLSTLDRSMRQKVNDIQELNS ALHHMDLIDIYRTLHPKSTEYTFFSAPQR TYSKIDHIVGSKALLSKCKRTEIITNCLSD HSAIKLELRKIKLTQNHSTWKLNNWLL NDYWVHNEMKAEIKMFFETNEIKDTTY QNLWDTFKATLNQEEVESLNRPTGSEIQ AMINSLGTKKLQDQTDSPSSTRDDMIV YLENPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSKLPFTIASK IIKYLGVLTRDVKDPFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIMKMAILPKVI YRFNAIPIKLPMTFFTELEKSTLKFIWNQ KRACIARSILSQRNKAGGITLPDFKLYYK ATVTKTAWYWYQNRDIDQWNITEPSET MPHIYHYLIFEKPDKNKKWGKDSL FNK WCWENWLATCRKLKLDPLTPYTKINS RWIKDLNVRPKTINTLEENLGNTIQDIGM GKDFMSKTPKAMATKAKIDKWDLIKLK SFCTAKETTTVRNROPTWEKIFAIYSSD KGLISRIYKELKQIYKKKTPSTSG*
1809	9860	A	276	842	2432	SLISCSEGSPPKASGPSS*EHCPAKPLGPG TWPLLTGPESGGGGPDVGLRAGQPMN AAPV*SSPCL*N/PGFLTPSGVSSV*MPVL LKEPAFQMAEKAPNGAVCAP/SFPASTS GLWSPA VGVPRSRSLHGSALPWGHAPR Q/SGYPGQSAPAGCGPRPPGGGSRSPGR SVPGSGAWRWPRGRSEACTAPRAWRSA LGESCGPAGSGA*AW*WQTAPSPHWGW IGS***VGHLLRAGCAPCWPLGTGCTG LPSRSGHKSLSLSVQQVQWLIRFFPLS* M*KPAACLPS*RERPSCAHWTAGGVMG FLSV*SVIR*SLSHCLAAESSPHPGAPQG TATQIGGGGSRYVQRG*NHRPCRS*PIQR PCGQAGSGGRVASTWCAQ*QTPPGSHSP PTANREINPGAAAADTRSCWGHKRSW RGWRGLAPWRLGFGSPWNSRDQGPAGI PAARRGGPTFGFLAHGPR*RRTPRDGRE GGKGAGAKPSETLTRSPVWRGKRGS NGFLSWVQILQYFAAGNGIWEMGRGLRI L
1810	9861	B	2760	1	1044	MGRNRSRKDENSKNQSASSPPKDRSSSP ATEQSWMENDFDELTEVGFRLNQEEV ESLNRPIRGSEIEAIINSLPTKKSPPDGFT AEFYRRYKEELVPFLLKLFQSYEKEVILP NSFYEASHILIPKPRDTTKKENFRPISLM NINAKILNKILANQIPQHIKKLNHEDQVG FIPGMQALFHIQESINVIHHINRTKDKNHI IISIDAEKAFDKIQORFMLKTLNKLDDMI VYLENPIVSAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSELPFTIAT KRIKYLGIELTRDVKDLFKENYKPLLNQI KEDTNKWKNIPCSWIGRINIVKRATLPK*

1811	9862	A	2761	1331	2175	TEPKTKTT*LSQ*MQKRPLTKFNNPSC*K LSIN/IVLEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIISAQNLLKLISN FSKVSGYKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWKNIPCSWIGRIN IVKMAILPKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARITKSILSQKNKAGGI TLPDLKLYYKAIVTKTAWYCYQNRDID QWNRTEP*EIMLHIYNLIF
1812	9863	B	2762	1	2898	MRQKVNKDTQELNSALHQEDLIDIYRTL HPKSTEYTTFFSAPHHTYSKTDHIVGSKAL LSKCKRTEIITNCLSDHSAIKLELTIKKLT QNHSTTWKLNLLNDYWVNNEMKAEI KMFFETNKNKDDTTYQNLWDTFKAVCKG KFIALNAHKRQERSKIDTLTAQLKELE KQEQTHSKASRRQEITKIRAEKETETQK TLQKINESRSWFFERINKIDRPLARLTEK KRKKNQIDAIDKNDKGDIITDPTIEQTTI
1813	9864	A	2763	3	668	
1814	9865	B	2764	64	1242	MINS LGTKKLQDQDTSQPSSTRDDMIVY LENPIVSAQNLLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSKLPFTIASKII KYLGVQLTRDVKDPFKENYKPLLNEIKE DTNKWKNIPCSWIGRINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKSTLKFIWNQK RACIARSILSQRNKAGGITLPDFKLYYKA TVTKTAWYWYQNRDIDQWNITEPSETM PHIYHYLIFEKPDKNKKWGKDSL FNKWC WENWLATCRKLLDPFLTPYTKINSRWI KDLNVRPKTINTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIKLSF CTAKETTTRVNRQPTWEWEIFAIYSSDKG LISRIYKELKQIYKKKTPSTSG*
1815	9866	B	2765	287	898	MNINAKILNKILANQIPQHKKLNHEDQV GFIPGMQALFHQIESINVIHHNRTKDKN HIIISIDAEKAFDKIQQRFMLKTLNKLDD MIVYLENPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQIMSELPFTI ATKRIKYLGIELTRDVKDLFKENYKPLL NQIKEDTNKWKNIPCSWIGRINIVKRATL PK*
1816	9867	B	2766	1	1443	MKLPEEASGSNICCYAIFAVLQPLLVIPK ETVSGVDLQQTPTDLQLSDLTPGRKTNK QKGIASPSTKRTSTPKPHLQANAQRFC HQACVTRVPKGSTKHGKEQLVPATAKT CQIVKNINAMKKLHQLTEIQITIREYHKH LYANKLKNLEEMDKFLDTYTLPRLKQEE VESLNRPIMGSEIEAIINSLPTKKSPGPDG FTAKFYERYKEELVSFLLKLFQSIEKEGIL PNSFYEASIIIPKPGRDTTKKENFRPISLK NIDAKILNKILANRIRQPIEKLIHHDQVGF IPEMKGWFKKCKSINVIHHNQTNNDKNH MIISIDAEKAFDKTQQPFMLKTLNKLGTI RQKKEIKGIQLGKEEVKLSLFADDMIVY LENSIVSAQNLLKLISNFSKVSRYKINLQ KSQAFLYTNNRHMESQITSELPFTIDTKR IKYLGIQFTRDVKDLFKENYKLLNEIKE DTNKWKNIPCSWIEESIS*
1817	9868	A	2767	1	966	
1818	9869	A	2768	1	216	
1819	9870	A	2769	3	2074	
1820	9871	A	277	721	1027	

1821	9872	A	2770	1	1632	MHCILPTPSGSGSFPVYTSQSOPKTPGAF SGTLSVREPLSPEPDVLLPGSAKCAALC WFSVLDAASPVTRWPVSRSPWECRCV PSPPVREAPVSPPFQCAPPYTDCLSPYL YEYTVCPSPCARVPIPSSTHPWEYKVPPP HAERLCPVSEDPPCLCNWKTRAAGARES SLVPCPYAARYPPSPPRVAWSSHSYRG LSPSLGPNKPGNPRGPSESPAAAASRPRA AAASAPPPGAARLPASPTPRLARDRGVS
1822	9873	A	2771	842	2353	TEPKTKTT*LSQ*MQKRPLTKFNNPSC*K LSIN/IVLEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIISAQNLKLLISN FSKVSQYKINQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRDVKDLF KENYKLPPLIKEIREDTNKWKNIPCSWIG RMNIMKMAILPKVIYRFNAILIKLPLTSFT KLEKTTLKFIWNQKRARIAKSILSQKNK AGGITLPDFKLYYKAIVTKTAWYCYQN RDIDQWNRTEP*EIMLHIYNLIFDKPEK NKQWKGDSL FNKWCWENWLTICRKLK LDPFLTSTYTKINSRWIKDLNVRPKTIKTP EENLGNTIQDIGMGKDFMTKTPKAMAT KAKIDKWDLIKLSFCTAQETTIRVNRQP TEWEKISAIYSSDKGLISRIYKELKQIYKT KTNNPIKKWAKDMNRHFSKEDIYAAKR HMKKCSSSLAIREMQIKTTMRYHLTPVR MAII/RIKSGNNRCWRGCGEI
1823	9874	A	2776	3	2077	
1824	9875	A	2777	3	1038	TAEGTWIAVRRLRLEGTGGEMSRVPAFL SAAVEEHLRSSSLIPLETALANFSSGP EGGVMPQPVRTVVPVTKHRGYLGVMIPA YSAAEDALTTKLVTLRGPRHHLRSSLP TRVIVVTLLSPAMGTLLAVMDGKCS*IA KRTAAVSCHLPPSFLKPPSSEVLCLGAG VQAYSHYEIFTEQFSFEVRIWNRTKEN AEKFADTVQGEVRVCSSVQEA VAGADV IITVTLATPILFGEWVKPGAHINAVGA SRPDWRELDDELMKEAVLYVDSQEAAL KESGDVLLSGAEIFA*AGEK*FKGVKPS /YCEKTPRC SKSLGMAVEDTVAAQTHP MIPWSSGK
1825	9876	A	2778	2	2037	
1826	9877	A	2779	3	194	TFFFQVKPDGTYVKPLASNKLTGYTMV FVRSFLVGEAARALS KACTIAIRYS AVR HQSEIKPG
1827	9878	A	278	615	2182	PQVIRPPWPPKVLGLQGLLTFRDVAIEFS QEEWKCLDPAQRTL YRDVMLENYRNLV SLDTSSKCMKMFSSSTGQGNTEVVHTG TLQIHASHHIGDTCFQEIEKDIHDFVFQW QENETNGHEALMTK/YQKVDECTERHD QRHAGNKPLKMSLDQAFIRICLKCTYFT PKGKLVIKLRLSTMLS/HVSASQRISCRP KTRISNKYRNFLQSSLLTQKREVHTRE KSFORNESGKAFNGSSLLKKHQIHLGD KQYKCDVCGKDFHQKRYLACHRCTG ENPYTCNECGKTFSHNSALLVHKAIHTG EKPYKCNECGKVFNQQSNLARHHRVHT GEKPYKCECDKVFSRKS/TLERHRIHT GEKPYKCKVCDKAFRRDShLAQHIVIH TGEKPYKCNECGKTFVQIHLVMHKVL HTGEKRYKCNECGKVFNHKS NLACHP* TSIPGRETFTRVMECGQGFNRKSNLER HHLRHTGKKS*KC/EICKVFRQQSNLAC HHLRYTGEKPYKCECDKSFQFQITP
1828	9879	A	2780	1	903	
1829	9880	A	2781	133	402	
1830	9881	A	2782	2	242	

1831	9882	A	2783	26	2229	RFRAGAADLDCHCHLGRCLLRQQLVVA MNPDLRRERDSASFNPPELLTHTLDGSPE KTRRRREIENMILNDPDFQHEDLNFLTR SQRYEVAVRKSAMVKKMREFGIADPDE IMWFKNFVHRGRPEPLDLHLMFLPTLL HQVATAEQQERFFMPAWNLAIEIGHFIAQ TEMGVHG\THLSRLSETTATYDPETQEFIL NSPTVTSIKWWPGGLGKTSNHAIVLAQL ITKGKCYGLHAFIVPIREIGTHKPLPGITV GDIGPKFGYDEIDNGYLKMDNHRIPREN MLMKYAQVKPDGTYVKPLSNKLTGT MVFVRSFLVGEAARALSKACTIGILYSA VRHHSEIKPGEPEPLILDFQTQQYKLFPL LATAYAFQFVGAYMKETYHRINEGIGQG DLSELPELHALTAGLKAFTSWTANTGIE ACRMACGGHGYSHCSGLPNYVNFPS TFEGENTVMMLQTARFLMKSYDQVHSG KLVCGMVSYLNDLPSQRIQPQQVAVWP TMVDIN\SPESL TEAYKLRAARLVEIAAK\ NLQKEVIHRKSKEVAWNLTSDLVRIAS EAHCHYVVVKLFSEKLLKIQDKAIQAVL KE/SLCLLYSLYG\SQ\NAGDFLQGSIMT GP\QITPSNPAV*RELLTIRSDAVALVDA FDFQDVTLGSVLGRYDGNVYENLFEW AK\NSPLEPKAEVHGIFTRHLEVHCQSQA LEVFTDRDKFKSGFQKAPVWQLQILWESF SNSNRL
1832	9883	A	2784	61	241	
1833	9884	A	2785	60	341	
1834	9885	A	2786	70	428	IGGPQGFSPTPSLKPRPRIFKTPPIRGNWG PRPPGVSPQFQFGGDTKFNLEILFVVL TFSV*AQSGDPAAPRSGP/RPGRGERE G*NEKSPVLPQCWGGWRHHPPSAALLW ALIW
1835	9886	A	2787	38	243	TPSTIDKSLTSLIKKK\KA*INNFRDKKGN IAKDIPEM*KIIREYYENIHANTFENLGDI DKNKIDQN
1836	9887	A	2788	2	114	
1837	9888	C	2789	50	214	
1838	9889	A	279	403	933	QQRWQQGWQAWGGQVPQEVGFWF LLSWLLSRLGVPAQGPARGVDPRPGS RGARGGCSASAAPPARASPGRPCCWNG SRPPAQHRRTPATRVGEAGQGEVRGVR RLPAPLLQAVQPRLSDRSYPAAPARPTA TSP/APPSPAPKAPIVGALS*GTADPGSD SYPPSRSHAPRP
1839	9890	A	2790	1	624	
1840	9891	A	2791	2	851	
1841	9892	A	2792	1	1116	
1842	9893	A	2793	53	1408	HRCCLWTFQCLSLGITFLIKEGKEGKL EPAREGPYLVLLTTETAVLLISITPTTNS NPTLERFCGLGAEVTGKDPMGFFKVLRO SLDADEGTAVDIQSFRPQKDFGRRRTLE ECHVTGKGGTGTKMSNRVVCREASHAG SWYTASGPQLNAQLEGWLSQVQSTKRP ARAIAPHAGYTYCGSCAAHAYKQVDPS ITRRIFILGPSHHVPLSRCALSSVDIYRTPL YDLRIDQKIYGELWKTGMFERMSLQTDDE DERSIEMHLPYTAKAMESHKDEFTIPL VGALSESKEQEFGLFSKYLADPSNLFV VSSDFCHWGQRFYISYYDESQGEIY*SI EHLDMGMSIIEQLDPVSFSNYLKKYHN TICGRHPIGVLLNAITELQKNGWMNMSFS FLANYAQSSQCRNWQDSSVSYAAWEHS RATEALNPQGCHLPHSSYSVRGSPA

1843	9894	A	2794	53	699	SLPSLTTPPGSRQTPAGRLNTEHHINEHIL MYSLDLNNSSSQMPSTKAQTSDEIFEVD GEMPNHLLPIKAHVEDLGMDDEGDDD PVPPLPNVNAAILKKVWQWCT/HPHKDD PPPPEDDEEQRKSVDDIPVWDQGIPGK FDQGTLF*NSFLGLQTYFRTSKGLLDVTC KTVCCQYDQKGKLP*EIRKPPFKSKMTFT EEEEAQVRKVENQWCEEK
1844	9895	A	2795	162	522	WVRRGTISPARQRQDGVGAAPANYAKV LEWQLAPSPRHKCCQRPGLHGCDSIGP LSPVGLPGLKG*PDNSSEGPCSS/QALPVP SSPGHPGSGGPKGQARSLLNCRGCPINW QHRCCRKI
1845	9896	A	2796	2	1214	QPFQSGGCVIALGRKMFSSVAHVLARAN PFNTPHVLQLVHDGLDLRSSSPGPTGKP RRPARNLAAAAVEEQYSCDYGSGRFFIL CGLGGHISCGTTHVALVPLDLVKCRMK VDPQKYKGIFNGFSVTLKEDGVARGLA KGLAPTFLGYSMQGLCKFGFYEVFKVL YSNMLGEENTYLWRTSLYLAASASAEFF ADIALAPMEAARKVRIQTQPIGYANT*EGI SFPKCIKEKGLKAFYKGVALLWMRQIT YTMN*SSPCLERTV*SHCTSLGVPKPRSE CSKPEQTGCNHLVAGYIARVFCANVSH PC*FVWYLVLNKE*SVAVSLLVFSVTL FKGVWKGFLFARIIMIGTLTALQWFIYY SVKGYFRT/LPRPPPPRDGQSLNNKFG TPVVRSKQIVD
1846	9897	A	2797	276	728	CFGFVFRSWPYGPLSTGDVPKLGPPN* AMGGFRPGKQVSLPGFAGGHACSPAS LPSGPGPAPPRACLPSPRGGRKSLGAPGG FPPGDSHGAPCSRVTVSPGNDLKPGHS PRTLQRGGSLPGRRWVWSCGVVCPVW WPVLSASISGWI
1847	9898	A	2798	451	1030	VPEALSPFEMEGPQFPTMCCCSAPPAMP FPTT*QPSEAAAGQGVPGPHRL*GGLAP AGRS*APAGAFWQGPAQRGEPAVSSK GGAAASTQRLV*HRRGHRGDASRGCP GDQNLQ*KLCSSRAEGGAVSQPGWPAL PHAAGEPLASALPGLHAAQAPAPAVVSG PTTIRSCSGNSGKIFPSSCLDSCFPSP
1848	9899	A	2799	1	933	
1849	9900	A	28	1230	1820	QEYRPSQTPHLALSPERVAPGRRAAGRL APEARAPRGSP/LPPHRVSEKTIRVVVFH PGARKAGGTPPRAPRGDTGGAPGAFTY STPLMSLHRARLESSSTGSSFPADSAPV PLAVVSLDSR*QWESRSSIHAVTN*AS SSSSSSSSSVSRVYPRFIEFLHFDIQTG Q/RITSRQHPPR/DLRDALF*LNSRIPL
1850	9901	B	280	73	207	ELGTQLRTCTLSGLASQVEAHHSLVLS HLKTLWKKISNTKYS*
1851	9902	A	2800	1	1563	MRREGFKFSRSKVVFQDEMTKKWHKSD LHWVSRIQCTVLGVLNATEMRSLPIES LFLIQCFVVSASRNEATDCSGECYSSM RETRGSKECAAARFIKVKGKVLQKVESY KLYHPYFLANWFSASFSGKLVEMRG QEEETLGTFAHVLMFQAASSRALVLPPT MQLELQNFNTCSYRKPNNASSMRSFL SDHGKYVESFRFLNHSTEHQCMQEFM DKKLPGIIGRIGDTKSEIKILSIGGAGEI DLQILSKVQAQYPGVCIQH*SCLRPSAG TNWPNYKELVAKTSNLENVKFAWHKE TSSEYQSRMLGEKGAFKSWDFYSI*FKM LYYVKDIPATLKFHSLALGTNAKMLIIV CVQGSSGWDKLWKKYGSRFPODDLC QYITSDDLTQMLDNLGLKYECYDLLSTM DISDCFIDGNENGDLLWDFLTETCNFNA TAPPDLRAELGKDLQEPFES/ALRKEG KVLFNNTLSFVIEGITIQQSKYIQKLYFE

						QLESLIYFHIKJINSSH
1852	9903	A	2801	1	6750	
1853	9904	A	2802	3	91	KKNIN*EILN*KQMEEPTLYVGNFPIQLT
1854	9905	A	2803	3	7501	
1855	9906	A	2804	3	3223	PPPEAAVVAFEWLKTSTLTGLHPQLPLSL PQPECALPYLVRAFSRGDYMGRIQEVG WVTAGLVIWAGTCYIYKFTKGRAQSV RTLARNGSTVKMETVVGVSQTLAINEA EIKTKPQVEIGAETGARGSPRAEVETKAT AIAIHRANSQAKAMVGAEPETQSESKVV AGTLVMTEAVTLTEVKAKAREVAMKEA VTQTDAGKIVKKEAVTQTKAKAWAL VAKTEAKREAMTQTKAETHILAEKETEI NRVMV
1856	9907	A	2805	1	374	NYFLSLRFDWHSSKS*GHPTCVHCF*/TK NE/CASCHCGAGLLGFLGSGEGASHPC PSCLPLEYRSLHCSLGHCGECMPGASGW GPWTGPGHCPNLCQDKGSKRISWRVGR NGWGRPSFDNAPVAL
1857	9908	A	2806	162	789	AGQNGVSGSAERCLSCLLIPLALWSIENI LLYIPNGHTFYASSNKLTNYVWYSERI*L SGIMMLIVTTVLLVLENNNNYKCAQSE NCSKKYVTLSSIIFFSLGIAFSGYCLVISA LGSCP*AIC/LAPLMGWGVCF*RALLGRF LTDS/SIWDSVPGNLAHVVEWNIILFSILIT LSGVQVVIICLRVVMQLSKILCGSYSVIF QPGII
1858	9909	A	2807	1	3282	
1859	9910	A	2808	136	447	
1860	9911	A	2809	3	3593	SSDPRPSSFWLVWVGLWSMVWRVPPFL LPILFLASHVGA AVDLTLLANLRLTDPQR FFLTCVSGEAGAGRGSDAWGPPLLEKD DRIVRTPPGPPLRLARNGSHQVTLRGFSK PSDLVGVFSCVGGAGARRTRVIYVHNSP GAHLLPDKVTHTVKNKGD TAVLSARVHK EKQTDVIWKSNGSYFYTLDWHEAQDGR FLLQLPNVQPPSSGIYSATYLEASPLGSA FFRLIVRGCGAGR WGP GCTKECPGCLHG GVC
1861	9912	A	281	276	565	WTSSVSTGQSDQA/GPAPALIQMQRPGC GPSPVPGGWLE*RDGQAGMGAAAAPA WVLLCIPAGQGPLPGPRLPFHIPILKFCYC GILVEKKEPRGCF
1862	9913	B	2810	85	283	MEKTELIRRSAWRVISSIEQKTD TSDKKL QLIKDYREKVESELRSICTTVLELLDKYLI ANATNPEX*

1863	9914	A	2811	1	932	KAKSRSEVGLASRPRRRGSSRGSSRCG SALALALLALRPGPGPAPAMEKTELI QKAKLAEQAES/RYDDMATCMKAVTEQ GA/QSLANEERNLLSVAYKNVVGRRS A\WRVSKHPSRKTDTSDK\KLQLIKDYR EKVD\SE\LRN\CTTVLGICLDKYF/ILANG NLIPESK\VFY\KMKG*FTFR\YLCLEVA CC\DRK\QTIDNSQGAYQEA\DISKK\E MQPT\HPIRLGALLLTFV\FYIE\LNPE ACLHAWLKTA*WRAIA*LDTLNEDSY KDSTLIMQLLRDNLPLWTS\DSAGEECD AAEGAEN
1864	9915	A	2812	199	214	PPSPLNSSTCCLAKTDEK*CKEKGSHLLH
1865	9916	A	2813	1	2176	QGPKLFMDAGIE\FSQDEWKCLDPAQRT LYRDVMLENYRNLVSLGICLPDLSVTSM IEQKRDPWTLQSEEKIANDPDGREGICKGV NTERSSKLGSNAGNPKCKNQLGFTFQLH LSDLQLFQAERKISGCKHFEKPVSDNSSV SPLEKISSSVKSHLLNKYRNNFDHAPLLP QEOKAHIREKAYKCNEHQVFRASASLT NQVIHNADNPYKCECGKVFSCSSKLVI HRRMHTGEKPYKCHECGKLFSSNSNLSQ HQRIHTGEKPYKCHECDKVFRRSSSLAQ HQRIHTGEKPYKCHECDKVFNQIAHLVR HQKIHTGEKPYSCNCKGKVFSRHSYLA HQT\VTGEKPYKCEECGKAFSVRSSLIT HQLIHTGRKPYKCKECDKVFGRKCFLTS HQRIHTRERPYGCSQCGKIFSQKSDL*R HRK\THTDEKPYNGNCKGTA\FREFSDLT HFLIHSGEKPYECKECKGVFRYKSSLTSH HRIHTGEKPYQM/CNRCGKVFRRSSNLV CHQKIHTGEKPYKCNQCGKVFNQASYL TRHQIHTGERPYRCSKCGKAFRGCSGLT AHLAIHTEKKSHECKECKGIFTQKSSLTN HHRIHIGEPYKCTLCS*GLSVTILTLHSF RGFHHEGPYKLC/DGKTIIMSSSINHQ* VHTKWYSYK*NVC\DTGFIKACQITGHHH ITVEDESTQMNCVYLGYYSR\TIAIEHDRI YTRSNSVSGSLILIYDIA
1866	9917	A	2816	26	736	EPIPVTPDHLVMTMTHIVANLLSCQQRPR LPNYEMLKEEQEVAKLGAPQKPCLP PPVIHNRN\TSPDHVRLVPVQ\HPLHE HLLRLGFIRFA\YSVKSRLDRKMVGEVN RGPKA*CLHRQSA*KIWGP\DFG\HLHEPI LAHQSSPPKFVWVPGPANDREASLRPG ALPVT\CPRTLASSIPRPAPRGQEVLP\TCI PLTPPSIPRPVPTAES\CSPLSSHAFLQWH SIKCICFW
1867	9918	A	2817	748	1637	DIMESGFTSKDTYLSHFNPRDYLEKYK FGSRVHSAESQILKHL\KNLKF\UFLADG VEGETCLNDIGFWAPLILSSSSCFVESF* GRIVRSLDYFR\TQEPGRELGRKWLEGKE ARGLFDWVPPM\VTMCLNLERETE\VKG PRRRRK\KLQ\AVKARCLKM*M*TQKPS HLGAVPL\PPG*TA\VPQ\AHLCLGCP\PCPR PPQPTCKGASGTLGQPYLKPRG\PSLVIM DAAQE\QPTYMIGE\QKFS\SLPLGREAVK A\AVKEAGYTIEWFEVISQSYSS\TMANN EGLFSLVARKLSRPL

1868	9919	A	2818	1	1538	MENPIVKS LAKARERLEDSKLEAVSDNN LELVNEILEDITPLINVDENVAELVGILKE PHFQSLLEAHDIVASKCYDSPSPSPMNN SSINNQLLPVDAIRILGIHKRAGEPLGVTF RVENNDLVIARILHGGMIDRQGLLHVGD IIEVNGHEVGNNPKELQELLKNISGSVT LKILPSYRDTITPQQVFKCHFDYNPNYND NLIPCKEAGLKFSKGEILQIVNREDPNW WQASHVKEGGSAGLIPSQFLEEKRAKAFV RRDWDNSGPFCTISSKKKKMMYLT RNAEFDREIYEEVAKMPPFQRKTLV LIGAQGVGRRSLKNRFIVLNPTRFGTTVP FTSRKPREDEKDGQAYKFVSRSEMEADI KAGKYLEHGEYEGNLYGTKIDSILEVVQ TGRTCILDVNPQALKVLRTEFMPYVFI AAPELETLRAMHKAVVDAGITTKLLTDS DLKKTVDDESARIQRAYNHFDLIINDNL DKAFEKLQTAIEKLRMPEQWVPISWVY
1869	9920	A	2819	1	1749	EFVLNYEPRVCRWGCSAAPVAEGEQRR RGATGSGGSGGAEAAEVRAAMQQVLEN LTELPSSTGAEEIDLIFLKIGIMENPIVKS AKAHERLEDSKLEAVSDNNLELVNEILE DITPLINVDENVAELVGILKEPHFQSLLE AHDIVASKCYDSPSPSPMNNSSINNQLL PVDAIRILGIHKRAGEPLGVTFRVENNDL VIARILHGGMIDRQGLLHVGDIIKEVNGH EVGNNPKELQELLKNISGSVTLKILPSYR DTITPQQVFKCHFDYNPNYNDNLIPCKE AGLKFSKGEILQIVNREDPNWWQASHV KEGGSAGLIPSQFLEEKRAKAFVRRDWDN SGDELDTIKFDRHEIYEEVAKMPPFQR KTLVLIGAQGVGRRSLKNRFIVLNPTRFG TTVPFTSRKPREDEKDGQAYKFVSRSEM KADIRAGKYLEHGEYEGNLYGTKIDSIL EYVQTGRTCILDVNPQALKVLRTEFMP YVVFIAAPELETLRAMHKAVVDAGIHH PRL*PNSDLKKTVDDESARIQRAYNHFD LDPSINDNPRPKPFELQTAIEKPENGPP QWVPQSAWVYLMIQ
1870	9921	A	282	1466	2353	RNVHLNLLIHFIYFKINVFHIDFPLGGEK NSGVLGFQAVQKQPRGSFFLPRIPQ*QN LRIGI*KGRRGPGSGWPAGDTQHPK GKGLPPLPACPSL**QQGRRCSGPGGRL GS*GCKHPECQWSQRGVRPLSVPLFQPP PGTGAGPTSWASASGSGAGACQPGS/PL GSVHTGSPSQAKSPPSRVK*QECQHPTH VSSPVSRPFGPKLPAGNRAGPAAPSPP RDTPAAPPPRPGPPSPGSLAQDAPGRSLP PPRTRRPAAQSPRPRSAESEAAARRGPVR RSRTGREEKSG
1871	9922	A	2820	14	230	FATLYPLKIFIFPKAFNPWREVGLCPPPK /CKGPSKSPGW/CLNRPPIGKKLIPCKPR LTWAPPRIL*NGPP
1872	9923	A	2821	170	303	RPLRGTPC*CAAWASSWWGCCSACCSH CCLLGPCWHSGPCSA*WAFWCSSG
1873	9924	A	2822	208	547	AAPGAMGPWPDRLCGSALPSCRLPCYSS ASVSLRCAAENTFTQAGPCCWAWPHRA HQDFPLQIPFRHLEAPRCSPPLSAWPPRH LLPAGDPDLQEQPPGIRGAP*RPLRGTPC CGSICGVAAGVRGCGPVWL*HPEPADSH TATAEPRI*AAPGAMGPWPDRLCGSALP SCRLPCYSSASVSLRCAAENTFTQAGPC CWAHPHRAHQDFPLQIPFRHLEAPRCSP PLSAWPPRHLLPAGDPDLQEQPPGIRGAP LSLRRLLL
1874	9925	C	2823	48	173	MVRKRMEMKMRKLSQLRASQGLKMM RMXMSIPRSRRPRGIX*
1875	9926	A	2824	183	423	

1876	9927	A	2825	147	588	TLAFFLIPCIGSPACPTMSDAA\VDTSSEIT TKDLKEKKEVVVEEAENG/REDRPCLTG NAENEVENGEQEA*QLR*DEE/EREGRIG REGGREGRKEG*LVEEEDGRLKIEEAES ATGKRATEDDEDDDCRYQSRRPDEDD LDSKKAKS
1877	9928	A	2826	1	77	SGRPFFFFFFF*CKGFLIGYM
1878	9929	C	2827	175	351	MKLIQLSCQPFNSRHHVLKKPLTFMILS HFQASLSSIFGFCSSLFRQSSFFSNILFF*
1879	9930	A	2828	56	380	KYLVDQHAGSPPVKNILAEAVQNIVQIL H*EIQKSVNHRYML*KLDTDSL**FIIQLQ EPTILGIKVDVYKHEYKDKDGHSDFSNY SSHQVFFLLIFNKNMAIN
1880	9931	A	2829	3	129	
1881	9932	A	283	134	385	CQIMDGMLAIQAWPTPQQVASNGTGLN PNAKVWQEIAPGNTDATPVTHGTSSW HEIAATSGAHPEGNAEPQKIYVKNMK*C I
1882	9933	A	2830	472	756	SSADSKCTLTIGKPAKSRVQLCHKEETFP NQTNAYRTCVD*CLMSPTLLGTSIF*SQ MIIRVVPICMPNIFLIISC*VLCIRKPVSEL PHLLGF
1883	9934	A	2831	1	170	
1884	9935	A	2832	1243	5595	
1885	9936	B	2833	2177	3174	MGKTTPMIQSRPSFDTWELQVPPSTCGD YNSSFIKELRASQSNVIKPPGPVKLKESV VENHAVLSYAVEEEHAYLGPTVKPDDK AKTLYEPLSSATVSTGSLSYENTDLSL TDPESFSEHMDDSKQESTTSKEEETNISS IVPSTQDIYQRQNSSDVHKSLLPAVDETT CGHTHFQQMIDKALYQSGKPETGHGIME EPELTLISTTDTSAEMDFANLTLEEKSEN EAKCFFQQSKTRLKRLKRVKHATFLPLA TEASDYPVSELSIEKPRTASTETPRRLTP VPGSLQEAFIGRKKSMERSHQRQKEIR NKIHVSENSQIKTVKEKPSISSIL*
1886	9937	A	2834	2268	2547	KYLVDQHAGSPPGKSLCCLEKSQORMMM ISQNLDVVLRV*TADDAN*EKCVPILANL FFQVSNLLH*WLVYHLLKVCVTTCFSIH CRQQRFMNV
1887	9938	A	2835	137	716	TTTMSSKKAKTKTTKKRP\QRATSNVFA MFDQ\SIQGVQRGPFNMIDQNRDGFHS DK/EKVLHMDLA\SLGKNPH*WHYLD MMNEAPGPIQFSPCFL\TLFG*GSLNGHQ IP*RCSFRKRLAFALDEEATGHPFREDYL /RELLTNPWGDRVYQIEEVG*TCTGEAP I*QKGGNSNYHRSFTRHPNWKAPKAQR
1888	9939	A	2836	2	437	LVIIESDLERAEEAELSEGKSDSWKNN* E*WIRP*KH*WLQRISKCAELEELKTVT NNLKSLEAQAEKYSQKEDRYEEEIKVLS DKLKEAETRAEFAERSVTKLEKSIDDLE DKFLCFTSPKTPSSWMSHLSELICLFFS
1889	9940	A	2837	1	834	GSRVRRAAAGLSHCSPPARLP SGAMAGS SSLEAARRKIRSLQEQADAAEERAGTLQ RELDHERKLRETAEDVASLNRRRIQAW FEEFVGFPKERLATAF\QKLAEAEKAA DESERGMKVIESRAQKDEEKMEIQEIQL KEAKHIAEDADRYEEVARKLVIIESDL ERAEEAELSEGQVRQLEEQLRIMSDL KALMAAEDKYSQKEDRYEEEIKVLSK LKEAETRAEFAERSVTKLEKSIDDLEKV AHAKEENLSMHQMLDQTLLELNNM

1890	9941	A	2838	9	1108	PDRATRPRPRARPADPALVLGPLAAVTM GAGKKKMRMLKLDKENALDRAEQAEA DKKAAEDRSKQLEDELVSLQKKLKGTD R*TGQIL*RLSKMPKEETWNWQEKKATD AEADVASLNRRIQLVEEELDRAQERLA TALQKLEEAKEKADESERGMKVIESRA QKDEEKMEIQEIPT*KRAKHIAEDADRK YEEVARKLVIIESDLEPCRGSGAELSEK CAEA*KEEFENL*PNNFEVHLEGSRLRK YSQKERPDMEEEIKGFPDKA*RRLETR AWSFAERSVT*NLEKSIDDLEDRAVTL QETEVQSHQRRSWDHALNGYDFHISFFA SLLPRLPRRSWMSHLSELFHLSYSPADPG SLS
1891	9942	A	2839	3	268	
1892	9943	A	284	305	1129	DICKEYEVMYSSSCETTRNTTGIEESTDG MILRPEDLSYQIYDVSGESNSAVSTEDLK ECLKKQLEFCFSREKLSKDLYLISQRSD QFIPIWTAANMEEIKLTTDPDLILEALRS SPMVQVDEKGEKVRPHTKRCIVILREIPE TTPIIEVKGLFKSEYCPKVISCEFAHNSD WYITFQSDTDAQAFKYLRKEVVKQFKA RPILAGIKAINTFFC*EWSNNGILESIVHP I*TQAQYASPVFMQPVYNPHQQYSVYSI VPQSWVSKSYTLL
1893	9944	A	2840	500	682	
1894	9945	A	2841	1617	2086	GLAASSRKHQMVDADAVGGPGGPGM AGCDGLPGGFGSDIRPLWLWLGPRLW SS*RGTNILASVPKKLLM/DCYALARD RTATLGTFDAISKTASNWIPDLWKETVF TKFPYQEFTHL/VKTHTRVSKQKTQVP AVATTAARQTMEGQAPVEYI
1895	9946	A	2842	55	665	AMAEDHGLSNGDGPVEVTQGLELLVSA AAQDIVLLDGIQGLFTLQFDNIWVWDH FLGKLPHRVFKGGGEKQHLAVPGQHPL DADALILVALSGYHDISLIQNKHLDLGI NELDLEHQSSSTVPGVPMTCISLIFWPLSN LLPRTA*ASFSSG*NLPCSITFPV*SASSY VGERHRHWGYLSDGSTRLSMAKTKAA VLPVPD
1896	9947	A	2843	43	548	
1897	9948	A	2844	1	876	
1898	9949	A	2845	222	482	
1899	9950	A	2846	3	218	SLFQLKTTKTQSRVMGAIYDSSWFQEDR QAAERFTDRSTHLRLRNAEAAA*TKPAQ GPGSIPILPATPSSL
1900	9951	A	2847	322	452	LCCSI*IYLN/NLLIC*QSFSVLK*DFRVD* KKKNPRMSHRVLNI
1901	9952	A	2848	3578	5288	TESREHFSPWYSVTAARRPQVASKAEEN LLMVLGTDMSDRRAAVIFADTLTLLFEG IARIVETHQPIVETYYGPGRLYTLIKYLQ VECDRQVEKVVDKFIKQRDYHQQRHV QNNLMRNSTTEKIEPRELDPILTEVTLMN ARSELYLRFLKKRISSDFEVDGSMVS*E VKQEHQKCLDKLLN*LAFLSCYHGRELI GLYVTMEEYFMRETVNKAVALDTYEKG QLTSSMVDDVFYIVKKCIGRALSSSIDC LCAMINLATTELESDFRDVLCNKLRMGF PATTFQDIQRGVTSAVNIMHSSLQQKGF DTKGIESTDEAKMSFLVTLNNVEVCSENI STLKKTLSDCTKLFSQGIGGEQAQAKF DSCLSDLAAVSNKFRDLLQEGLTELNST AIKPQVQAWINSFVSFHNIEEEFNDE ANDPWVQQFILNLEQQMAEFKASLSPVI YDSLTLGLMTSLVAVELEKVVLKSTFNR LGGLQFDKELRSLIAYLTTVTWTIRDK FARLSQMATILNLERVTEILDYWGPN GPALTWRLTPAEVRQVLALRIDFRSEDIK

						KAALVS
1902	9953	A	2849	233	801	VVTLTGSNLYFYCSLFIFSVLDPQDVSLV *ICYLSLPLDIVCFNCVKIOFFFLSLESYY *FLTIFPHCFYLLKTPFKHRELFILVFGL LKIFQ/LC*FFYLILLRIFYFINFCFLDLF LFWIFIWYFVIFACSWFIGVSLKFLLVPL/ CSFFLRCRHSPLF*GAS*TDLYILGCIPFP* VCLLWEFCGGL
1903	9954	A	285	1053	1403	TFTQDSAGSLVVHSPMTSIWKTAESVDQ GHFPIIILFVYLLFETGSHSVTHATMQW CDHSSLQPQTP/SGSGDPPTLAC*VPGIIG MCHHTWLIFTFAETGSHHVPRLVSNP LA
1904	9955	A	2850	170	494	
1905	9956	A	2851	70	1474	RESGTWQPGKAGTQTGAKFWEVISDEH GIDPTGTYHGDSDLQLERINVYNEATG GKYVPRAVLVDLEPGTMDSVRSGPFGQI FRPDNFVFGQSGAGNNWAKGHYTEGAE LVDFVL\DV*RKEA\ES*DCL\QGFQLTHS LGGGTGSGMGTLISKIREEYPDRIMNTF SVVPSPKVSDTVVEPYNAILSGH\QLVEN TDETYCIDNEALYDICKTLKL\TPPFG DLNHLVSATMSGVTTCLARFPQQLNADL RKVAVNMVPPFRLHFFM\GGFAPTDQA GASQASTRALTVPRSSPKQ\MFDA\KNM MAACDPRAWAAYLDGLPPCFRGPHVPL KEVDE\QML\NVQKQKQPAIFVE\WIPQQ CEKRAVCDIPHLRGLKNVRPPSFGKQAR PIPGAFSKPHLPKQFHGPCFRRKALPSFIT GGEGMDEMEFHPRPESNKNDLVSEYQ\ QY\QDATAEE\EGEFGRSLGRKVA
1906	9957	A	2852	284	359	QQEANPSAPLQHVSTSN/CVLTCCCKGA EGLASCCYCHCLCNECCQGACGPDTHL AHCCRCQHSSKPPGGPRI/ASTQTCYY*C PCRLPGGSRT*CLASCPYHWCPWTSPLG SPVPNKAPP
1907	9958	A	2853	295	478	
1908	9959	A	2854	1	1167	

1909	9960	A	2855	3	1328	SGILGTTTPSPFVGVVLRVECPCLCPGPAP MSVPAFIDISEEDQAAELRAYLKSKGAE ISEENSEGGLHVDLAQIIEACDVCLKEDD KDVESVMNSVVSLLLILAEPAKQAEALIE SLCAEKLGNFREGEPRLRLQFVKATF STGMD*EILPVKIHVSICSLVKVAAASCGI AIQYHPQLEPGIKFRKWDFLNWNLTG KKSTPLLKTTFMKALVDCCKSDAASKG MVELLGSYPGGQCPRARVDAHRACIV RALKDPNAFFPDHLLTLKPRQVFWKGE LI/HIVPF*PNFVSA*MGHHMSRFYPD*LR TFH*IPLGPVTMDPGIWPKMRLFLW MGQ*ENRÆISFWTTMPARNFRIGADDV EAFVIDAGKELKMVYQONWSRPQRKV VSHSTHRTFGK\QQWQQT\YDTLNAW KQNLNK\VKNSLLSPSGYLKFLCL
1910	9961	A	2856	377	2393	FSLECLGHENR*D*ITIYKITS LGTGKVF KIQHPFTIKKK*KTLNKLIEGNFLNLK GIYEPMVSIILNGEGLDYFPLRSETRQG CLLWPFLFN/IVLDSQERAIRQENKIKVI* VGKEEV*LNRMGDDMVVLCIVIQKVI* KIQRHDLINKFSKVTGYRI/NICRKLVI HI*YQLNKSQNDVKKTI*FSTMVKLGGL C/RVIPTLWESEAERLLEARRPAWETVRS HLYKNKQTKNNKQTKN/TLDVMTLICRL SYSEAEV*GWLEPQSSKLQ*AITGSLQSS LDRQS*TLTQKKTKKKRKL TASERVKY QYN*GSRNID/PHLSSN*LLENSA*GQFQ WGGKIVFFIK*CLETWISTWQNNGNWDS YLILHIKINSELT*DLNVRANIVSIFKEN/M GVNLSDFELGNDFLNK*/PLKTQATKEEN R*IKIKTICVSKDNKKAKIQPTE*DNFF*N HVLVKGGICI*NM*RTVTIHKRHIIQFLKI QQGVWN*QFSKGGYTKGPLRHMEKVSQ PSLAIREMOMRSTMRHYHTPLE*YINQS DNIKCW*GCREIGTLMHCWWYPRDIKT NVYTKTCAQMFLPALFI*AQK*NGP*FLS \LTSALTKTWHIHT/MEYYSSQ*KKEMKV LIWPPTTMEKPLEKPYPSEECPRHERPTY YMISIYMKCPRTGEYI
1911	9962	A	2857	3	445	GEFADSF/SSMGSPVNAQDFCTDLAVSSA NFIPVTVAISTSPDLQWLVPALVSSVAP SQTRAPHFPGVPAPSSGAYS RAGVVKT TGGRASIGRRGKVEQETDQLEDEKSAL QTEIANLLKEKEKLEFILAAHRPACKNPD DLGFPE
1912	9963	A	2858	295	1622	DEMSVAGSFLFTAACGTGNSPHLCPEHA RSRRLSPSVLF*DFCTDLAVSSANFIPTVT AISTSPDLQWLVPALVSSVAPSQTRAP HPFGVPAPSAGAYS RAGVVKTMTGGR \QSIWQEGARWEQVRNF*RTLPGNVGAG WEAAPEMQEPSTEDEAT*WGLLAHP*LG ALAPSPFHPNSDSEFSP*EVLS*FLP*VSY RMLSDWALLCSLAEDLILNASHT*SATA GQKWFHSGVPGSREAAGASSTGVGEWR *WQTLNVLNGLFL*LF*LSPEEEERIR ERNKMAAAKCRNRRLTDTLQAGRY VGCSFLKLKGKVGRLHKG*VRLCLYA FPLSLCQ\ETDQLEDEKSALQTEIANLLK EKEKLEFILAAHRPCLARFPDGPAGFPE EMSVASLDLTGGLPEVA/TPESSEAF/TLP LLNDPEPKPSVEPVKASA

1913	9964	A	2859	3	1467	PHLQRATEKPRLSRRPRRSEAVTVLLPS SASQRPPVSAPRPLARLCLTATMMFSGF NADYEASSSRCSSASPARD\SLSYHSPA DSFFSMGSPVNAQDFCTDLAVSSANFIP TVTAISTSPDL\QWLVQPALVS/SLWAPS QTRAPSTFSESPPPTAGAIYSRAGVVKT TGGRASIG\RRGKVEQLSPEEEEKRRJR R\ERN\KMAAAKCRNR\RR\ELTDTLQA\ ETDQLED\RK\SALQTEIANLLKEKEKLEF/ LSLAAHR\PA\CKIPLIDLGLPRKE\MSVGS \DLTGGLPEGS\TPESEEFTLPLNDPE AQGPQWEPVQGGISRHGS*KDRGPFDDF LFPSIHGPGSGFLRTARSVPDMGPILGPF YGRQIRGAFSHSGSLGMGAHGHRGWEP LCTPVVTCTPSCNCLHVFPRFHLPRG*LL PQLCSCPPQGGQQQ*AFL*LAQLTHAAG PVRGQGRGGSRHPQVPLPELVHYREEKH IFPRGFL
1914	9965	A	286	259	506	PGYRRGHGGAEGRQEPAAHRNPVRE DADGGD/RPRSAACPGTSTAPPGT*GS\G QAHRDGARPAAPRPSHPSAGPAAGPSG
1915	9966	B	2860	1	196	MAEGNHRKKPLKVLES LGKDFLTGVLD NLVEQNVNLNWKEEEKKKYYDAKTEDK VRVMADSMQEKQX*
1916	9967	A	2861	1	988	MGSLEGNHRKKPLKVLES LGKDFLTGVLD DNLVEQNVNLNWKEEEKKKYYDAKTED KVRVMADSMQEKQRMAGQMLLQTTFFN IDQISPNKKAHPNMEAGPPESGESTDALK LCPHEEFLRLCKERAEEIPIKERNRTR LALIICNTEFDHLPFRNGADFDITGMKEL LEGLDYSVDVEENLTARDMESALRAFAT RPEHKSSDSTFLVLM SHGILEGICGTVHD EKKPDVLLYDTIFQIFNNRNCLSLKDKPK VIIVQACRGANRGELWVRDSPASLEVAS SQSSENLEEDAVYKTHVEKDFAFCSSTP \KYSWCCHLEEVFRKHCSQ
1917	9968	A	2862	12	914	GSFQRCKKGQRLFPMAEGNHRKKPLKV LES LGKDFLTGVLDNLVEQNVNLNWKEE EKKKKYYDAKTEDKVRVMADSMQEKQR MAGQMLLQTTFFNIDQISPNKKR**IGVTE AEITTYVLQYPAAHPNMEAGPPESGRIL PDCLKVLCPHNEEFLRLCKERAEEIPIKER NNRTRLALIICNTEFDHLPFRNGADFDIT GMKELLEGLDYSVDVEENLTARDMES ALRAFATRPEHKSSDSTFLVLM SHGILEG ICGTVHDEKKPDVLLYDTIFQIFNNRNCL SLKDKPKVIIVQACRGGEC
1918	9969	A	2863	12	1353	GSFQRCKKGQRLFPMAEGNHRKKPLKV LES LGKDFLTGVLDNLVEQNVNLNWKEE EKKKKYYDAKTEDKVRVMADSMQEKQ RMAGQMLLQTTFFNIDQISPNKKAHPIM EAGPPES\GESTDALTLCPHEEFLRLC*RK ELKEIYPIKGRRKQPHTAGLFF\ICITEFDH LPPRNGVADFDITGMKELLEGLWDYSV GVGRRFLTARGMDSALRAFATRPEHKS SDSTFLVLM SHGILEGICGTVHDEKKPD VLLYDTIFQIFNNRNLPQV*RDKPQGSSI VQACRGANPSGN*WVRDSPASLGKW PSSQSSGEPWRKDAV*QDPHV/ERRDFIG FPGSFKRPHNRAPWERPAQWGSIFITQLI TCLPRNIPWCC/HTLEEVFRKGTAIHLETP R\AKAQMP\TIERTVR*QGYFYLFPGEFE NWEHGKQSPSLNPTFKEAPFFVTACIF
1919	9970	A	2864	66	392	
1920	9971	A	2865	131	551	KIRGVSCPSAPKSGEQTQGHNNINTGFHP LPLGAVTSPVPQGGDRLCPPSSPEPAQ PAQ/C*PCSDSGRSPGPGKAWTVAPC PEPSVFCLQSPGFEPWVLAHPPSSERR ASSSGLDDDLPAQETGNGSGATRTCS

1921	9972	A	2866	943	1109	LMVLSDFIFKLI/WPGAVAHACNLSTLG GRGRWIT*GQQFETSPASIVKPPSLLKI
1922	9973	A	2867	112	1078	ESSRQALLAKPLSACAEQPARAEVGAAT ALPVRWASGEMAPSGSLAGPLAALVLV LWGAPWTHGRR\TNVRVITDEM\WRELL EGDWMIEFYAPWCPACQNLQPEWESFA E\WGEDLEV\NIAKV\DVTK\QPL\SGRFII ITALPTIYHACKDGEF*AVIQGPRTKKDFI NFISDKWKSIPEVSSWFGPGSVLMSSMS ALFQLSMWIRTCHNYFIEDLGLPVWGSY TVFALATLFSGLLLGLCMIFVADCLCPSK RRRPQYPYPYPSKLLSESAQPLKKVEEE QEADEEDVSEEEAESKEGTNKDFPQNAI RQRSLGPSLATDKS
1923	9974	A	2868	1	448	
1924	9975	A	2869	1	536	
1925	9976	A	287	1	2072	FRRSPSPAASVSLGLGVAVVSSLVNGSTF VLQKKGIVRAKRRGTSYLTDIVWWAGTI AMAVGQIGNFLAYTAVPTVLVTPLGAL GVPPGSLASYLLKEKLNILGKVGCLLSC AGSVVLIHSPKSESVTTHAELEEKLDQS RVGGLPCASLLVMLAAAHLLDPCRPMG PPTSWSTSASAPCWADTPCLPPRASGWR PKTSCITTRPVREPSACAWYSWPCSA SSSSSGTRNKALECFDSSVFGAIYVVFT TLVLLASAILFREWSNVGLVDFLGMACG FTTVSVGIVLMRVFKEFNFLGEMNKS DTWRQSSPLIVAPRDHFHLERGVOFQNM NSVMGSHLVMVALSPGVDFIPQDDPAA LLVTELFANRLVSGYAPATGLQGILQY GNTLMEVMPKICRLPRHECGSPGPGSC APPPSPHSTR/RRPPRSAD/CGPCKGTGTR RERAPGAG*AEAAGPGEVGVGAGAANA GAGAADAGAGGADAGAGGAGAGAGAGG AGAGAGGAGAGAGGAGAGAGGAGAGAG AGGAGAGAGGAGAGAGGAGAGAGGAGG GAGAGAGAGAGGAGAGAGGAGAGAGAG GGAGAGAGGAGAGAGGAGAGAGGAGAG AGAGGAGAGAGGAGAGAGGAGAGAGAG RAGAGAGGAGAGAGGACAGAGGAGAGAG AGGAGAGAGGPVAGAGGAVCSQTIFTR SHGGLHLWRPC
1926	9977	A	2870	1	5193	
1927	9978	A	2871	1	356	
1928	9979	A	2872	1	401	
1929	9980	A	2873	151	5459	AGARRRGRGGEAPLLPGLAAAEPPRAR PDGLAEPVVRGRRVGSGRPTMSAKVR LKKLEQLLLDGPWRNESALSVELLDV LVCLYTECSHSALRRDKYVAEFLEWAK PFTQLVKEMQLHREDFEIHKVIGRGAFGE VAVVKMKNTERIYAMKILNKWEMLKR AETACFRENRDVLVNGDCQ\WITALHY AFQDENHLYLVMDYYVGGDLLTLLSKF EDKLPEDMARFYIGEMVLAIPIHQLHY VHRDIK
1930	9981	A	2874	1	764	MEKIPIRLSLRAREQQAGKDVTLQGEHQ HLPEPGCQQTVPVSVGRRPPDTPGPETNS MEAAPGSPPGEGCPACSRCLRWEPPPGR PCE*PEESPAGT/PAPCPCGSPG\GPAAQS LPPLPG/PLPQSRPSA\SGPAPGHRHPEG GAGQAAEGQ\GPRGQPRSSLQTSP\PRPL AAPVPM\PRGLAWQDVSEPP\GCSGL NSSQKSPLSERPGPPVSGE\GP\DGSSHS AQRLQPPNRAGSGLESVSVSLEGQSRGA RD

1931	9982	A	2875	1	1641	MKVCSSIAEVSDDTNPPSRNTHGHTSV LKQALKDPCRTRHYRLVLTLETEVL DLFIERFCMTGGNSPICYLKAYHTNLYLS ADAKEVREAIDEGIAAATIFSPSRDVVVS QSQLRVAFDGDVLFSDSERIVKATLD RFFEHEKAHENKPLAQEQGSTSFPDKVE AFRSPSVPLPITGHSANVYQTPTCARRRT TRPLVNWELIPRDNPPLPRAFRDLGQS PAFSDAVATTSAVPPFGDCHLSEVRGAE TRQPAFAMKRPKEPSGSDGESDGPIDVG QEQQLRSSKLEKAEVLQMTVDHLKMLH ATGGTGFFDARALAVDFRSIGFRECLTE VIRTPTIWLLPGRSKAVESQSQFTGAHS TLGEPTAKKVA*SNPQVYMDIKIGNKPAG CIQTLRLSDVVPMTTENFLYMCTH/SKGL GFKGSSFHRIIPQFICQGSDFTNHGGTRG KSIYKKKFDDENFIFKHTGPGLRRHGTK CPMAHLALMEASKGQDQHPLLRKERA QQVHDVVKLTRGRGRGISLKRIARSLCK DKETGLCTLTWH
1932	9983	A	2876	1	949	
1933	9984	A	2877	185	339	
1934	9985	A	2878	673	1085	GEPTAKKVA*SNPQVYMDIKIGNKPAGCI QTLRLSDVVPMTTENFLYMCTH/SKGLG FKGSSFHRIIPQFICQGSDFTNHGGHQGS AQVHGTKCPMAQFGPHGGLKRAGPAPSS TGKERAQQKQGESAITSQPRSWKLT
1935	9986	A	2879	141	1959	PRPANLLKKGQITMSATVVDVNAAP LSGSKEMSLEEPKKMTREDWRKKKELE EQQKLGNAPEVDEEGKDINPHIPQYISS VPWYIDPSKRPTLKHQRPOPEKQKQFSS SGEWYKRGVKENSITKYRKGACENCG AMTHKKKDCFERPRRVGAKFTGTNIAP DEHVQPQLMFDYDGKRDWRWNGYNPEE HMKIVEEYAKVDLAKRTLKAQKLQEEL ASGKLVEQANSPKHQWGEENPSQTEK DHNSEDEDEDKYADDIDMPGQNFDSKR RITVRNLRIREDIAKYLRNLDPISAYYDP KTRAMRENPYANAGKNPDEVSYAGDNF VRYTGDITSMGQTQVFAWEAYDKGSE VHLAQADPTKLELLYKSVFKVKKEDFKE QKESILEKYGGQEHLDAPPAELLAQT EDYVEYSRHGTVIKQGERAVACSKYEED VKIHNHTHIWGSYWKEGRRGNKCCHSF SKYSYCTGEAGKEIVNSECIINEITGEES VKKPQTLMEHLQEKLEKKKKKKKKKK KHKRSSSDSDEKKHEKLKKALNA*EA VRLHVKETMQIDERKRPYNSMY*TSR PJEEMEAYRMKVRQRPDDPMASFLGQ
1936	9987	A	288	1	390	ITLGPDSIIGIWSGNQHKQDPYIASMEHH TDWVNDIVLCCNGKTLISASSDITTVKVW NAHKGFCMST/YKDT*ASSLSGNKDSIYS LAMNQLGTIIVSGSTKVLRVWDPRTCA KLMKLIGHTDNVKAALL
1937	9988	A	2880	711	1140	GVGVCFPPVPSSRLRVLGRWAFCALPGR SLRKSRLWGWGTGHTQS*EGELPWKAG/ WQRCFWRGGRQTLPLTCSPTTRGCRA AQEGAGCKARGAWWVRSRGRAGRPLR RGGSRVTLNSQMGSDATGETEWIKEMK PKKKKKMS
1938	9989	A	2881	1	649	MAGALVRKAADYVRSKDFRDYLMRVT QQPYKVFNSGPWAFSSSSYSRPSAHISS LIVSRVGSSTSFQGGGLGAGMGVEPLDP HENLYVDFYRGFHNCQNLEANKMSFG RSQSEKAAAYLVPTTQRSKGKIMELVE RSVVARVEHFVGPVANWGLPIAANDM KKSPEIISGRMTFVQPRNWLLFACHATN EVAQLIQGGRLIKHEMTKTASA

1939	9990	A	2882	1	389	
1940	9991	A	2883	27	554	LAVGCRGVGLGVIGSGKRQQRQGLGV SVSAQPCAGALVRKAADYVQSK\DFRD YLMSTHFWGVPANWGLPIAINDMK\ KSPGDYSVGRMTFALC\CYSLTFMEILP YKVQI*PLNWL/LCFACHGTNEVRPSFIQ GEGRLIPNTRMDLKRASGINQWGKGKN KVFEGLSLCPGCC
1941	9992	A	2884	1	162	QCAEKIASNPKIVVAMAKESVNAAFKIT LPEG\DDRKEGMPFVEKRKANFKDQ
1942	9993	A	2885	1	196	
1943	9994	A	2886	148	427	CLLGFTHHSASHDQPLPAGAGGTQRLTR AVGKSLAMEMVLTGDRI SAQDAKQAGL VSMICAVETL*CLLGFTHHSASHDQPLPA GAGGTQRLTRAVGKSLAMEMVLTGDRI SAQDAKQAGLVSMICAVETLVGGAIQC AEKIASNSKIVVAMAKESVNA
1944	9995	A	2887	1	1484	EATLTRPRPAGGPAAGWYCPSAKTSGQL GAGFTFSPLERHCPLSPSHLAVHPAGAGP VQQANREAPASPIFGLACCSGPVVDLNA AGTPRIFTSPLRPLARGANFEYIIAEKR GKNNTVGLIQLNRPKALNALCDGLIDEL NQALKTFEEDPAVGAIVLTGGDKAFAAG ADIKEMQNLSFQDCYSSKFLKHWDHLT QVKKPVIAAVNGYAFGGGCELAMMCD IHYAGEKAQFAQPEILIGTIPGAGGTQRLT RAVGKSLAMEMVLTGDRI SAQDAKQA GLVSKNCPF*DTGWKEAIQFAEKIASNS KIVVAMAKESVNAGRSPNLSECIYLEGV AVPRACRWLEAGYSEESILKERRLLSPE VFGKVVL PWERMLAPALEPQRLPPSAHL DLLCLASCKERAWNEQSQRSSWCRPRP ALALVLSFLVFI LGYFSLFAAPLPPHSLSS RAQFAISPFIQFLSLLGAVGYRSVTFGGH SRAVGSARSPLGQCL
1945	9996	A	2888	1	946	GRGVQRAMAALRVLLSCARGPLRPPVR CPAWRPFASGANFEYIIAEKRGNNTVG LIQLNRPLPVNWLCDCLID*LNQGLKIF EEDPAVGAIVLTGGDKAFAAGADIQ GK LQNLFSRDCYSSKFFGRHWGPPSPRVK KPVIAAVNGYAFGGG\CELCH*CVDIIL/ YAGEKAQFAQPEILIGNLPRVRGGTQED SPVPVGKSLAME\MVLTGDPDPQPQDA QASRVLSKICP\ETLVEEAIQCAEKIA\ SNSKIVVAMAKESVNAAFEMTLTEGSKL \EKKLFYFNLWPLDDRERRG*PRFVGKE KGPTFKDQ
1946	9997	A	2889	1	384	VRDYNLTEEQKAIKAKYPPVNRKYEYL DHTADV/QWIVLHRA*YFFRLHAWGDT LEEAFEQCAMAMFGYMTDTGTVEPLQT VEVETQ/GWGEEFSLSKHPQGTEVKAITY SAMQVYNEENPEVFVIIDI
1947	9998	A	289	1	1050	FRVNMQDGGPSPAEHSKAESAGMEAR FLGLPDAAGSSGPTPARRCPAPRPAGVS YVIRDEVEKYNRNGVNALQLDPALNRLF TARRDSIIRIWRVNQHKQDPYIASMEHH TDWVNDIVLCCNGKTLISASSDTTVKVV NAHKGFCMSTLRTHKDYVKALAYAKG* \ELVASAGLDRQIFLWDVNTLTALTASN NTVTTSSLSGNKDSIYSLAMNQLGTIIVS GSTKVLRVWDPRCTAKLMKLKGHTDN VKALLNRDGTQCLSGSSDGTIRLWSLG QQRCIATYRVHDEGVWALQVNDAFTHV YSGGRDRKIYCTDLRNPDIRVLICEEKAP VLKMELDRSADPPPAI

1948	9999	A	2890	1	332	RDYNLTTEEQAIAKAKYPPVNRKY*DDL QSLLFHFLDEWLYKFSADFFIPREVVKVL SIDQRNFKLRSIGWGEEFSLSKHPQGTEV KAITYSAMQVYNEENPEVFVIIDI
1949	10000	A	2891	3	425	SFMAQEEEDVRDYNLTTEEQAIAKAKYPP VNRKYEYLDHTADVQLHAWGDTLEEAF EQCAMAMFGYMTDTGTVEPLQTVEVET QVHADEFFIPREVVKVLSIDQRNFKLRSIG WGEEFSLSKHPQGTEVKAITYSAMQVY NE
1950	10001	A	2892	91	598	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTY LDHTADVQ*V*REFIPLKPRQ*ED*MFQS WLHAWGDTLEEAFEQCAMAMFGYMTD TGTVEPLQTVEVETQGDDQLSLLFHFLD EWLYKFSADFFIPGWGEEFSLSKHPQG TEVKAITYSAMQVYNEENPEVFVIIDI
1951	10002	A	2893	359	938	IYFFRLHAWGDTLEEAFEQCAMAMFGY MTDTGTVEPLQTVEVETQK*LVVLLF HFWDWLYKFSADFFIPGKLCIAIVF*K RL*RP GAVAYACNPSTLGSRGWIT*GQ EFETSLTNKEVKVLSIDQRNFKLRFN*GW GEEFSLSKHPQGTEVKAITYSAMQVYNE ENPGSFCDHWTFTKTTQKIKRLPTGKK
1952	10003	A	2894	220	345	LKKEKSLMEKHFF*QTDSSVSNLEKNHE PSDIVNSLQWAMVS
1953	10004	A	2895	1	281	
1954	10005	A	2896	83	425	
1955	10006	A	2897	1	3600	
1956	10007	A	2898	1	197	
1957	10008	A	2899	1	963	
1958	10009	A	29	376	610	FPAFWESQVRWIASASGVQDQPDQYGEI LFLKLQKLGGHGG/IR*EDHLSLGGQGC KEPRLYHCTPAWVTEHYLVSKK
1959	10010	A	290	1	366	FPNSSRLIWPECNRIKEESLVASPGSFCK PHLDLALGLGL/GVGLMVELGLKLGLFL GLGFDLGVGLGIGL/GVKLGLSDGY/GLG FRLGLGL*AGLVGLGIRVGLKPGLGLEI FVGLILCICI
1960	10011	A	2900	49	247	DLTRNHSPLQTVHDVRWFMIFQV*YRR IKFVKRNASPSGI*NII*TINTFVCIYK*IFR YKNMHI
1961	10012	A	2901	1066	1768	NPQSSSSESGR*DFPRLTVNRLLVQRSE VTQAPGQYTVDVEGHGCTFIQATLKAYN VLLPKKASGFSLSLEISKELLFDCF*P/RQ VNLQYTGIRNKSSMVVIDVKMLSGFTPN PCHPIELENKGQSD*SKNDPCSFY LENVFGQPDSPFFC*AEQPLCSTFQGP SHGLTDY*YEKEEYALAFYQHRTVVPVSE *DKAITRRVGEAISCNKLILLYQTWKKIM NHLTS
1962	10013	A	2902	620	1124	ETPAPCLQAWVPQACREGPLAFRELLGG VLALSTPGERCSVSSEFETRARTQ/PC WGSPKFLSPPHAKPAITLPELKEAPWP APSLGPPGGLSTPPSGIPCPQCCQGHVA LCRGLRPSPW*TE*PVCWKMPRCPEKLP PGIFGNETYLVPIVNWPTGTSEFSTY
1963	10014	A	2903	2	399	WKESQGRCEW*VARGL*ADLT*GFHWH LPGAPPWGLLTGGGQGRGHGHRGGWA LSGRPPRGFHWHLPGAPPWGLLTGGG QGRGHGHRGGWALSIGIPRLQSFQVWA ESPLPQLPWGCVAGISVHTGVSWLP

1964	10015	A	2904	73	867	GRAEQTSDTTASTSACSHNLTMSCPN YCSGNSNSGSLRTSRHIPLTSIDLCPSTVS CGDVL YLPTSSQDHTWVTDCQETCGE PTSCQPVHCETGNLETSCGS/SHC/CTTCP GPCQGSSFLPASFFSSCLPVSCRTTEVC/ RPAAVRPLRAVVQ*FTSP*GDCVAQCLAR PQFCLKSKCQPQNLLTSGCQPSSCLAYRP QSLHVVSSSLRPLGPLFSGCQPLTHVFST VSSHLALEHGSPNICFLQSSILLHRSSSRA VCSSALF
1965	10016	A	2905	1	478	
1966	10017	A	2906	800	1209	LFSSGAVPQRTSPHQAPKNMQTSGRLS/ NVAPP\CILRKNPPSARNGGWET*CPNSL NSNQQLVDLKLTVDGLEKERDFYFSKL RDIELICQEHESENSPVISGIIGILYATEEG FAPPEDDEIEEHQQEDQDEY
1967	10018	A	2907	1	3961	MSSKHLKSEQIKDQIRVPVISLIPKIHSAQ EEQLSSTAVCSCPARVFCVTKVVAVFQ MWMLHDLVQMVPRSLQWLPHIFTLFSN PLILYHSHELAPSFAEQRECKLAYMPVS SASAHLLQLAFDFNLSVLSLARNML ANSASVRILIKGGKVNDCTHEADVYI ENGIIQQVGRELMWRGQGLVIPGGIDT STHFHQTFMNATCVDDFYHGKVMLLF AKGGFLFGFILLGLLQTRLMASLAKS D
1968	10019	A	2908	48	308	NPRCGPGGSRFVSSWCSVFPEAGGG*RK EPGMRGAGYKQRMGS*SKGPFAFIMPF PRPRPGFVLPPPHLPDLNKGPHFSQKKK KK
1969	10020	A	2909	3	214	
1970	10021	A	291	49	418	FMINPPNQVGRYRNINLTNIYQKPLAP VIL/HGEIFKIFLTGIGVTQRYPLSPFKV FLAALDRK*REGAGEEVNGIENKRIKLSF VSDMIVYVENSKEKNGQLELMRGICKT ATKLQKL
1971	10022	A	2910	312	387	
1972	10023	A	2911	3	216	NCLLRPKNKSVRWGPAGAGAALLRPSA ALGAGSRACSVPPAAPAQTPRPQVSAPA WGPGRARGSGRMERRMKAGYLDQV PYTFSSKSPGNRLAR\TLIGPLGKLMDP GSLPLDSEDLFQDLSHFQETWLAEQV PDSDEQFVPDFHSENLAHFSPTTRIKKEP QSPRTDPALSCSRKPPLPYHHGEQCLYSS AYDPPRQIANQVPCPWCLDSRPYSFPFG QNGIS*DPLAPPSPTLAMGTSGNIAPSSS SPWDICHSFTSQGG/APG/HPSQAPYQH LSEPCPPYPQSFKEQYHPLYGTGGAS QAVGTRGGGSMGAQ/RYPGAGVVIKQE QTDFAYDSVDTGCASMYLHTEGFSGPSP GDGAMGYGYEKPLRPFDDVCVVPKEF EGDIKQEGVGAFREGPPYQRRGALQLW QFLVALLDDPTNAHFIAWTGRGMEFKLI EPEEVARLWGIQKNRPAMNYDKLSRSL RYYYEKGIMQKVAGERYVYKFVCEPEA LFLAFPDNQRPALKAEDRPVSEEDTVP LSHLDESAP*PPYSGLAPRPSVRAPGHA RYPPRLQPRRPLRSRPLGAPAVRREG AAGWSSG
1973	10024	A	2912	119	444	GFGVGTTPALTCPVTPSYSPKARPS*T/EL EPPSRCQPQCQTLGPQAEQNQMSSAPSL ASPPSKQPPLMANRCCCVPRSIHLGCIQ NRLGFWDSDREERGGDATWVSVD

1974	10025	A	2915	1	574	GADGGGAFRLSGPGP*APPGSSALMMP SSCPWRTGALGPSPAGSRALGRCTSSVG PGSRWLTRTSSPGCAYQNLNEDDGAQ ASPEPDGGVGTRLGPPIAE/PSIRSFVV LQHHSAAPSAPTTPAAAGPNTL*SRRT AEWCWPPSCSCCLGPGADPGRGNWRR PPLPRCLQRQSSSCRAFLLLVPGV
1975	10026	A	2916	355	511	LFLETESCFVAQAGARWAVITHCSLKL/L GPCNPPISAL*VARTTGMSHTEP
1976	10027	A	2917	1815	2152	INKEMSGQARWLTPVIPALWEVKVVDH LRPGVRD\HQPQQQSETPVSTTIQK*ARY GGMCL*S*LLRRLTQQNHLNQGGRGCSE LRSRYCTPAWARQSKTSSQEKKKEKEM PW
1977	10028	A	2918	315	480	
1978	10029	A	2919	1	1845	
1979	10030	A	292	5	377	FMINPPNQVGRYRNINLTNISQKPLAP VIL/HGEIFKIFLTGIGVTQRYPLSPFKV FLAALDRK*REGAGEEVNGIENKRIKLSF VSDMIVYVENSKEKNGPILLELMRGLSK NATKLQKLI
1980	10031	A	2920	407	802	
1981	10032	A	2921	914	1134	QESLLLQFTKSSSCPSETTSARTLLSILLS AFWAKPFNKSLGSSKLSHIFLSSSDPSK/A VPTSAYYPVPKSLPH
1982	10033	A	2922	1	447	
1983	10034	A	2923	218	544	SGFSLSLRGSISFSL/CFKVGMCVTPRCY C*SPVP*KPLIKPGWVSELPKPMNWASC SRTLASFLLQAARSHPWTPMKMETMEQ SKLRSQCKPAAGAVDPRAVVHGT
1984	10035	A	2924	3	260	
1985	10036	A	2925	1	534	
1986	10037	A	2926	198	562	LKCGKQWSDPITSPQTESQLLGSSQQQL HQQRHLQGP*K*NRDSPLCFSLSSCPIPK TYTNRHILLP/SSSKSLCKFL*PA*ISPQKM GFSFLSQSVCKFSKLLCSASLIKLFKAFNSI QVTS
1987	10038	A	2927	72	270	
1988	10039	A	2928	325	535	
1989	10040	A	2929	492	696	
1990	10041	A	293	346	489	QLQAMAIFEYLKKTFLRPGTVPHSCNPS TLAGGRGGWIT*GQELEASP
1991	10042	A	2930	822	1759	SSAEPSPSSPAPSQQTAAAGAPPLCAVS PMASASGAMAKHEQILVLDPTDLKFKG DG*VFIRPEQYYTV*KWCKRSKRHGPF PFTDVVTNLKLRNPISDRKVCVKVTT VPS/RRYCVRP\NSGNDPGSTVTVSVML QPFDYDPNERSKHKFMVQTIFAPPNTSD MEAVV/WKEAKPDELMDSKLRCVFEPP NENDKLNDEPSKAVPLNASKQD\GPM PKPHSVSL\NDTETRKLMEECKRLQGEM MKLSEENRHLRDEGLRLRKVAHSDKPG STSTASFRDNVTSPPLSL\VVIAAIFIGFF LGKFI
1992	10043	A	2931	2	417	FVAQQLQGDSLHFMQALYQGHFPIEVR HYLSQWIESQA/WNTYDRCPMELVRCIR HILYNEQRLVREANNSSPAGSLADAMS QKHLQINQTFEELRLVTQDTENELKKLQ QTQEYFIIQYQESLRIQAQFGPLAQLSPQ
1993	10044	A	2932	1	855	
1994	10045	A	2933	1	810	

1995	10046	A	2934	224	2606	TMAVWIIQAQQLQGEALHQMQUALYQGH FPIEVRHYLSQWIESQAWDSVDLDNPQE NIKATQLLEGLVQELQKKAHEHQVGEDGF LLKIKLGHYATQLQNTYDRCPMELVRCI RHILYNEQRLVREANNSSPAGSLADAM SQKHLQINQTFEELRLVTQDTENELKKL QQTQEYFIIQYQESLRJQAQFGPLAQLSP QERLSRETALQQKQVSLEAWLQREAO LQQYRVELPEKHQKTLQLLRKQQTIIID DELIQWKRRLQLAGNGGPPEGSLDVLQS WCEKLAELWQNRQQIRRAEHLCCQLPIP GPVEEMLAEVNATITDIISALVTSTFIEK QPPQVLKTQTKFAATVRLLVGGKLNH MNPPQVKATIIEQQAKSLLKNENTRND YSGEILNNCCVMEYHQATGTLSAHFRN MSLKRIKRSRRGAESVTEEFKFTILFESQ FSVGGNELVFQVKTLSPVVIVHGSQ DNNATATVLIWDNAFLQEPGRVPFAVP DKVLWPOLCEALNMKFKAEVQSNRGLT KENLVFLAQKLFNNSSSHLEDYSGLSVS WSQFNRENLPGRNYTFWQWFDGVMFV LKKHLKPHWNDGPILGFVTQQAHDLLI NKPDTGTFLLRFSDEIGGITIAWKFDSE RMFWNLMPFTTRDFSIRSLADRLGDLNY LIYVFPDRPKDVVYSKYTPVPCESATA KS/VLDGYVKPQIKQVPEFVNASADAG GGSATYMDQAPSPAVC/PPQAHYNMYP QNPD*VLDTDGDFDLEDTMDVARRVEE L/LGRPMDSQWIPHAQS
1996	10047	B	2935	123	219	XPPTGMTMDKSELVQKAKLAEQAERYD DMAAA*
1997	10048	A	2936	1	1815	
1998	10049	A	2937	1	510	
1999	10050	A	2938	107	961	VVGLGRKRSSRSGASLGRVFPVCPPTG MTMDKSELVQKAKLAEQAERYDDMAC SSERHVTEQGHERLQPKKRNLSSVAYK NVVVGARRFLPGRVISSIEHENREGMKKK QQMGKVEYP*EDRRQNLQDICK*CFWEL LADKYLPN/AVTQPE*GVLL*KLKGGYF RYLSEVAS*DNKQTTVSNSQPGFTREHF EISKKEMQPTHPIRLGLALNFSVFYIEIL NSPEKACSLAKTAFDEAIAELDTLNEESY KDTLIMQLLRDNLTLWTSNQDGED AGEGEN
2000	10051	A	2939	208	1178	EGRGHLARSFARKGLCSLQPSHGRVSRD LGRYKKCILPRLWIEKQEEHWTWSQGM TMDKSELVQKAKLAEQAERYDDMAAA MKAVTEQGHELSNEERNLLSVAYKNVV GARRSSWRVISSIEQKTERNEKKQQMG KEYREKIEAELQDICNDVFELLEQISLFP NATQPRKVKVFLEK*KGDFRYLF*K WQS*RRQTQPTCVETPQQSLPRKQFEISK KEMQPTHPIRLGLAPKFPQSFYIEIPKL PLKKA*AWAKTALCFRHF*SNLLNL DTLEWKSLLKSDSTSDSWQLLRDNLTLW DIRKTRGDEGDAGEGEN
2001	10052	C	294	140	172	
2002	10053	A	2940	1	459	IEIHIKCGGIPAVLAAPAMGLEFLDLVS QPSRAVYIFAKNGIPLRLTVDLVKGG HKSKEFLQINSLGKLPTLKDGFILTE/SA NRSVYLQGGCWHITEMRFSKCKAEGPA KRSRSLIYLSCKYQTPDHWYPSDLQAR ARVHEYLGWHAD
2003	10054	A	2941	2	310	
2004	10055	A	2942	205	454	

2005	10056	A	2943	5	437	AQESRDCGDHBRATALQPGQSEILLQ RLPPENA VD*VALEGSQPL*TLACLSCK YQTPDHWYPSDLQARARVHEYLGWHA DCIRGTFGIPLWVQVRRANLPFLSFPLAP VPSLQLHVKLCTDKTLSVLGSASILRCSI HTS
2006	10057	B	2944	307	447	XSAILIYLSCKYQTPDHWYPSDLQARAR VHEYLGWHAD CIRGTFGIPL*
2007	10058	A	2945	2	384	
2008	10059	A	2946	1	1278	MPGLGFREKKGGSRTVIPASRGCLPAPI LCTKWELPLSGSSRCLAAAALQGTVWT AESSSLTPAFQSRGWGLIPYFPARRDPAT AAAHTALSAFTAIPAVLAAPAMGLELFLA DLVSQPSRAVYIFAKKNGIPLELRTVDLV KGQHKSKFELQINSGLKPLTKDGDGFLT ESLAILIYLSCKYQTA DHWYPSDLQGF GARVHEVPWA WHADLHPVGTFWYYP WGVQGVWGHSLGVQVPEEKVGTQTRT AMDQALQWLEDKFLGDRPFLAGQQVTL ADLMALEGS*CKPVALGYELFEGRPRLA AAWRRRVEAFLGAELCQEA/HTSILSIL EQAAKKTLPTPSPAEAYQAMLLRNRPGS PEGSGMGAKEISNKDSFCYLLAPFYLSLL PQSLLSKLQCEALHRQRHSSVLWQVLLL LRCKHT
2009	10060	A	2947	298	456	NIYQLE*K*FKNGQVWLGAVVRACNPST LGGR/WIPWGQEFGTSLANMVKPRLY
2010	10061	A	2948	59	190	ARSFHSDAPQGHLECHWCPGVLEL*GHR NPDTCPHLEQGISSK
2011	10062	A	2949	319	460	HFSYIHWFYTEKYKIKITHQDYLKQFIHY/ CTEEKHAYH*PNKILFIT
2012	10063	A	295	2008	2438	WSLHRPRGPLLWHMPPRVPPLTGL*SSP HDSVGPQPWKSPPTTSFNSPDPPENVQN HPGKPVAKSPFPQRNGH/PPKR/PTWGS STCWGEVIRSGSPPTTKPVWPTSCEFGS VLPPEDETVFPVHPFVSLILFAISFALVCG D
2013	10064	A	2950	78	3703	FQELGAREPFGNMYDADEDMQYDEDD DEITPDLWQEACWIVISSYFDEKGLVRQ QLDSFDEFIQMSVQRIVEDAPPIDLQAEA QHASGEVEEPPRYLLKFEQIYLSKPTHW ERDGAPSPMMPNEARLRNLTYSAPLYV DITKTVIKEGEEQLQTQHKTFIGKIPIML RSTYCLLNGLTRRDLCELNECPSPDAGR YFIINGSEKVLIAQRKMATNTSFCRLQK TDSKYAYTAGECRSCLNSSRPTSTIWVS
2014	10065	C	2951	162	293	MGNLLKVLCTDLEQGNFFLDFENAQP TESEKEIYNQVNVAL*
2015	10066	A	2952	286	1327	AGAKFFP*F*KVADAQPTSESEKEIYNQV NVVLKDAEGILEDLSYRGAGHEIREAI QHPADEKVAKKAWGAVVPLVVGKLLK FYEFQRLEAALRGLLGALTSTPYSPTQH LEREQALAKQFAELHFTLRFDLKMNTN PAIQNDFSYYRRTL SRMRINMYPAEGEN EVANELANRMSLFYAEATPMLKTLSDA TTKFVSENKNLPIENTTDCLSTMASVCR VMAGNTVEYRSQILQNEETVSFLSWRAM VGCS*YSYDHR TSSGEAFCLKLPKFD MK GCIKVLKDQPPNSVEGLLKSLRYTTKH LEWMRLPPSKLKSMLPITILGIKHPAVDR RQYSAMTENAVF
2016	10067	A	2953	75	478	AVKMCDF T*DQTA*FKEAFQLFDR TGDG KILYSQCGDPKSDEMNVKVLDFEHFLP MLQTVAKNKDQGT Y*DYVEGLRVFDKE GNGTVMGAEIRHVLVTLGEKMTEEEVQ MLVAGHEDSNGCINYEELVRMVLNG
2017	10068	A	2954	2	343	

2018	10069	A	2955	34	353	
2019	10070	A	2956	2	303	
2020	10071	A	2957	1	999	
2021	10072	A	2958	255	528	ARYKIHTGKGTDSETGKVLSHSAPCGR CSRPARHPDRSMPHKRIFVDTNQLLSS CPATSISTSSSVNLPRCD/FPEDQTAEFK EAFQLFDRTGDGKILYSQICGDMRALG QNPTHAELVKVLGNPKSDEMNVKVL FEHFLPMLQTVAKNQDPGSPMGFMSKE LRVFKYK\EGNGTVMGAEIRHVLVTPG*\ KLTEEEVEMLVAGHEDSN\GICINYEAFV RHTPVGVTPGWAGASSAWC
2022	10073	A	2959	26	518	AVKMCDFTE\DQTAEFKAEFQLFD/RKPG DGKIPCTAQCGDMRALGQNPLPNAEV LKAPGEPPRSDDMSVKEHDCEHFLHIL QTVAQNQ\QGT\YEDYVEDFRVFDKEG \NGTVMGAEIRHVLVTLGEED*QRKKV EMLVAGP*RTANGLVSNYEELVRMVLN G
2023	10074	C	296	165	290	MCHRAGPASLSAGQFIHIFLVTPMAAPRI SAVCGPESRHQG*
2024	10075	A	2960	453	744	
2025	10076	A	2961	736	1062	
2026	10077	A	2962	295	782	PLLCNPDPGWYWWVKQSEISKESQEM DARPKLDLGFKEGQTIKLCIGNITNKKGG ASKPRTARGGGLSLLPPP*GKVTPPPSS /VKLPSTNHVTPPSIPKSNHGGSDADILLA DLDSPAPVTTPAPTIVSVSN\DL\WGDFS TASSSV\NQAPQPSN\WVQF
2027	10078	A	2963	192	324	
2028	10079	A	2964	1	1044	
2029	10080	A	2965	1	811	
2030	10081	A	2966	1	750	
2031	10082	A	2967	493	1946	
2032	10083	A	2968	539	1215	
2033	10084	A	2969	414	1762	
2034	10085	A	297	883	1095	GSGV*DQPG\QHGKPPSLL*LQNLAEERG GHL*SQLLRRLRQENHLNPGGRCC\SELR SRHCTPAWATRAKL
2035	10086	A	2970	449	1305	SKSRMSAEVIHQVEEALDTDEKEMLLFL CRDVAIDV\TPPNVR\DLL\DLRERGLKLS VGDLAELLYRVRFDLLKRIKMDRKA VETHLLRNPHLVSDYRV\MAEIGEDLDK SDVSSLIFLMKDYMG\GKISKEKSFLDL VVELEKLN\LVAPDQLDLLEKCLKNHRI DLKTKIQKYKQSVQAGTSYRNVLQAAI QKSLKDP\SNFR\HNGRSKEQRLKEQLG AQQEPVKKSIQSEAF\LPQSIPEERYKMK SKPLGNLPLIDWHWALRTELSFEDTFTS LGY
2036	10087	A	2971	473	1164	SKSRMSAEVIHQVEEALDTDEKEMLLFL CRDVAIDV\PPPNVR\DLL\DLRERGLKLS VGDLAELLYRVRFDLLKRIKMDRKA VETPLFKDPPLVSDYGV\MAEIGEDLDK SDVSSLIFLMKDYMG\GKISKEKSFLDL VVELEKLN\LVAPPDQLDL\LEKCLKNIP QK*P*RQKSQKYKQSVQAGTSYRNVL\ QAAI\QKSLKDP\SNFRMITP\YAHCPDL KILGNCSM
2037	10088	A	2972	482	692	EKPL*SYLSSFFHFLEMGSHPRLVCSGV IVAHCSLQLLGSSDVPTS/ASR*LGLTGSH TTIPSLGLFLN
2038	10089	A	2973	1	358	AQLVEFGEHSMAPPAHFRALLYHPGTAT LVPHPASISQSPSPWGNA/RG*PV*RQR HLTAPRSPPHPRFRHKPGKDPRENPSRW PEVPSLPQTHVVPQAAWDTVNTTVCK NRSTKPQD

2039	10090	A	2978	136	500	GTLPNSSLCESNNGHPRQRGRGSCPSRY TGVPPSPRLSRIQSWIR/HLHPPSPTRPSY SSPQASASPVGLRGHPAQWTTCRSRVP SPVRFSSGSDGEKRLGQSCPHGNDPGAA CISRPPYA
2040	10091	A	2979	242	9991	FKLELHQESDMEFNNTTQEDVQERLAY AEQLVVELKDIIQKDVQLQQKDEALQE ERKAADNKKIKLKLHAKAKLTSLNKYIE EMKAQGGTVLPTEPQSEEQLSKHDKSST EEEMEIEKIKHKLQEKEELISTLQAQLTQ AQAEQPAQSSTEMEEFVMMKQQLQEKE EFISTLQAQLSQTQAEQAAQLSSMQQVV REKDARFETQVRLHEDELLQLVTQADVE TEMQOKLRVLQRKLEEHEESLVGRAQV VDLLQ
2041	10092	B	298	191	494	MKLKRGAGSCKKPGSSGWPVAVGEFHS VQNICARREYQRQDYMADAMAEKQKLD AEFQKRLEKNKIAAEEQTAKRRKKRQKL KEKKLLAKKMKLEQKKQEGPX*
2042	10093	A	2980	3	211	
2043	10094	A	2981	1	519	
2044	10095	A	2982	291	686	GLGTFAYISQDVWKSLEYVQAEVCCRGR VFLVCSCGSCWSKSSRCEPPYAVLSIQVE AAHMHEIWCRDSDRDLPWESSCSLLLE KDPP/SGPQTDQPKKHLTNFKSDKGDTF YPWTQNSGAGHGLGRQPSLGV
2045	10096	A	2983	1	639	
2046	10097	A	2984	2	423	GFLVLLTSRMKLRLTAKQRRHILSVDPK LRRRSRTGKAAPFWCLIIAGTPLIIHPRFK GVRPCRDACLGPSPLAASPAFLGEGQEL ATSARNLTTRPRNACSPGFLLSRVHLCG TPLEI*PPGQGMPPAAQDSS*AVSICAGPH WKSDCSTHLAGTPRAPGILAQGSL
2047	10098	C	2985	80	106	MRMKFGLD*
2048	10099	C	2986	259	531	MSPAHKNFQTPEPQRPPIPPEPPPGACY KCQKSGHQAKECLQPRIPKPRPICAGPH WKLD CPHLASTPRAPGTLAQGS LTASQ IFLA*
2049	10100	A	2987	3	505	
2050	10101	A	2988	1	1056	
2051	10102	A	2989	1	1482	
2052	10103	A	299	2	478	SGRLPWLAQPPPRCDHRGPRKSRSS PRMRREEQKLERLMKNPDKAVPIPEK MSEWAPRPPPEFVRDVMGSSAGAGSGE FHVYRHLRRREYQRQDYMADAMAEKQK LDAEFQKRLEKNKIAAEEQTAKRRKK/R PQS**KKNLLAKKMKLEQKKQEG
2053	10104	A	2990	399	567	ACYKCWKS GHRVKECLQPRIPKPCPIC AGPH*RSDCSTHLAATPRAPGTLAQGS L
2054	10105	A	2991	1	468	
2055	10106	A	2992	1	984	
2056	10107	A	2993	1	900	
2057	10108	A	2994	1	522	
2058	10109	A	2995	3	1150	
2059	10110	A	2996	3	500	LEGASYGETKADVAEGKSQKKATEWRS QGQRRKGEETSQKDKCRTNQLSVKRT NQLSVIWTNQQDVGSYANPLMAAEPAQ AVKLGWRPSPKPHIGDKSVFWLLWMG SVQQGQKIGP/PSQGNACRPRNSS*SHVP CGGGPHWKLD CSTHLAATPRAPGT LAQ GSL

2060	10111	A	2997	3	603	GHSRPRNWSQWSPRFLWLEAHRPSPGSP DSAEQRSQVSDCLGTSRHGTGALFLALG IYAASCYVARFIRVRPHRDAYS LQGRLS DHSPTFQGCQTTQGRLPWSFTLSGKSRF SGEGATTSPA HKNFQTPEPQWGPPEPP PTGACYTCRKSGHWAKECPQARIPPKPH PICVGPH*KSDCSTHLAATPRAPGT LAQG SL
2061	10112	A	2998	1	669	
2062	10113	A	2999	1	762	
2063	10114	A	3	32	474	LYALRNQIKPPPHVTGGQ*QKQERTKPA WRPPRP/GPPPFIALIGFCFSSVPVAVVEL RVEPPGGHWPLSPLGEVRGEWRRPLSGL AS/VGQWLVP RSPEGGGGGWAGSPQVS GGWPPSAHLRNPPLSLGDILPAPQHPALS PGGPKLCG
2064	10115	A	30	147	766	GALHLIRKGSPLHGQA HKHVAQQGRGIL SRVHRPTHVHTQGRKATRLGLCSAHR APHPSFLPLVPVCCS/WHHCETPRPCPLL PCPPSSGASTSRTASSPVLSLTD*PYLSE TEEQVSPGLTHKASLEPRSDSAKTSSH PRDWPHPMVDCAAALSWTQPLWMFCG SRLAFHDAPAPAHMRAIWASRAIPAARP GPHLGLAAASC
2065	10116	A	300	72	409	VCSETGFILYCRN/DCKWDAPILETVWFF VRS*TLDMNCTPAIPFLFIYPLEMYGHA Y*MTCTRIFMAALFIIATNQKSPKCSINSI HATKYIYIAMKLIQLYPYVATWINKVF
2066	10117	A	3000	1	519	
2067	10118	A	3001	1202	1315	
2068	10119	A	3002	1	930	
2069	10120	A	3003	132	248	
2070	10121	A	3004	3	439	
2071	10122	A	3005	1	357	
2072	10123	A	3006	1	765	
2073	10124	A	3007	1	1434	SVAFVFACPAVDYLVKISWELQGDEEQD GLRNMWQTLQKTKDYEDVRIQNAINI AQGASEAIGQRQSSAAKPRRSGKESVRE PWARVPGALGVAARKYQKMKGIEIKRR ERLKC GAKIERRKRLKDREVGESKKRP LTGFEIEPPKVTVM PKNQSFTGGSEVSIM CSATGYPKPKIAWTVNDMFIVGSHRYR MTSDGTLFIKNAAPKDAGIYGCLAKAPK LMVVQSELLVALGDITVMECKTSGIPPP QVKWFKGDLELRPST/CFLLSILAP/PLQS LPSLNFNFSFHFLDFLAATPRAPGT LAQG SLTDSFPDLLGLAAED
2074	10125	A	3008	166	421	RPRSERLLWGTSPLS/CALTL*GDPPTTSG PQTNQLKEHLTNFKSGPHWKMDCPHP AATPRAPGT LAQGS LTDSFPDLLGSAAE D
2075	10126	A	3009	1	434	
2076	10127	A	301	92	617	DRVLSLLPRLECSGSILAH CNVCLP/GFK RFS\CLSLPSSWDYRHTPPCP/V*LVFLVE MGRHFSQAKSRTL/TGDPPASASQKCW NYRRDNLAWLASALNKVINLLKSEIPSF FLVQLSGFSRTLLQGF LNFNHYHTLVYS NNLPIMQFTFTQDFGRISGKPPGIMILCN REILYIM

2077	10128	A	3010	1478	2240	WQVPLSWGRGKYPSTSPSPPLAASPTFL GQGQVPLNPFSTLSGKSRFPAGASTPQ PLLLHPQRQVPLSWGRGKYPSTSPSPSA ASPAFLGQGQVPLNPFSTLSSKSRFPRG QETPNRLFHPNLLSLHPNPLFHPDLLS LCPNPLFPCLNPFSAFLEGKNPPPLRVST LFSGLASFTMGACYTCQKSGHWAKECP QPGIPPKPCISVGPH*KSDCSTHLAATPG APGTLAQ/GLTDSFPDLLGLAAED
2078	10129	A	3011	1	624	
2079	10130	A	3012	321	512	
2080	10131	A	3013	1005	1251	KGGWSQRHSQGACYTCRKSGHWAKEC PQPGIPPKPRPICVGPH*KSDCSTHLAANP RAPGTLAQGS LTDSFPDLLGLAAED
2081	10132	C	3014	18	56	MAINSIRSLQLM*
2082	10133	A	3015	188	364	
2083	10134	A	3016	602	2459	FWGEGEKATAFLICNLAGCLRCPVDMN S\QGS DSNEEDYDPNCEVEKEEEEEED\DP GDIEDY\YVG VASDVEQQGADAFDP EE YQFTCLTYKESEG\ALNEHMT\SLSFLSL KVSHSSWLNLYLVNFHWQVSEILDRYK SNSAQLLVEARVQPNP/SQKHVPTSHPPH H\CA GCGMQVCAKRENLL\SLWACQL*F CRSCWEQHCS\VLVKDGVGVGVSCMA\ Q\DCPLARNTSGTFVFPALLPNEEFEEKY RRYLFRDYVESHYQLQL\CPG\ADCPM\V IRVQEPRA/RARVQC\NRCNEV\CFKCR QMYHAPTD\CAT\RKWLTKLQDDSETA NY\SAHTKDCPKCNICNEKDGG\CNHM QCSKCKHDFCWMCLGDWKTGSEYYE CSRYKENPDIVNQSQAQA/RREALKKY LFYFERWENHNKSLQLEAQT YQRINHEKI QERVMNNLGTW\DWQYLQNAAKFFGQ GSFSSLLQCRYTLQYTPYAYYMESG PRKKLF EYQQAQLEAEIENLSWK\VERA DSYDRGDLENPD\IITEPTGGTNPCLKD FHD TLSWDVDVPGVRKISLARS PRAAH TACLAGSAFHDPQATAQGPTPERHWQH LLVDFCFLFLSLFVSTQGRRPC
2084	10135	A	3017	103	769	GPCCIIQQLILFQCFKHFGSLCFQLCK LMMPSKSLVMEYLAHPSTLAGLAVGVAC GMCLG\WSLRV\CFGMPLPKSKTSKTHTD T\ESEASILGRQPGSPG*FLVVRN*L*RWG KGERGCPSASHAAVSSPTKQISKKKSPE MAQNNGEYWWASPKVGGSKVPDEETLI AL\LAHAKMLGLTVSLIQDAGRTQIAPG SQT VLGIGPGPADLIDKVTGHLKLY
2085	10136	A	3018	99	478	
2086	10137	A	3019	2	87	
2087	10138	A	302	367	619	ETRCRGHPPRDREPPPS*PGIQSSPGVP/PS RPSNKA YPRLPIRPQPPGLSFRISTPPRSP \KPPCPPHIGRHVQPTKTS AVSILS
2088	10139	A	3020	1	921	

2089	10140	A	3021	1	2203	MGGASARPAAPSGRWGVPLGRPFWEV MSPSARPPRLGGVPNSSLRTHGDDGG FVEQRRGKGDSEQLGLRIKLVRVFSW QLVMAFDKAELPSSPKVLVLTTRATG GVGLQTLRRLQERPQIGQLGALCLICTVR LCGHEEMTSTFNPCKLSKQEGQNYGF FLRIEKDTEGHLVRVVEKCSAEKAGLQ DGDRVLRINGVFVDKEEHMQVVDLVRK SGNSVTLLVLDGDSYEKAVKTRVDLKE GQSQKEQGLSDNILSPVMNGGVQWTQ PRLCYLVKEGGSYGFSKTVQGGKGVY MTDITPQGVAMRAGVLADDHLIEVNGE NVEDASHEEVVEKVREGPRRVGYGFDR QQMAAALQKRGLTVKNKQTESNNNINK KRPHKNPIQSAASKIEELEKNYFKIQYG SKKEPVQVKTTSKKNKAGGITLPDFKL YYKVTVTKTACSRFHWKMNLCVILLIL /VFPMVPFLQLAYFIVSNIRLLHQRLLF SCLLWLTMYFFWKLGDFFPILSPKHGIL SIEQLISRVGVIGVTLMALLSGFGAVNCP YTYMSYFLRNVTDTDILALERRLLQTM MIISKKKRLRGPVVGFLIYSPVGQIAE DLTIQEQVDALEELSRQLFLETADLYAT KERIEYSKTFKGKYFNFLGYFFSIYCVW KIFMVKFWSQHISFILVGHIVTSIRGLLITL TKFFYAISSSKSSNVIVLLLAQIMGMFYV SS
2090	10141	A	3022	2	215	
2091	10142	A	3023	50	1598	GGLWPQRAVASGSGKWRQEPSLHFAMS FLIDSSIMITSQILFFGFGWLFMRQLFKD YEIRQYVVQVIFSVTFASFCTMFELIIFEIL GVLNSSSRFHWKMNLCVILLIL/VFMV PFYIGYFIVSNIRLLSPLSQA*TTDWL FSCLLGLTFMYFFGKLGDFFPILSPKHGI LSIEQLISRVGVIGVTLMALLSGFGAVNC PYTYMSYFLRNVTDTDILALERRLLQTM DMIISKKKRMAMARRTMFQKGEVHNKP SGFWGMIKSVTTSASGSENLTIQEQVD ALEELSRQLFLETADLYATKERIEYSKTF KGKYFNFLGYFFSIYCVWKIFMATINIVF DRVGKTDVPTRGIEITVNYLGIQFDVKF WSQHISFILVGHIVTSIRGLLITLTKFFYAI SSSKSSNVIVLLLAQIMGMFYVSSVLLIR MSMPLEYRTIITEVL/GEELQFNF/YIHRW FDVIFLVRRFSLGILFPLFGLHKQAPEK/Q MAPLNLKPYLQTDKRPSGFQKFRI
2092	10143	A	3024	1	158	
2093	10144	A	3025	2	1067	AAELGTFAQTQSGAWRAERSWHNRGP MMWRPSVLLLLLLLRHGAQGKPSPDAG PHGTGRVHQAPLSDAPHDDAHGNFQY DHEAFL*REVAKEFDQLTPQESQARLGRI VDRMDRAGDGDGWVSLAELRAWIAHT HQRHILDSVSAAWDTYDTRDGRVGWE ELRNATYGHYAPGEEFHDVEDAETYKK MLARDERRFRVADQDGDSMATREELTA FLHPEEFPHMRDIVIAETLEDLDRNKDGY VQVEEYIADLYSAEPGEEPAWVQTERQ QFRDFRDLNKDGHLDGSEVGHWVLP QDQPLVEANHLLHESDTRDKDGRATKAE ILGNWNMFVGSQATNYGEDLTRHDEL
2094	10145	A	3026	2	860	

2095	10146	A	3027	2	1681	FGTLGSAPFESCPFQKEDGMKIFQIQGIH VQERVTFKDVAVVFTKVI*LALLDKAQI NLYQDVMLENFMNMLWIPVVSFQLG SANGESQEQGRDKSEVRIFIPFGFSLEV AVEWLYSISIDQRDAHPKTDPKLRPEEA QRKSLSRNVKMHCFVKPRAAPQTEPTLE PTLFPSYPGVRPVPWRMRKEAYGLQSPE SPARSSGHSQGYPGEDLHRAEQRPERFA GSAWTWSLQRLATWKRIQRTGQNTWLE ALANLLANMTQLPGHFSTFLVSAPHPAA EKPLLHSILTHRPVHLLATVTLPAEEAP LMADITAQAILTPQLCSGTLALLAHVAAR AHADTNLQHVGIAPAGDTTGDMASMTLL PGSDTVDLKDTAPCIVAAPVPAMAKKG QGIAQAIASEGANPRPWQLPRTVGPVVN GEGKCGVGAPRVPTALPSGAVRRGPPS SRPQTHQQLPPCAWKRCRHSTPAHENSQ VGYTLQSHRGRDAQGLGSSSLASACLD VRHGVKGDYFRTLRFNDPCAGFQTGMG PAAPLFCLISPFQNGGIYPKAVAPLYLGS N
2096	10147	A	3028	51	569	SLRTVPPHYLQGSPTPIPPSSLGPASGTR RVES/CVAAPNEQEGSSKGGARPVTICDS QNRPCPPPPSPALPQADPSLKTWLLN HIRWDTDSMICMEDSS**GFK/PNKDSIK VQVRLRGVQGVGHCMGGAALPSTSLSS CLTPFPAPLNSRHITLAPPLQPENPAQR TTP
2097	10148	A	3029	2	395	
2098	10149	A	303	2	519	FPLFLFLLLLLAFPVALTTTRRIQGVQTL VLQAKRVNTSRPHPD/GS/QPPTSASFNQ LNPTNSTPQLRSHVASGYVG*KQMOPY H/PPQHAPAPPQPCPWQVDTFLPAPTRPL LGSGPGSPRRSPGGAPPPAGKGPAPGPE CPPTAQRPTR/RQYLGPLFKGDPRNSPRE KPRS
2099	10150	A	3030	2	1038	GLLEPFSKLLSFVIONAVFTLAYLVELCG LCYRAFTKERDKFYLSRSGCSKSFRRLL KLKSLPDTNLLLLVQFILPDAGTKLD*V NNPEQADDSLCTWDVGTAAAMECVRQY INEVLDFMADMHTLTKLKSHMKTCSQA SDEDTFGGHLKVGLAQIAAMDISRGNH RDNKAVIRYLPWLYHPPSAMQQGPKEFI ECVSHIRLLSWLLGSLTHNAVCPNASSP CLPIPLDAGSHVADHLIVILIGFPEQSKTS VLHMCSLFHAFIFAQLWTVYCEQSAVAT NLQNQNEFSFTAILTALEFWSRVTPAIL QLMG/HINKVMGRKWVLLSMWISLMGG NLPGNAIWT
2100	10151	A	3031	3615	5322	EVPPNPACYQHQA*SVCLCLHLKSSLTSS RR*/CTDKCHDCGAILEEYDEETLGLAIV VLSTFIHLSPDLAAPLLLDIMQSVGRLAS STTFNSQAESWPPTASSRSCSKARSKVIH PLRIQAPQICLIPDTQTLNPIVDFPDGTF RTLASSLMDFNELSSIAALSQLEGLNNK KNLPAGGAMIRCLENIATFMEALPMDSP SSLWTTISNQFQTFKLPVLPKSLLE PFSKLLSFVIONAVFTLAYLVELCGLCYR AFTKERDKFYLSRSVVLELLQALKLKSP LPDTNLLLLVQYENKMNEKAERLVKL LNSAQQQFQFICADAGTKLAESTILSKQ MIASVPGCGTAAMECVRQYINEVLDFM ADMHTLTKLKTSVLHMCSLFHAFIFAQL WTVYCEQSAVATNLQNQNEFSFTAILTA LEFWSRVTPSILQMAHNKVLIPMWLPM IQSNIKHLASAGLQRLQAIQNHVNHSLR TLPGSGQSSAGLAALRKWLQCTQFKMA QVENPVLGKQPLNFILYEWTPSAPQCQH SGLAIMGLKTNNLDPQAGWGNHIGYLY

					NPLS
2101	10152	A	3032	3	1078
					FFSSVFPA AIEPGERASARRRVSRAGCLA LTL PALLLVTHQVPAEAAVSRAMAE LAT ALES LIEMGFPRGRAEKALALTGNQGIE AAMDWLMEHEDDPDVDEPLET PLGHILA GREPTFSEQGGLKDLVLA VAGEGKPALS */EERQEQT KRMFGAWLAQKGSRE RE EREGREVALERERQRR RQGQELSAARQ RLQEDVKMRR\AAA EERRREKAEE LAAR QVR EKIERDKAERAKKYGGSVGSQPPQ VVAPEGP VPSSP SQEPP TKGEDDKCRI QVRLPRWDPH*PQTFRAREQLAAVRL VY VEL HRGEELAGG GARDPVQIASVAFPRR AFLRSLTMER PLQELGMAAKTRNQD
2102	10153	A	3033	2	565
					IHFQQEHWP S QLLRESLEDMM LHSALG LC LLLVT VSSNLAIAIKKEKRPPOPLSRG WGDDITGVQTYEEGSLCSKK*GSH*WV IHHLG DCQYSQALKKVFAQNEEQEMA QNKFIMLNL MHETTDKNLSPDGQYVPRI MFVDP SLTVRADIAGRYSNRLTYEPRD LPLLIENMKKALRLIQSEL
2103	10154	A	3034	73	262
2104	10155	A	3035	29	867
					PLEGIADNRFP HGETSTLPATFCSPSAPEL ASMSVVPNRSQTGWPRGVTFGNKYI QQT KPL\TL\ERTINLYPLTN\YTFGTRAP LTRRTSSV AARFQRIEGKNFDKIGMRRT VEGVL VHEHRLTPWCYLLQLGTNFLP NYLGWLN LTPGEDEV EGLKTA**PEIPG SVQDGV LQD\WGPLTDCHWVTWWRP KFLNPPSVSHIFPAHIT KPKE/HIRKLFPG SSLQEKALVLQFPKFTSW*PATPLFELY DNA PGYGP ISSLPQLLSRFNFYIN
2105	10156	A	3036	2	817
					RARIPKMAAVKDSCG*GEMATGNRRRL HLGIPEAVFVYYSY*RKMYHYFMKQP GNETADTVLKKLDEQYQKYKFMELNL AQKKRRLKGQIPAEIKQ TLEILKYMQKKK EISTNFNGRPRFFAGRLTYLQKLSVPPT R*RG/CLGLGANVMLEYDIDEAQALLGK DLASTATKILDSRGGRTLFLARDQFTTTE VNMARGLLIGDVKKEGNKD DSTKNKA LMLGQFKNVGLVFPNMFIFKYPPIPYRFD INFGMFNQPRNFKEKINTILFIY
2106	10157	A	3037	3	468
					ERIMEWHRHTMTECSAQEPKSHDIYLRRL LVKLYRFLARRTNSTFNQVVLKRLFMSR TNRPLSLSRMIRKMKLPGRENKTA VVV GTITDDVRVQEV PKLV CALRVTSRARS RILRAGGKILTFDQLALD/SPYVRSKGRK FERARCRRARRGYKN
2107	10158	A	3038	1	693

2108	10159	A	3039	105	756	VDHPPYKRTEKVRAQRSPKSQYIYLSLL LKLRYRFSGPEEPNSNIQTRVVLKRLFMSP HQTGPPLSLSRMIR\KMKLSWPGKQRR VVC/VGPITD\DVGRSRRYPKLKVCCTAP *PSRAPQAAILKAGGK\ILTFDQLALGLP LKG\CGTVLLSG\PSKG\RKVYRHFRQRP QEPPHKPHQNPTFRSKGRKFERARG\RR AS\RGYKKLTLDPTLLYKKIFA
2109	10160	A	304	444	920	NPSLRCWLGSLSPGKLAGARGRTVHVG GPEGPCTHSTSTKRM\AKRHPEVSTGGGG KAP*/SQGIRGQGAGQG\GARSGVAGNG GGGARSRLRLSPAAASATA/SGPEGS\GP GSGGRSRVPVEAAPP\CP\SDV\PAARGA AAAGPGGTWLPASQVGPSPGPWG
2110	10161	A	3040	301	390	
2111	10162	A	3041	1	737	MWFAYSPFTFCHDWKLPEASAEAKRMP ALCFLYSLQHPLCEDGVCAHEAGVWGI GGLIIAYVKGYEEVSQKFTSIRRVRGDNY CALRATL\FQAMSQAVGLPPWLQDPELM LVVFVAILLHSHLECREPLILSLYMGA LVRCTTLCLGYKNIHDIIPDRSGPELGG DATIRKMLSFWWPLALILATQIRSRPIVN LFVSRDLGGSSAATEAVAILTATYPVGH MPYGWLTEIRAVYPAFDKNNPSNKL\ST SNTVTA\AHIKKFTFVCMALSLTLKDSVQ KPDISLTGRLVQTLPTMRHQRGESKDV APLASWLSEPSTSSEASQTSSKLTINSQG EGKAKQKLECGTSLIVLRSCEKNQERIK AAEKRNRSWTTL\CGLGAWRPLL\FELPVI VQTPDQTNRFQFRYPAKTQSGLC\SFHFS FDLLTLEAFVKVWFPGLLILLCFVMFW TPNVSEKILIDIIGVDF\AFELCVVPLRIFS FFPVPVTVRAHLTGWL/QGPGAHAGCFC SHFASQSPGMPGAPAHDPDLLVHGRTCA LHHPVPGLLQEHSRHP*QKWPGAGGR CNNKKDAELLVAFGSNSGHTENQSAYC QPLCFPGPWWQFCSHRGSGDFD\SHIPCG SHAIRLV\DG\NPCCVSCFRQE
2112	10163	A	3042	889	1577	RGKKNTVLKKIRSQFTIRESFDLRYKEHI PLPKLEFPLDTKVFGLLGEDMVCTGPTG VALKGPHWKYIGI\DEGKDLVNF\SYQKL VFRTSWSTWLPRGPRVLLRDCSLKTPKP AAQAQEPTVHLRPRRQGFSGSMRSLID WVSLTHSDGDVIVPIVLSNERYHWPV\VL GWVGGVDCDEFFRVVLGEARLHLDGV AHQH*GKKEPFPTCSKTTSVSHLVEVVP QKLSWVI
2113	10164	A	3044	2188	2706	RESIDQGFSNFFFLRRSLDSVTQAGVQ WHDLSSLQPPPPGFK*K*F\SCLSLLSS*DY RSPATMPGLIFLYFFFLVETGGFTVLAR\ MVSIS*PQ/CDPPASASQ\SAGIQKNSFFFL ETRVS\AFVAQAGVQWCDLGSPPPPPG V\QPFSCLSLPSSWDYRRTPGPANFAVC N
2114	10165	A	3045	33	198	
2115	10166	B	3046	6	125	MAGQFRIYLWDPLLILSQIVLMQTVYYG SLGLWLALVDGL*
2116	10167	A	3047	1	110	
2117	10168	A	3048	260	798	RPGHAQTLGSPSLALGMAGQFRSYVWD PLLILSQIVLMQTVYYGSLGLWLA\WVD GLLRISPSLDQMFD\AEILGFS/TPFQGRLS MMSFILNTLNSA\LGLLYFIRRGK\QCLDF TVTVHFFHLLGLLGSNS\SPFSPGG*TLV GLGPKPVVALHSLAVIGEYLCMRTELKE IPLNSAPKSNV

2118	10169	B	3049	1	528	MRRQDCPNPMKKIRSSSPVQQERVSSLY FQSARGGLGVDVSALGTVTHVSPSSAR VAMAMSAERGCSMGHIMGYRGVGRFT RGNGDHARVGYKGNPPEVSISGYDDNW YLGRTDATLSCDVRSNPEPTGYDWSTTS GTFPTSAVPRAPSWSSQTQWTVCSIHRL HITNAVDGPR*
2119	10170	A	305	504	935	AYLQSSMIAQSRATRTGLATWHQHKL DRHFPRLSSRHPLFETCSSPPCKRWGEKS HFRACKEGRESAPCGIPRPFKVHTPRG KLRMRPVPRRFGGSRLGPRSRKRRTK QPR*PAAPRDSGAPAAPPTPRPSAARNG GG
2120	10171	A	3050	31	206	GSSCRSRLVVVLSIVLEGAPAPGDPQT SPSALDKLKEFGNTLEDKARELISRIQS ELSAKMRVPLRPRHEALPVAPGGGGSV DRLGRPSPPRGPPDVSQCLG*AEGVWK HTGGQSGTHQPHQTE
2121	10172	A	3051	21	353	SAAGTGPEPEPEPHRHLNRPADRPQSG PRASGRAQSPGPMARAAALLPSRSPT PLLWPLLLLLLLETGAQDVRVQVLPEVR GQLGGTVELPCHLLPPVGLYISLVTWQ RPDAPANHQNVAAAFHPKMGSPSPKPG SERLSFVSAKQSTGQDTEAELQDATLAL HGLTVEDEGNYTCEFATFPKGSVRGMT WLRVIAKPKNQAEAQKVTFSDPTTVAL CISKEGRPPARISWLSSLDWEAKETQVSG TLAGTVTVTSRFTLVPSGRADGVTVTCK VEHESFEERALIPVTLVRYPEVSISGYD DNWYLGRTDATLSCDVRSNPEPTGYDW STTSGTFPTSAVAQGSQVLVIHAVDSLAFN TTFVCTSQPNPWALARAQVIFVRETPQ ALAPRCGPAGVGGRGGDTAGAAASGW GVLGLHPCMRVRRRRKSPGGAGGGASG DGGFYDPKASGVGWPRLLDTSSPWS HGTRWQG*GGGGGGREGRRPHVASTP STSRMTWSPSWTAPSSHGG/PVYV*PGPP WPGPLPSCRRDRRRRRCCGRCCCSW KPEPRMCEFKCYPRCEASSGAPWSCRAT CCHFLDCTSPW
2122	10173	A	3052	1	1620	MARAAALLPSRSPTPLLWPLLLLLLLET GAQDVRVQVLPEVRGQLGGTVELPCHL LPPVPGLYISLVTWQRPDAPANHQNVAA FHPKMGSPSPKPGSERLSFVSAKQSTG QDTEAELQDATLALHGLTVEDEGNYTC EFATFPKGSVRGMTWLRVIAKPKNQAE AQKVTFSDPTTVALCISKEGRPPARISW LSSLDWEAKETQVSGTLAGTVTVTSRFT LVPSGRADGVTVTCKVEHESFKEPALIP VTLVRYPEVAISGYDDNWDLGRTDAT LSCDVRSNPEPTGYDWSTTSGTFPTSAV AQGSQVLVIHAVDSLNTTFVCTVTNAV MGRAEQVICVRETPNTAGAGPTGGIIGI IAAIIATAVAATGILICRQQRKEQTLQGA EEDEDELEGPSPYKPTPKAKLEAQEMPIS HLFTLGA*EHSPLKTPYFDAGASCTEQE MPRYHELPTLEERSGPLHPGATSLGSP VPPGPPAVEDVSLDLEDEEGEEEEEYLD VNPIYDALSYSSPSDSYQKGFMVMSRAM YV

2123	10174	A	53	408	2708	DPSSGHWLH RPPAAGWSPRSGRAA ARAQSPRRREHGAPGRTGPGGGPRLLLL AVLLAAHPGAQDVRVQVLPEVRGQLGG TVELPCHLLPPVPGLYISLVTWQRPDAPA NHQNVAAAFHPKMGPSFSPKPGSERLSF VSAKQSTGQDTEAELQDATLALHGLTVE DEGNYTCEFATFPKGSVRGMTWLRVIA KPKNQAEAKVTFSQDPTTVALCISKEG RPPARISWLSSLDWEAKETQVSGTLAGT VTVTSRFTLVPSGRADGVTVTCKVEHES FEFPALIPVTL SVRYPVPEVSISGYDDNW YLGRTDAT/L*ACDVRSNPEPTGYADWS TTSGTFPTS AVAQGSQQLVIHAVN/SVLFN TTFVCTVTNA\VGIGAGAEQVIFVRETP RASPRDVGPLVWGAVGGTLLVLLLAG GSLAFILLRVRRRRKSPGGAGGGASGDG GFYDPKAQVLGN GPDVFWTPVVP GPME PDGKDEEEEEEEKAEKGLMLPPP ALE DDMESQLDGLISRRAVYTPSPVPGSA GAAAVACTDPVPSSGVHGHNDHKNSSS MFRMKALAQLSPYKTPNTAGAGATGGII GGIIAIIATAVAATGILICRQQRKEQTLQ GAEEDLEGGPSYKPPTPKAKLEAQEM PSQLFTLGASEHSPLKTPYFDAGASCTEQ VGAHGKTKEMPRYHELPTLEERSGPLHP GATSLGSPVPPGPPAVEDVSLDLEDEE GEEEEYLDKINPIYDALSYSSPSDSYQG KGFVMSRAMYV
2124	10175	A	3054	115	467	
2125	10176	A	3055	315	431	
2126	10177	A	3056	53	442	PRVMAM/ATKGGTVKAASGFNAMEDA QTLRKAMKGLGTDEDIAISVLAYRNTAQ RQEIRTAYKSTIGRDLIDDLKSEL SGNFE QGAGTDEGLIEILASRTPEEIRISQTYQ QQYGRSLAEDDIRSDTSF
2127	10178	A	3057	186	1268	PRDMAMATIGGTVKAASGFNAMEDAHT LRKAMKGLGTDENAIISVLAYRNTAQR EIRTAYKSTIGRDLIDDLKSEL SGNFEQ VIVGMKMPT*RDDVQELRRAMKGAGT VDEGLIEILASRTPEEIRISQTYQQQYQ RSLEDDIRS\DT SFMFKRVLVLSAGGR DEGNYLDDALVRQDAQDLYEAGEKKW GTDEVKFLATVLCSPKILLLHVFEYQ KDIHRRRIEPEVLNSETSGIFWKIALGLI VKCMRNKSAYFAEKL\YKSMKGLGTD DNTLIRVMVSSSQKMD\MLDIPAHTSKR LLWKSPLY\SIKNRVATSGDYRK\VLLV LCGREMIKIPGRDREGSSTLLNFF
2128	10179	A	3058	1	4608	
2129	10180	A	3059	1	465	
2130	10181	A	306	163	387	IRQKKAIFVIVAFKRRGLRKTID\YYYAR GG*FVKNKYRGFIELGTTGKYFLFCTL AIIDPSDSNIIISMPEQT
2131	10182	B	3060	109	192	GSSSNEYL YERFGLLA VPSIRSLSVQSK*
2132	10183	A	3061	1	1542	
2133	10184	A	3062	1	4226	EAVLCSSRGRPDSSMPDCCRNAALEARS CQSM TSLFSNTVSPTQDGTSSLPRRQSSF AKPPLRALYDLLIAPMEGGVVESTEPLG TSRSGFASGTALFWLGDNGKAASPPGVS VSSLENNEDNTQCNRL EQGYREAAVPD WTQDLALCLLPTLQSLKARTAPHL CVPS SCYKAWYTLAVSKVSGMVEGKAWIILL LLAASTHALLQRPQEGDITPLAGSRAAA VSCQARPFTSFGLMHSSGPVGRHRQLIL VLE

2134	10185	A	3063	2	4195	ALDFPGRFRPTASFIWASVLFETIRHEA EVSTDYKLSLFDLQTSSYQALQRLVLSL GHHDEALAVAERGRTRAFADLLVERQT GQQSDPYSPVTIDQILEMVNGQRLVL YYSLAAGYLYSWLLAPGAGIVKFHEHY LGENTVENSSDFQASSSVTLPTATGSALE QHIAVREALGVESHYSRACASSETESA GDIMDQQFEEMNNKLNSTVDTPTGFLRM VRRNNLFNRSCQSMSTLSFNTVSPTQDG TSS
2135	10186	A	3064	8	665	SAQMAVTTADPRVRPRVRTQLCSLATSN RHAWCILSPEEKSAVTALWGK\NVNDE\ VGGKALGRLL\VVLPVPDRFFE\SGDL STP\DAVNGQTPKV\KVSWSRKCLGAIFS DGPGETWDNLQGSPLPTLK*ACTC*QAC TWDP*RTFRLPGGNVAGFVVAWAHSL GKEFQPHQCKLA*SRKLVGLVLAKCPW PHKYHLKLAFLAVQFLFKGFLWSLKTN Y
2136	10187	A	3065	8	531	SAQMAVTTADPRVRPRVRTQLCSLASLI QTRMVHLTPVEKSAVTALWGK\NVNDE\ VGGKALGRLL\VVYPWTQRFFE\SGDL STP*SLLRANP*GERLHGKKSASVPFSDG \LAHL\DNLKGTF\AHEVSLHCDK\LRG SLKNFRLGQRAWVSVAGPIHFWEKNF NPTSCRLA
2137	10188	A	3066	91	951	TPHFHQGTGKRAAWPTWFNPAGPGIFLR R*GPGKAQRRRSIAPRPVGFSPGPIVRC PHGFGYPHERLRAGPRLPALRKL RVAGI HKEGWPGPIG\SVDPKPDQVPRSLQ\A NVQRLKKYASNILFPQSRAPKKGDR SAEELKLGHPSTGPIVMPVRNVYKKE KARVITEEEKNFKAFASLRMARANAPAL RHTGQKEPREAAEQGC*KAHNKALPGD LESVGQSCWVSTWCVSWEQLGLGWGFT AVTSSCQGIWGFLEQSKPWIMLNLVL KPCWLFG
2138	10189	A	3067	1	1603	MKLLKSILLTILLDFSLHTCASLVPALQW ILLLLITVLVVEGIAVAQKTQDQONIGIK HIPATQCGIWVRTSNGGHFASPNYPDSY PPNKECIYILEAAPRQRIELTFDEHYIIEP SFECRFDHLEV RDGPF GFSPLIDRYCGVK SPPLIRSTGRFMWIKFSSDEELEG LGISEQ IIPFIPDPDFTYLGRYFKFPS/HDCQFE/HL RELDGDSAALVR*NKRRKQNGQAFD\C IWDL*/MPFQK\KIYLRFLDYQMEHSNEC KRNFAVYDGSSSIENLKAKFCSTVAND VMLKTGIGVIRMWADEGSRLSRFRMLFT SFGGASPAQAALSFCNSNM CINNSLVCN GVQNCAYPWDENHCKEKKKAGVFEQIT KTHGTIIGITSGIVLVLLIISILVQVKQPRK KVMACKTAFNKTGFQEVFDPPHYELFSL RDKEISADLADLSEELDNYQKMRRSSTA SRCIHDHHCQSQASSVKQSRTNLSSMEL PFRNDFAQPQPMKTFNSTFKKSSYTFKQ GHECPEQGPGKDRVMGGRFPC
2139	10190	A	3068	163	392	HQELLFLLSSRRLSRSPSEGSRPTM/AL GEKKIGFPSLLWCFPPSAAGASSQIKWIQ PCGSGAPPLPGCSGKRA
2140	10191	A	3069	190	352	HQELLFLLSSRRLSRSPSEGSRPTMVL EKRK*GFHPHSCLRWRLKVCEGKS
2141	10192	A	307	131	395	LWAARAAVLTSLPTGSPSAALSGCCRP GGQGRYSVAACRGRAAGGVAPVPAHT* AAAPLGHFSLLGIVSPAPEPHFELGHYY SGLS

2142	10193	A	3070	1	794	MSRERPPGTDIPRNL5FIAAL/DGARLLP* PAAQPRGGAGGGARRGRDAVRGPIPRSR TESGP/SGPDLHQPEAAGPGRP/CSRSPDT RKRVRFADALGLELAVVRRFRPGELPRV PRHVQIQLQRDALRHFAPCQPRARGLQE ARAALEPASEPGFAARLLTQRICLERAEA GPLGVAGSARVVDLAYEKRAPAAYAGP APPPRADRFAFRLPAPPIGGALLFALRY RVTGHEFWDNNGGRDYALRGPEHPGSG GAPEPQGWIFI
2143	10194	A	3071	133	1079	ARRILQNFSLYPSGEDLKGYKVIQAQTA FSANPANPAILTEA\SAPIPHDGNLYPRLY PELSQYMGLSLNEEENRANVAVVSGAP LQQQLV\ARPSSINYMGGLLLTG*LMLGI RRSR/II*GKGFREVILCKDQDGK\GLRL KSIDNG\VFVQLVQANSSSLIGLV*EFGDQ VLQINGENCAGWSSDKAPRWSNRPF*E KITMTIRDRPFERTITMHKDDSTGHVGFIF KNGKITSIVKDSSAARNGLLTGPNLCGN SMGQNVIGLKDSQIADILSTSGTVGTITI MPAFIFEHIIKRMAPSIMKSLMDHTIPEV
2144	10195	A	3072	242	512	AWVPCLLRHCDREPAPRGRTSPSLWPQE GT/P/GQDRGGGPWLGPQLQ*QRSHGG HLPAPQGPLGGPHDNSSFRPGRGGAGRG QGIEQGSK
2145	10196	A	3079	184	561	GQRGRGLRKSGSAGAGMMEHTHTEA HPHTWVCTSTHTCTHTLGDIDYMHHLV CVSIHMYV/CPHT/MSLALGMSAHTLHM FSHTKLLSR*HAGRHVPMPKQVTCTYVP TPSPTHVLGHACGCRPHAS
2146	10197	A	308	327	598	GPARNPAQCRWAGTAGGPSTLSAAAGP GAKPLMPGAA/GAGQAGWLL*VQGPSP RPPGTLAGPQARHTALVPARASPSTPPC KLRGGLRP
2147	10198	A	3080	63	426	GLLFPQHCPAHRPRRCLRPSSAGRGSA PALSRLPSALCHLCLPRSSLAPRSVSPAA TPHH*ALQGLVEPWGPLHSAPLHR*APA SGPAGNVRAWPACRGWCLSRPLPGTV GEGAASRAF
2148	10199	A	3081	1	588	
2149	10200	A	3082	81	289	
2150	10201	A	3083	3	387	
2151	10202	A	3084	2	290	RPPGPSRSPPAPPPSSRRPLPKMACCACC ARVTAGPVPGLGWGVGGPGQRPVTRR ARPPSGLLGFEARPLVPWTSRSPFRQCCT ACGHLVEFVL
2152	10203	A	3085	2099	5383	VIQTSLSPPATNDRGHFPFLDNWTGKP VHSMVAHLDAVTCLAVDPNGAFLMSG HDCSLRLWLDNKTVCQEITAHKKHEE AIHAVACHPSKALIASAGADALAKAHKE QGGKRLHLPVEDDGFQAQAPPCWEEVP QGTNAQFLGCKGLCPSPAPGSEHTRKD GGRCLDTQDMAAFCWDSHLPFRKKGAE LQSPPLLPQIPAPGSGVSFHIQIGLTREF VLLPAASELAHVKQLACSIVDQKRPRVQ VPRP
2153	10204	A	3086	2	426	EDGSLATFLGRRQFAFAEMRHSKRTHCP DWDSRESWGHE5YRGSHKRKRSHSST QENRHCRPHHQFKESD/CCSMCIPLEASH SVEEDTHPSHYLEARSNERDYDRRYV DEYRNDYCEGYVPRHYHRDIESGYRIHC SRS

2154	10205	A	3087	39	1514	GDGAAAILWGVCRSGRGKTA VWRHFS AEGPFAFAEMRHSKRTHCPDWGSIESW GHESYRGSHKRTRISHSR\QENRHCKPH HQFKESDCHYLEARSLNERDYRDRRYV DEYRNDYCEGYVPRHYHRDIESGYRIHC SKSSVRSRRSSPKRKRNRHCSSHQSRSM KSVDTLGEGAFGKVVECIDHGMDGMHV AVKIVKNVGRYREAAARSEIQVLEHLNST DPNSVFRVCVQMLEWFDHHGHVCIVFEL LGLITYDFIKENSFLPFQIDHIRQMAYQIC QSINFLHHNKLTHTDLKPENILFVKSDYV VKYNSKMKRDERTLKNNDIKVVDFGSA TYDDEHHSTLVSTRHYRAPEVILALGWS QPCDVWSIGCILIELYPWGSQFFRLQ**K EHLAMMERNIRTPYPQHMIQKTRKRKY FHP*PSLDWDEHSSC/AGRYVRRRCKPL KEFMLCHDEEHEKLFDLVRRMLEYDPT QRITLDEALQHPFFDLLKKK
2155	10206	A	3088	2	175	
2156	10207	A	3089	1	534	
2157	10208	A	309	1	630	
2158	10209	A	3090	1	325	LEKERDFY/FGKLR/NIELICQENEGENAP VLQRIVDILYATDEGFVIPDEGGPQEEQE EYYSLGPAEQHGYSLQIMCLTVKYSLL LSLEDSLVSFHKQKVPLLKVPVF
2159	10210	A	3091	3	930	SSRGRAGGVWRFERDEDGTGAGCGQW TRFCREPKMAVNVYSTSVTSDNLSRHD MLA\WINESLQNLTKIEQLCSGAAYCQ FMDMLFPGSIALKKVKFQAKLEH\EYIQ NFKILQAGFK\RMGVDKIISVDKLLKGK\ FQDNFEFVQWFKKFFDANYDGKDYPV A\AR\QGQETAVAPSLVAPALNPKPKPL TSSAAPQR\PISTQRTA\AAPKGWALGV VRKNPGVGNGDDEAAELMQGQRI*NL LFEDLGGERDFYFGKLRNIELICQENEG ENDPVLQRIVDILYATDEGFVILDEGGPQ EEQEEY
2160	10211	A	3093	337	903	CNRNTSTLTRCTNVCINTPRPAPPLA/P QATLHFQFP*/PPLPL**QPQALSATRLSL/ VCHGSGRLRLPLLQAAPGWLPSLGPLSL FSCRGRVLLC*PGWSCYLGLKLSSHGL PKCWDDRPKPPSPASFEWAPTRPNLPQ HGTQSQCCLFSVGEAPRPHSGSAYYTNQC LQCSRPCSERTRRLGVLLPK
2161	10212	C	3094	821	1051	MAMELINNKHWPVSRALCWNTVLAYVI GEGVNSGRSCLAQTLVTFRKGSAFRD WVLGPAPGGNGALRLFRKILFC*
2162	10213	A	3095	1	594	
2163	10214	A	3096	3	761	TSRGRVGTQAGEPRDLRPPPCSSPLRV/ AVV\CLEQPERGAWAENIPQPNGDSAV RSFG\TGTHVKLPGAPD\NPNVY\DFKTT YDQMYNDLLRKDK\ELFTQNGILHIAGR NKRIKP\GPERFQNCCKDLFDLILTCEERV YDRVGWKI*ISR\EQGDLSPVHV\NLDI QDNHEEATLG\ARFLICE\VCQCIQHTED M\ENEIDELLQEFEESGRTFLHTV\CFIL FSFLDICF
2164	10215	C	3097	129	314	
2165	10216	A	3098	1	1434	
2166	10217	A	3099	1	831	
2167	10218	A	31	1	365	FFFLLLILFLLLIQYHYIFYTFLWLRLLV LTGSI*C*KCKITMNST*IE/TVFKDYEH LYVCKLKNLEKTDKVLTIHNLRLNQ*E PEVLTRAKMYKIYNDIE

2168	10219	A	310	101	520	RRLQKPGCLIWTRGST*CPLTLLPSRGA GLGTC/KPAMPEPPTHSMGTCAARASPT STTPCST/CAQSHRPGRNKQPKG*GMRA HGAGLAGSSTCSPGVGSTG*SQGL
2169	10220	A	3100	1	1251	
2170	10221	A	3101	1	5355	MAGWLRWLDGWLTGWLAGCMSEW MMDGWMDGWIDGWMDGWNPIVPETQ VLHEEIELPGSNVCLRYLSSRTAGYKSL KITMTQSTVPLNLIRVHLMVAVEGHLFQ KSFQASPNLAYTFIWDKTDAYGQORVYG LSDAVVSVGFYEYETCPSLLWEKRTALL QGFELDPNLSGGWSLDKHHILNVKSGIL HKGTGENQFLTQQPAITSIMGNRRRSI SCPSCNGLAEGNKLLAPVALAVGIDGSL YVGDFNYIR
2171	10222	A	3102	205	393	
2172	10223	A	3103	2	158	
2173	10224	A	3104	1	1923	MRPPPALALAGLCLLALPAAAASYFGRQ SRSLMPSRDPHAGALSAAILASGEPSLPR TPSPPSAFALRSGDREGWVDGWGLFPV SGQRIVRVQGEWGKPRTSFAFDYNTKCF GILIREYANIRRAGNIYVFGPLMNDPQQ MASSLQAKTWAFAHQCSAAKQQLHTE LLHEDALKKWTSPAMGWERSRSHDKPR RLSRPLVPPRPFPRAPCAGSSRVRRGLAD QKGQQFPTQRSLLPTGSASFTPDRCAES WCLRPRALIGCSLTSSNPAAPRWAREGG GCGWRCASDKPESHFQSQVDFVPTIGGV APPLHGRGQTSSSAPLLMEPHLLGLLLG LLLGGTRVLAGYPIWWCWAQGCVAVNI FADIYLVVRAILLHLYIHVILYAGKWSQ WAMGAGEKVLRESEATRFFSVRQPVPR EHSGYPRQVHEIQSCMGRLDADKQSG HIVENEIQASIDQIFSRLEILSSKEPPN KRQNGR/LFRVNSLKYDVQHLQTALRN FQHRRHAREQQERQERAFRC/RSKPFTT *TLDTTITNWDRIHLQF*LPSLPRKFHN GHGIDLILDGHNLDGLRTQRLATLKGT QKKILDIANMLGLSNTVMRLIEKRAFQD KYFMIGGMMLTCCVVMFLVVQYLT
2174	10225	A	3105	1	566	FSGRPTPRPGAVACRAGMDPLFQQTH KQVHEIQSCMGRLETADKQSVHIVENEI QASIDQIFSRLEILSSKEPPNKRQNAK LRVDQLKYDVQHLQTALRNQFQRRHAR E/QRRRQRAEELLSTFTTNGTQKKDPLTL PNMLGLSNTVMRLIEKR/AFQDKYFMI GGHPA*PLWALFLWFQYRT
2175	10226	A	3106	53	151	
2176	10227	A	3107	432	649	GSHPFAQAGVQWVCSTLQP/LNS*SSNL SLHSCWDYKFKLVCICKGDGKEFLHMHI LKKDVTLTEKLIPRYV
2177	10228	A	3108	2	677	PPSFQPSDGRGDASGRNAAMAAQGEF QLVLVDGGTGKTTFFVKRHLTGEFEKK YVATLGVFVHPLVFHTNRRPIKFNVD TARQEKFGGLRDGYIIQAQCAIIMFDVT SRVITYKNVPNWHRDLVRVCENIPIVLCG NKVDIKDRKVKAKSIVFHRKKNLQYYHI CAKSNYNFEKPFLWLARKLIGDPNLEF/V AMPALAPPEVVMDFASTYEHDLEVA QTTAL
2178	10229	A	3109	1	549	

2179	10230	A	311	411	640	ADIDSRGPKMSLQSSS*SRGSWMSGN*W SFSSDPTYSGSGGSAPSPNPTQGAEECGR TAPGLAGSSTCSPGVGSTR*SHFRPTHPS LENLEDIALTNVLQNRVRAEPASLKSPV IALLCMSDLTVGTTVTQLQHLNMTMGVIG SQDGRDQVAALNHQKQGDWPFPRVTV LWRKGIDQTFWGLLNTGSELTLPIDPK CRCSPPVKVEAHGCQVINGVLAQIQLTV GLVGPRPVPSTTQGAEECGRTAPGLAGS STCSPGVGSTR
2180	10231	A	3110	2	822	APALAPASAASPAFEFTLPPSFQPSDGR GDASGRNAAMAAQGEQVQFKLVLVG DGGTGKTTFFVKRHLTGEFEKKYVATLG VEVHPLVFHTNRGPIKFNWDTAWPWR NSGGLARDGLYIPSPRVPIIMFDVTSRVT YK\NVPNWALGDLVTSV/CENIPHLCCVA NK\VDIKD\RKVKAKSIVF\HRKENFQYY DISAQKVPTNLKKPFLWALLGSLMGDP* LWNLLPMPLLSPPPR/EVVMPEQLWPAT SMKHDLEVASDNCLPPDEDDDPVKK
2181	10232	A	3111	116	599	PQVISLPKCCDCRCEPLHLAAEKSLPTVR ETTKVPGEAKSEFHKNKMDGRGGKPMG GCEGPDAMYVKLISSDGHE\FIVKRDHG LTSGTE*KPMLSGPG/QFAGGKTHNEVN FRIEIPSH\AIRKVCNVFFTYKV/RATPNS SHPRFPEFPNLAPGNLHWELA
2182	10233	A	3112	84	348	KYTIKTKTVLKSGIFSTCPKPKSCYDFV PLNAGPIPPKSILGTNGPTHLEMLD*RL NKPTPISPQRSPLTQVGHR*TRPTRRRPR T
2183	10234	A	3113	122	518	KSLEFFPPALSPSPALILCHLMQAPYHLK VSWEPTDPPT/ALEMLD*RLPLPHA*HKG ETHTCGPLSDHTFKAPPDPLQICLLSHQG PASPSQQTHPYQPSEVTADSGGTQVDKA NQEEATNTKHHEQEEEQD
2184	10235	A	3114	1	1452	MSAYCLQLGGLQALLALTQTPGHRDSL DAQPAAVLVCGWPWLASFSERTIVGHK EWTIKDKLKNKFKDEFDIVSLPCTLGSH QPQDPMLKLPWSITYGRCLAPGDHTVSL VIKLVESASLSLAVSNMLSDMIRWMPAG CGRCLLGLQSESRAVCGQCVGMEQVCR VSGPHIRWIPQQLHSCFLFLYPSYPLEP SSNTSFICPHSRTYNGSLLSCIPNSAAAAA PPTPQATSFSPSCPSPKQRLPTGRVVEGSD HRVHEARLPGNHSRSGVDSAPPTLAHA GLLLTEEKTLKENGRRAEALRVGVHWR HGTSQGPGRTLWAEKVKPHFRTRGQVY DASSAPVTEHTATELPAGNQGSQPGLOE GGLEGTVVTLVSWKVT/MVSRRC*CRY GQRPH/HHLKVLGNQR/PTHLEMLD*RL PLPQRLTPKGKHTPVVPLLQPFKAPPD PLQICLLSHQGPASPSQQTHPYQPSEVTA DSRWDTR
2185	10236	A	3115	1	414	

2186	10237	A	3116	112	1655	QEH LQRASPRLLQLLPPLPPPPPPAFGGS LSSLGSRMSRQVVRSSKFRHVFGQPAK ADQ\CYEDVRVSQTTWDSGFWC/SVNP* VLWALICEASGGGAFLVLPLGKTGRVDK NAPT VRR*HS/APVLDIAWCPHNDNVIA/ SGSED\CTVMVWEIPDGGLMLPLREP VV TLEGHTKRVGIVAWHTTAQNVLLSAGC DNVIMVWDVGP\GAAMLT LGPEGPPDA NYRGDWEP\DGGLICTSCRDKRVRIIEPR KGT VVAEKDRPHEGTRPVRAVFVSEGKI LTTGFSRMSERQVALWDTKHLEESPV/S LRKLHTRNGVPVAFFGPDTNIVYLRGK GSGPIRVFENTSEAPFLHYL\SMFSSKES QRGHGLHGPNRGLEVNK\CEIAGFYKLH DGR/CVSPMPKPVPRKSD\AQE\DLGPTQ PQGPDPCLHGLKEWLGGRDAGPLPSSPL KDG\YVPPKSRELARVNRGLDP\GRRRAA PEASGTPSSDAVSRLEEEMRKLQATVQE LQKRLDRLEETVQAKL
2187	10238	A	312	375	519	GMLFPKQITPQSI*VETNAKNV*GGDIAS FMGSTHALFEFPDSSHSA
2188	10239	A	3122	200	469	RGGGAGPLTGHVGLLGIAHAAADQFD RLAAGICGSHSPHPGLPGLHCCAPLWS GPQQN*PTADVAESLQLVTVHQSETEDG EFTECNN
2189	10240	A	3123	1	2520	
2190	10241	A	3124	1	1950	
2191	10242	A	3125	1249	2166	
2192	10243	A	3126	1	2424	MVAIHSALESSLLFQEQSLLYLVLTVHE NLNFMAGFTDGSVTLNKGDIRDRHSK TQILHKGNYPVTGLAFRQAGKTTHLFVV TTENVQDLQFIVAGDECYLYQPDERDC RDDHVFSLYFMIPFFFTL/VIALPQLVPIT GVCGRYLLLCWQTFVAVGILGHFSKT MLLFFMPQVFNFYSLPQLLHIICPRHRI PRLNIKTGKLEMSYSKFKTKSLSLGTFI LKVAESLQLVTVHQSETEDGEFTECNM TLINLLL/QSPWAHT*EKPHIAPAAAAAFS FLCDHWHWPGRFLPSADY*LDFTYGFLQL ATLSLSIPSLQPIGTIGKLEPSYVIRKFLD AQRIHNLTAYLQTLHRQSLANADHTTLL LNCYTKLKDSSKLEEFIKKSESEVHFDV ETAIKVLRQAGYYSHALYLAENHAHHE WYLKIQLEDIKNYQEALRYIGKLPEQA ESNMKRYGKILMHHIPEQTTQLLKGLCT DYRPSLEGRSDREAPGCANSEEFIPFA NNPRELKAFLEHMSEVQPDSPQGIYDTL LELRLQNWAEKDPQVKEKLHAEAISLL KSGRFCDVFDKAWFQQIMHYHMQHEQ YRQVISVCERHGEQDPSLWEQALSYPAR KEEDCKEYVA AVLKHIEKNLMPPLL V VQTLAHNSTATLSVIRDYLVQKLQKQSQ QIAQDELVRVRYREETTRIRQEIQELKAS PKIFQKTKCSICNSALELPSVHFLCGHSF HQHCFESYSESDADCPCLPENRKVMD MIRAQEQKRDLDQFQHQLKCSNDSFS VIADYFGRASPNFIFYVV
2193	10244	A	3127	1	411	
2194	10245	A	3128	2	243	
2195	10246	A	3129	1	1176	
2196	10247	A	313	640	975	VPWEAGGSMSCIFYPRQSEQSHNIVKSK RPVTFQQNRCQKGGGHSADVSSTCQCF QCSHREQGFAKQFSYL*NGGSNSFYLT GCFDNLITSVFCSVRFIHPKAIKGYH
2197	10248	A	3130	2	496	
2198	10249	A	3131	2211	2568	

2199	10250	A	3132	100	2726	AMMGPLPGPHLLDPLLPSSFCPLPPGITV CDSCRGS LVFGDMEGQIWFLPRSLQLTG FQAYKLRVTHLYQLKQHNILASVGEDEE GINPLVKIWNLEKRDGGNPLCTRIFPAIP GTEPTVVSCLT VHENLNFMAIGFTDGSV TLNKGDI TRDRHSKTQILHKGNYPTVGL AFRQAGKTTHLFVVTENVQSYIVSGKD YPRVELDTHGCGLRCSALSDPSQDLQFI VAGDEC VYLYQPDERGPCFAFEGHKLIA HWFRGYLIIVSRDRKVSPKSEFTSRDSQS SDKQILNIYDLCNKFIAYSTVFEDVVDVL AEWGSLYVLT RDGRVHALQEKDTQTKL EMLFKKNLFEMAINLAKSQHLDS DGLA QIFMQYGDHLYSKGNHDGAVQQYIRTIG KLEPSYVIRKFLDAQRIHNLTAYLQTLHR QSLANADHTLLNLCYTKLKDSSKLEVEF IKKKSESEVHFDVETAIKVL RQAGYYSH ALDLAENHAHHEWYLKIQLEDIKNYQE ALRYIGKLPFEQAESNMKRYGKILMHHI PEQTTQLLKGLCT*LSAQPRRPQR*GGPR LAGPTLR SFIPFANK/HPRDLKAFLEHMS EVQPDSPQGIYDTLLELRLQNWAEKDP QVKEKLHAE AISLLKSGRFCDVFDKALD LCQM HDFQDGGLYLYEQGKLFQQIMHY HMQHEQYPAGQSA/CCERHGEQDPSLW EQALSYFARK\KEDCKEYVA AVLKHIE GNLMPPLL VVQTLAHNSTATLSVIRDYL VQKLQKQSQQIAQDELVR RRYREETRI RQEIQELKASPKIFQKTKCSICNSALEPS VHFLCGHSFHQCFESYSESDADCPTCL PENRKVMDMIRAQGT EPRFSMNSQHQL QVLQ
2200	10251	A	3133	11	707	AKMGAYKYIQEVLWRKKQSDVMRFLLR VRCWQYRQLSALHRGSRPHR/RPDKVH RLGYKQAKQGYVIYRIRV RRYI*DSCSR DRRGGRKRPVSKGATFGKPVHHGVNQ AKVWFYPTSAE\ERPGRHCGALRVL NSYWVGEDSHLPNFLGVIPHGSHSHKAI R\RN*PPQWITQTQSHKHREMRGLTSA RPERAVGL\GKGHKFVHTIG\GSRAAW RRRNTLQAPPLPI
2201	10252	A	3134	1	333	
2202	10253	A	3135	1	1530	
2203	10254	A	3136	1	554	ILSQVRCQAQLAQQAAGGGLSFRAASSL PVSPSLAVSMKAFSPVRSIRKN/SALSDH SLG\SRSK\TPVD\DPDGALLYNMKDCYS \KLKEL\VPSPPEQRR*ARWEILAQHVIRL TSWDLADSPWDLAFPLIVQPGIHQRTRG RNQ\RSRTP LGPPSTRDISILSFAGLLEFPS ELMSNDSKIALCG
2204	10255	A	3138	3	251	
2205	10256	A	3139	1	1674	
2206	10257	A	314	22	297	GKEKLSHSAWAPKSQNSNSSASSWSN QSQAQPRFKGEDI/ESHLLMGREALS*IQS /GRLVYLQSL*TRFSTASPEQLDTECRL VHSQTL
2207	10258	A	3140	1	648	MSLRKLTIMVEGKGGPNIPHACGCRQRS SIKVSLPAVTSKSESPKEPEQLRKLFIGG LSFETTDESLRSHFEQRRTLTDCAVMRD PNTKCSKGFGVITYATMEEKYHTVNGH SCEARKALSKQEVASASSQR/GRSGSGN FGGGHGGGFGGNDNFHGHENFRGHSSF GGSHGGSGYGGSGDDYSGFGNDGSGNFG GGGSYNDFGNYSNQSSNFGPM

2208	10259	A	3141	579	2102	SPKEPEQLRKLFIGGLSFETTDESLRSHFE QWGTLTDCVVRFGDKAVKQPISLAYL GAVFSECL*K*LIAL*LELCWQRNVLL*F *KLTS*I*G*WETGRTFYKRLV*SFLLPYS KLK*QKLLRSDFLVHLKTLFSGVMRDPNT KRSRGFGFVTYATVEEVDAAMNARPHK VDGRVVEPKRAVSREVSFFFFFLNLL GYVLL*T*DSGVF*TYQNFLFEYRLC*SK PMVFLLLDSQRPAGHLTVKKIYVGGIK EDTEHHLLARDYFEQYQKNEVVEIH*LDR VGQWPRKRGFAFVTDDHDSVDKIVSKY QIVAFSGSTICMAF*TLIPCCIIYVFFLVQ KYHTVNGHNCEVRKALSKQEMASASSS QR/GYACCLIKP*R*L*VTPV*MI*CLNFM S*GRSGSGNFSGGGRGGGFGGNDNFGRG GNFSGR/GYVWFIYM*F*LLTIFAMKILQ YGNCIQNVTLSPSHT*NLKFLTGFGGS RGGGGYGGSGDGYNFGNDGKFFRNK
2209	10260	C	3142	42	152	MIXXXXXXXXXXXXXXXXXXVSPSAFA PXXXXKSLG*
2210	10261	A	3143	3164	3255	
2211	10262	A	3144	12	336	SPVQL*F*LFLVFC*LWSWSAVVYLGPL GTPSADAHT/AGLSKTPPHWAARARLDD VFSLRTFSSHSLNMELVQDLTASAPMYS STSRDPP/CLGLPKCWDYKREPPRAH
2212	10263	A	3145	602	744	TPASLKIPVE**NTLLAKMVIS*PRDLPA SASQSAGITGVSHRARC
2213	10264	A	3146	269	483	
2214	10265	A	3147	2	988	KYPPPAVLWFFGFFVLRRLALSPLRECS GMISAHCKLCLPGSRHPASASRVAGTT DVHHHAQLI/L/YVFLVETGFHRVSQDGL NLLTRLHLPKCWDYR/R*ATTPGLCFVF* KKRNAREGGRQPPDHKS*FL/VFFFLFFL KWSL/DSVSKAGVQWHGLSSLQAPPRGF TPFSCSLPSSWDYRRPLPRPANFFVFL** VGGFTVLARMVLIS*PRDLPASASQRAG VTGLSHCAWSEFF/CFFKTGSHSVTHARV QRHNLDSLEA*TPGLN*SSRLSLPSSWD YRSTPPSPANFCSFSRDGVSPC*PGWSRS SDLVIRPPRPKVPGLQA
2215	10266	A	3148	2	608	RDSPPRSLDSGARRDAPPHSPAECRAH AATWRLKPRPHRPHSLTAPLPVHWAGT TEPLSPRPATGTRERPPLHFPATPRSHS/ WRLARPCRQGPS*DRLFSAGAGPGVVS CLDREEKNAGHWLSSAFALVWLWLTEH WLLLVGFIGYVKAGSVYPGCRACFFW AVLAGLGCLPAVSGIPRERFWVPRLHL VPWLALWE
2216	10267	A	3149	131	453	
2217	10268	A	315	152	437	GLRLCLSRPLTRPGDDSVGGSAMASGAG GVGGGGGGKIR\TRRCHQGPIKPYQOGR QQHQVWDPDAAVAVRWGKLGWRGRA VRGPGAPRGADRA
2218	10269	A	3150	403	787	MGRIFLDHIGGTRLFSCANCDTILTNRSE LISTRFTGATGRAFLFNKVNNLQYSEVQ DRVMLTGRHMRDVSCKNCNSKLGW IYGWVPLKDSQRF*GKGRR*SGERVLVS EELRALEEHVPPDNS
2219	10270	A	3151	171	382	KNSYKCEECGKIFNEYSHLIARK/RIYT*E KLYQYKDCEKAINVCSHLTQHQRV/H*K KYYKFNYCQKVQKI
2220	10271	A	3152	76	195	VHLLNPQHMLPLSTHKQRRITL*KGHAE HLQYYLNNQKLS

2221	10272	A	3153	2	634	VVWESLNREDLWPCFLRRILGGSSYSTA EMVSGQTLQRAHLREAASISLNSQGVW RKSARFSHQLERGTEEQQLQIPDLGQHP SKAPVFPQVQAHPRFQTGPHGHKLQRN QDPGQLQ*IPMLGQTPWTQATGPTI*TQP SGRSPCSHYSGMSTDSGFMALHSLTQVS SQPTCRLLEACPWTSSGGLPRISGWT RQVFGSVDRDLISP
2222	10273	A	3154	275	463	GKFFSLCETLFPSSGVGSFFSSCTMDSSRS LGVGSKNSHFSLA*NTDLRLSLCPFPGW KEDIKF
2223	10274	A	3155	5904	7919	FMFINMSVCRLITTKYLLLLFLHESLILLS ENLRKDVEAVTGSPASQTSICIGILLRSA ELALLHPVDQANTLKSPVSESVSPVVP DYLPTENGDFLSSKRKQISRDNIRSVT VNHMSDNRSMSVDLSHIPLKDPPLFKSA SDTNLAKRAFFMDYLSKHLGKISEDE SSGLVYKSGSGEIGSETSDKKDSFYTDSS SILNYREGFRIYLSFG*VMGNQNILSSTL TSKGNETIESIFKAEDLLPEAASLSENLD ISKEETPPVRITLKISQSSLSGESLRERLPH PNLGFPLVFSYKNMKRSSSQMSF/EATIS LDSMILEEQLES DGS DSHMFLEKGNRK NSTTNYRGTAESVNAGANLQNYGETSP DAISTNSEGAQENHDD\LMSSVVFKITGV NGEIDIRGEDTEICLQVNQVTPDQLGNIS LRHYLCNRPGSDQKAVIHSKSSPEISLR FESGPGAVIHSLLAEKNGFLQCHIVENFS TGFLTSSLMNIQHFLDETVATVMPMKI QVSNTKINLKDDSPRSSTVSLEPAPVTVH IDHLVVERSDDGSFHIRDSHMLNTGND LAKENVKSDSVLLTSGKYDLKKQRSVATQ ATQTSPGVPWPSQSANFPFESFGLHLGE QLMEENESLKQELAKAKMALAEHLAE KDALLHHIKKMTVE
2224	10275	A	3156	149	382	ARHCGSCP*SQHFGRSR*AEHLRTGV*D QPAQRGETPSLWKNTKIRRAQWWCPPVI PATSGGLRQENYLNPGRQRLQ
2225	10276	A	3157	162	342	
2226	10277	A	3158	1	1995	FRLVTPGVPAFSGCGRRHGRGTGRRAM ASCVGSRTLSKDDVNYKMHFRMINEQQ VEDITIDFFYRPHTITLLSFTVDSLMYFAF TTDDSV*DNWRGILSGILLFLIKV*AFP NGPLTRPHPALWRMVFGLELYFLVFLV LLFPEFEQAKSLMDWLDPNLRYATREA NVMEYAVNCHVITWERIISHFDIFAFGHF WGWAMKALLIRRYGLCWITISITWELTEL FFMHLLPNFAECWWDQVILDILLCNGGG IWLGMVACRFLERRTDHWASFKDIHTTT GKIKRAVLQFTPASWTYVRWFDPKSSFQ RVAGVYLFMIIWQLTELNTFFLKHIFVF QASHPLSWGRILFVGGVNSFPQLRQYYA YLTDTQCKR/L*GTQCWVFGVIGFLAVI VCIKFGQDLFASKTQILYVVLWLLCVAFT TFLACLGYMIWYAEHYGHPKRPTPECE DGTYSPEISWDHRKGTKGSEDSPPKHA GNNESHSSRRNRNHSKSKVTNGRWER NEKPWVNSKMFPECLGTEEGKWELHLG TPRGGGSAHRGKPGRGEGTLGVILRLSL SLCFPTDLGRVQADHRLGGPFANVGSLL TSALDMRSPVAARCVERETVAISFHSCQ EQLRAMLDRCGSVNIFPSDEALTPWLMD WSPVFNFIYESTFPID
2227	10278	C	3159	410	538	
2228	10279	A	316	3	609	
2229	10280	A	3160	4	334	FFPKALIFCREVGPISPPPKIRFP/SPKFPGN RFSPPRVVKPPPGP/SPFKRPPIRKKILPCQ PP*TLAPRIL*KGPP/PSSSSG*NPYYLFIQ QKTEYLLWSRPCPWHCEQR

2230	10281	A	3161	1	1130	PLLPTSLSVEDAAILLQQVMRAFASKQAST VVFSDTVVVSEKFINDCTELFRELMMHQK AEKEMKNNPVHLITEEDLKQISTLESVST SKKDKKDERRRKATEGSGSMRGGGGGN AREYKIKKVKKKGRKDDSDDESQSSH TENEESGYDKKDENILEDVKWGKTSQFL EIFQDIEKARDKTLEADSELESVFMSSTT SASGTGRKRTIKDLQEEVSNLYNNIRLFE KGMKFFADDTQAALTKHLLKSVCTDITN LIFNFLASDLMMAVDDPAAITSEIRKKIL SKLSEETKVALTKLHNSLNEKDQHALLV KYQGLVVKQLVSQSKKTGQGDYPLNNE LDKEQEDVASTTRKELQELSSSIKDLVLK SRKSSVTEE
2231	10282	A	3162	20	2478	RVCSSSASTASQAVMADAWEEIRRLAA DFQRAQFAEATQRLSERNCIEIVNRLIAQ KQLEVVHTLDGKEYITPAQISKEMRDEL HVRGGRVNIVDLQQVINVDLIHIENRIGD IHKSEKHVQLVLGQLIDENYLDRVGQEV NDKLQESGQVTISELCKTYDLPGNFLTQ ALTQRLAIIIGHIDLNRGVIFTEAFVAR HRARIRGLFSAITRPTAVNSLISKYGFQE QLLYSVLDELVNSGRLRGTVVGGRODK AVFVPDIYSRTQSTWVDSFFRQNGYLEF DALSRGIPDAVSYIKKRYKTQLLFLKA ACVGQGLVDQVEASVEEAISSTWVDIA PLLPTSLSVEDAAILLQQVMRAFASKQAST VVFSDTVVVSEKFINDCTELFRELMMHQK AEKEMKNNPVHLITEEDLKQISTLESVST SKKDKKDERRRKATEGSGSMRGGGGGN AREYKIKKVKKKGRKDDSDDESQSSH TGKKKPEISFMFQDEIEDFLRKHIQDAPE EFISELAEYLIKPLNKTYLEVRSVFMSS TTSASGTGRKRTIKDLQEEVSNLYNNIR LFGKRGWKFFADDTQGWLLPKHLEV QCVLISLNLIFNFLGFGILMDGQ*DDPG RPFTSELRKELSKLSEETKVALTKLHN SLNEKSIEDFIFCLDSAAEACDIMVKRG DKKRERQILFQHRQALAEQLKVTEDPAL ILHLTSVLLFQFSTHSMHLHAPGRCVPQH AFLNSKIPEDQHALLVKYQGLVVKQLV SPSKKTGQGDYPLNNELDKQEDVAST TRKELQELSSSIKDLVLKSRKSSVTEE
2232	10283	A	3163	1	389	IPSEISRSVAFSL/LPLLSVSGLEAIQRTPK NQVYSRHPENGKSKFLNCYVSGFHPSD IVGDLLMNGERIE*A*HSDLAFRKDWAF YLLDYTEFTPT/EKDEYACRVNHVTLSP KICKWDRDMLSASMEA
2233	10284	A	3164	2	409	RPRVRPRVRSIRAEMSRVALAVLALLS LSGLEAIQRTPKIQVYSRHPAENGKSNFL NCYVSGFHPSDIEVDLLKNGERIEKVEH SDLSFSKDWAFYLLYYTEFTPTEKDEY ACRVNHVTLSPKIVKWDRDM
2234	10285	A	3165	26	299	
2235	10286	A	3166	11	486	
2236	10287	B	3167	198	282	XPSLEDLSNSIQKLHLAENAEPEEQSAA*
2237	10288	A	3168	80	827	AQQAVLARSKLESCLRELHGHNRSLKEE GVQRAEEEEKRKEVTSHFQVTLNDIQL QMEQHNERNSKLROENMELAERLKKLI EQYELREEHIDKVFKHKDLQQQLVDAK LQQAQEMLKEAERHQREKDFLLKEAV ESQRMCELMKQQETHLKKQLALYTEKF EEFQNTLSKSSEVFTTFKQEMEKMTKKI KKLEKETMYRSRWESSNKALLEMAEE KTVRD/ERTGGPAGKNPTAGEAVPGTAD RAQ
2238	10289	A	3169	1	2511	

2239	10290	A	317	1	949	MGSCAARASLTSTTPCSTAPSPINHPKAE ECERTTAQDWQAAPPAAPVRDPLGEP WAPESGGDVESLYIYLRDCKYTNQHPVF SSRFVNPPIDTLYLALVGPWKTFMSSS GIVNTPIGTLYLAQVTVPPPLHTRFFALSP RQPRSFKNGLLFQTGTTLNPLSGYSSDY KGFGRFRNHPQTGFSPAGANQRGPLVAT LSGPGGEGQSAVPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSPTGKR SATAINLKVKHTSQHPVFSSRFVSAPID TLYLALVRTWRVFMSSSGIVNTPIGT YLAQGL
2240	10291	A	3170	93	517	GRGHLGG/VWC*RSQERAQKIKEASAEIT /CSWLQMKQNRKPSQEKTRDTRMENP DRGFVPGKECSFEQLEHVREMQEKLARL HFSLDVCGEEDDEEEEDGVTEGLPEEQ KKTMAADRNLQLLSNVGSCLGALVPGG MRGGE
2241	10292	A	3171	3	348	FFAFFLGLIPFNAPLPHSTWGAAEHPPES VKSHSLKMRGAVW/CLRGTPTR/HCS SGSAFSARCSFWIELLRSSRLSSWSRLR SAIVFFCSSGKPLSDPNPLPHRPPPHTH PG
2242	10293	A	3172	2618	5946	PGCNFSLDVCREEEDDEEEEDGVTEGLP EEQKKTMAADRNLQLLSNARGRAWQL APMEPELLVRKVSALQACVRGFLVRRQF QSLRAEYEAIVREVEGDLGTQWTEGRI PRPRFLPEKAKSHQTKAGDRVANPEQ GLWNHFPCEESEGEATWEEMVLKKS SSANQGSCLCRDHSSWLQMKQNRKPSQE KTRDTRMENPEATDQRLPHSQPLQEL QYHRSHLAMELLWLQQAINSRKEYLLL KQTLRSPEA
2243	10294	A	3174	16	319	LGTRPAHRSSQ*GKGSPLPPGAPLIS GAKEGGPGDRAAHADFLPAEEGAHGM/R GSHGSPLIAPLPTYPHPPSGLFPLGALPLA RPRHQGAALGSVHEIQ
2244	10295	A	318	1	4425	
2245	10296	A	3180	417	736	YGLGAVAHACNPSTLGGQAGQITRLAV QDQPDQHCETPSLIKMQKN/LPGHGGVC LQSLLRGLRQGNCLNQGGSCEPRSH QCTPAWAIE*ESVSKKKKKKKLVV
2246	10297	A	3181	1	2061	MGA VRDELHSLVVPPLMGRGAQT PMAAALRDPAGQCVTFEDVTIYFSQEEWV LDEAQRLLYCDVMLENFALIASLGLISFR SHIVSQLEMKGEPWVPDSVDMTSAMAR GAYGRPGSDFCHGTEGKDLPEHNVSVE GVAQDRSPEATLCPQKTCPCDICGLRLK DILHLAEHQTHPRQKPFVCEAYVKGSE FSANLPRKQVQQNVHNPIRTEEGQASPV KTCRDHTSDQLSTCREGGKDFVATAGFL QCEVTPSDGEPHEATEGVVDFHIALRHN KCCESGDAFNKSTLVQHQRHSRERPY ECSKCGIFFTYAADLTQHVKVHNKENP YECFEGGKFFKPA\SLVKHRRVHTGES P HVCDCGKFFSRSSNLQHKRVHTGEKP YECSDCGKFFSQRSNLIHKKRVHTGRSA HECSECGKSFNCNSSLIKHWRVHTGERP YKNECGKFFSHIASLIQHQIVHTGERPH GCGECGKAFFSRSSDLMKHQRVHTGERP YECNECGKLFSSQSSSLNSHRLHTGERP YQCSECGKFFNQSSSLNNHRLHTGERP YECSECGKTFRQSRNLRLKLVHKPDRP YECSECGKAFNRPTLIRHQKIHIRERSM ENVLLPCSQHTPEISLRTDLIRALSSTML NLVHPSTHTGEVP*EC*LCWKLSGDKLH SLTVEFISVFSLLGL

2247	10298	A	3182	441	1074	Q R V Q R S L K K * C W G / F N W G H S G G K I * K Q I G P Y L N T G / T R L K S K W I I V P Q N C I S R R Q Q G K R V H L G L G K D F L N P T P K A Q S M / R G K I D K L Y F I K I E N F S L K G T I R R T K R Q A V E W Q K / Y L Q N I S D K * V A S R L H K E V S K L N K V K P I V D L M R C F / R P E L A A S G P C S L S F S I C F Q H * I Q N V L L E I Q V R S H Q P S E L S N R R P W H S K V H N S L Q C W A K H E A P L F S L L
2248	10299	A	3184	178	488	V S S T V F G N T V R N K T E D D S G G N W E P P R T I L Q A S G K L K N P K A R L A S E C L S P F D S T G K A I H L C Q V C G R A S R S H Y S L G H H / M R H S H V G E * S * K C P G C G K G F S T K L D L R W
2249	10300	A	3185	7	310	K K R S H C A Q A G L E L L S G Q L G * T S S V Q K I R K L A G C G G V H P W S Q L L E R L R W E D S L P Q G G Q G C S E P * S H H C T P A W A T E * D P V S N N N K Q K Q K P K E S N L S R A T S R P
2250	10301	A	3186	65	203	K G D F Q G H Q G P W D A P P * P A F W W Q R E A R G E G E A M S Q S P C R G R G N A E M Y R P S A Q P E T G P A S G * * T E A A R G S S G W A E P W P R G * K P P E F P M R L G W P F P T P G A F S L P I L C D E E R P * G Q R S S G C E S Q Q E L R S P R E T E L Q V T S P T C F S A G P R R P G P A P G G P Q A A R A Y C C H L K T S S E P T F H Q A P T Q A E V S W E F S P A / P P A D K E M T S M A T P E K C P T S Q A P A I R K A A L P H P E R G N Y F L S A A W P Q G A P F P L W G S A S P F V A L P W S P R A G A A P L C P G K A P P S K T R L G R A V T F P * A E G G T G R G R G H V A V P L P W E R Q R G N V
2251	10302	A	3188	1	2559	
2252	10303	A	3189	259	3222	
2253	10304	A	319	160	747	V L N G S G R P S Q S K K H F P P K P G T F G G A S V H Q M F I M S L P A / G P D L S G F D E D D K G W P E N Q L D M S D Y S S S Y Q D V A C Y G T L P R D S P R R N K E G C T S K T P H A L T V S P F K G I F S S A T K V F Q A P N A C K R G A * G K G * P W E G K A S S K P G R D F L R E G R K M S W K L F N R K L I S S Q P Y V P V G V C L T S V F T I A S L G E Q G M V F P L K V D L F K L T G
2254	10305	B	3190	114	2876	M D K F L D T Y T L P R L N Q E E V E S L N R P I T G S E I E A I I N S L P T K K S P G P D G F T S E F Y Q R Y K E T V V C R L S P P S F N G G L P L G S D L V F Y A P G P Q K I I W V M V H V G A L A L K D G F S P L D V G V H G F C R F R N H H Q T G F S P A G A N Q R D P L A A T L S G P G G E G Q S A V A R L T G E K K N H P G A Q Y A N R L S P R V G R F I N A A G T T G F P T G K R A V S A T Q L M V K D D V T Y A I K L S C W P G L D I I P S C L A L H R I E T E L M G K F D K G R L P T H P L M L R L A I E

2255	10306	B	3191	1	2640	MEIRGRVEQRVGYTIEQINHM RDVFGTR LRR AEDVFPPVIGVAAHKG GGVYKTSVSV HLAQDLALKGLRVLLVEGNDPQGTASM YHG WVPDLHIHAEDTLLPFYLGEKDDVT YAIKPTCWPGLDIIP SCLALHRIETELMG KFDEGKLPTD PHLMRLAIETVAHDYDV IVIDSAPNLGIGTINVVCAADV LIVPTPAE LFDYPSALQFFHMLCDLVKNVDLKGFEF GELAPLYGCWGLRTGI AVACAPHHASL NLHGLNQIRNVKKQSVYLMNLRKSGTL GHPGSVDETTYERLAEESLDSLAEFFEDL ADKPYTFEDYDVSFGSGVLTGKLGRDL ATYVINKQTPNKQIWLSSPSSGLKRYDW TEKNWVYSHDCVSLHDVLA AELTKALK TKLDLSSLAYS GKELDAQPGYYMLHAQ YMLRPPLSSPMQH RAPETGPTSRNSVLN AVTPPAPTTPPSPLFDSRGSPRRKTYQNV QQFIDEGNYTSGDNHTLRDPHYVEDKG HKYLVFEANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQS AKKRDAELA NGALGHIELNNDYTLKKVMKPLITSNTVT DEIERANVFKMNGKWYLF TDSRGSKMT IDXGSPXKIRLFYTDYSGKHYGKQSLTT AQVNVSKSDDTLKINGVEDHK TIFDGDG KTYQNVQQFIDEGNYTSGDNHTLRDPH YVEDKGHKYLVFEANTGTENGYQGEES LFNKAYYGGGTNFFRKESQKLQQS AKK RDAELANGALGHIELNNDYTLKKVMKPL ITSNTAAANQESSHVQQALALEQQFLE RTQALEAQIVALERMR AADQTTAKQGM CTQVHLTNTSRHAGRPSKQCFSTRRQR HRLSDPKQDLGNRRFSPPP*
2256	10307	A	3192	1	454	MERRNRRTGRTEKARIWEVTDRTVRTW IGEAVAAAAADGVTFSPVTPHTFRHSY AMHMLYAGIPLKVLQSLMGHKSISSTE V YTKVFALDVAARHRAIRVPRQQGDYRT RIWK FEDGLSNVLVIQLNKLIICVMCLVR DCDVLKTYFHL
2257	10308	A	3193	2758	2946	
2258	10309	A	3194	2372	3570	EALLPGDQDSQSGKGVAAREVWFLPSSF APVLLRLVGNHHVGDNSIDSWKNAGR/V FKDS DKFDANDPILKDQTQEWSGSATFT SDGKIRLFYTDYSGKHYGKQSLTTAQVN VSKSDDTLKINGVEDHK TIFDGDGKTYQ NVQQFIDEGNYTSGDNHTLRDPHYVED KGHKYLVFEANTGTENGYQGEESLFNK AYYGGGTNFFRKESQKLQQS AKKRDAE LANGALGHIELNNDYTLKKVMKPLITSNT VTDEI

2259	10310	B	3195	1	2232	MKLMETLNQCINAGHEMTKAIAIAQFND DSPEARKITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQRVGYTIE QINHMRDVFGRRLRAEDVFPVIGVAA HKGGVYKTSVSVHLAQDLALKGLRVLL VEGNDPQGTASMYHGWVPDLHIHAEDT LLPFYLGEKDDVTYAIKPTCWPGLDIIPS CLALHRIETEFMGKFDEDNAGMVRVL QPFTSDEKKSIVSTLTFPGKHLRRDKSLT TAQGCDKINNKTSPPTSPDLALKGLRV LLVEGNDPQGTASMYHGWVPDLHIHAE DTLLPFYLGEKDDVTYAIKPTCWPGLDII PSCALHRIETELMGKFDEGLPTDPHL MLRLAIETVAHDYDVVIDSAPNLGIGTI NVVCAADVLIVPTPAELFDYTSALQFFD MLRDLLKNVDLKGFEVDVRLITKYSNS NGSQSPWMEEQIRDAWGSMLKNVEPE NGEVGKXGSPQLINQEKMFIRNRSYI DRDSEYLLQENEPDGTLDQKLEDLQKK KNDLRYIEMQPFPLVSSSRVWVKRGELT AYVEDTVLFSRRTSKQQVYFFLFNDVLI TKKKRRSDSSLREGDNQKAYKETYGVS HITRHDMLQIPKQQQNEKYQVPQFDQST IKNIESAKGLDVSDAGMVPVLQPLHLTE KSGYSTLTIPVNLRTSLTQRKVMCQNL VTHLKSTEWKHKTIVDGERKTYQKRS AVFRMKGILHSATTIR*
2260	10311	A	3196	1260	1340	LPMALAVGFCFRNHHQTGFSPAGANQ RGPLAATLSGPGGEGQSAVARLTGEKK NHPGAQYANRLSPRVGRFINAAGTTGFP TGKRAGFCFRNHHQTGFSPAGANQRG PLAATLSGPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINAAGTTGFPTGK RAGFCFRNHHQTGFSPAGANQRGPLA ATLSGPGGEGQSAVARLTGEKKNHPGA QYANRLSPRVGRFINAAGTTGFPTGKRA QAQAK*WHYREPLLLRAQLTNPPSGQQL KSVDQWPVQKQFSSGSDLYQLHPFHVQ HFLEPCFPRHPEFAPPSTGTESHYYCWIW
2261	10312	B	3197	200	2602	MQLARQVSRLESGQVKHEGQHTKMSQ VLWRSQEENPATLGNNIQLFDWIPQNDL LGHPKTKAFITHGGTNGIYEAIYHGVP VGVPMFADQPDNIAHMKAKGAAVEVN LNTMTTRPGGEGQSAVARLTGEKKNHPG AQYANRLSPRVGRFINAAGTTGFPTGKR AVSATQLMDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPVSLVKRK TTLAPNTQTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQVSRLESG QILPDFGPHHQTEFSPAGANQRGPLAAT LSGPGGEGQSAVARLTGEKKNHPGAQY ANRLSPRVGRFINAAGTTGFPTGKRAVS ATQLIPKVDKTTKIGKKQSRKTGNSKNQ SASPPKESSSSHATEQNWTFDELRE EGFKRSNCSELQEEVQTHGKEVKNEKK LDEWLTRITNEEKPLKDLMEKTKAQEL RDKCTSLSSRFNQLERVSMEDQMNE MKREEKFREKRIKRNEQSLQEIWDYVKR PNLRLIGVPESDGENGTLENTLQDIIQD FADFGTTIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTAPNTQT ASPRALADSLMQLARQVSRLESGHQAPC MKSNNALIVILGTVTLDVAVGIGLVMPVL PGLLRDIVHSDSIASHYGVLLALYALMQ FLCAPVLAALSDRFGRRTVLLASLLGATI DYAIMATTPVLWIYPLVNSPSC*

2262	10313	B	3198	1	3198	MKLMETLNQCINAGHEMTKAIAIAQFND DSPEARKITRRWRIGEAADLVGVSSQAIR DAEKAGRLPHPDMEIRGRVEQRVGYTIE QINHMRDVFGRRLRAEDVFPPVIGVAA HKXSPVIGVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNPDQGTASMYHG WVPDLHIHAEDTLLPFYLGEKDDVTYAI KPTCWPGLDIIPSCALHRIETELMGKFD EGKLPTDPHMLRLAIETVAHDYDVIVID SAP
2263	10314	A	3199	1	2259	
2264	10315	A	32	603	855	GGWIMRSGVRDQPDQHGETLSLLKLQK LAGHGGACL*SQLVRLRQEYHLNPGG GGCSEPRF*GHCAPAWATE*DSVSGKKK KKK
2265	10316	A	320	1812	5065	PNKTGGKTVSDGLHHPSQLHSKLENDQ GFYNVDSSTGFHNKTNPVGPFRKSPFLV MGVDWAETRRSMMMQMRRAPMSDDIL ARDRGSRLSRGNRRNGGGGCRDDDDG GGAGAVRTGEGATEELPPVGGRVRPQH RGELFVLSSAGDLHRDRDTHRGAGSG GGSAMASGAGGVGGGGGKIRTRCHQ GPIKPYQQGRQQHQVSSSRPDLSGFDED DKGWPENQLDMSDYSSSYQDVACYGTL PRDSPRRNKEG
2266	10317	A	3200	1	2418	
2267	10318	A	3201	1907	5097	TSKKIVKQAPVLTFTTA/LLAGGAIQAFA KENNHKAYKETYGVSHITRHDMLQIPKQ QQNEKYQVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHVVFALAGS PKDADDTSIYMFYQKVGDNDSIDSWKNA GRVFKDSKFDANDPILKDQTQEWGS ATFTSDGKIRLFYTDYSGKHYGKQSLTT AQVNVSKSDDTLKINGVEDHKTIFDGDG KTYQNVQQFIDEGNEGILPISEPPIKQDFR LLG
2268	10319	A	3202	891	2136	GATQAFKENNQKAYKETYESAKGLD VWDSWPLQNADGTVAEYNGYHVVFAL AGSPKDADDTSIYMFYQKVGDNDSIDSW KNAGRVFKDSKFDANDPILKDQTQEW SGSATFTSDGKIRLFYTDYSGKHYGKQ LTTAQVNVSKSDDTLKINGVEDHKTIFD GDGKTYQNVQQFIDEGNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGTENGYQG EESLFNKAYYGGGTNFFRKESQKLQQA KKRDAELANGALGIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMNGKWYLF TDSRGSKMTIDGINSNDIYMLGYVSNL TGPYKPLNKTGLVLQMGDPNDVTFTY SHFAVPQAKGNNVVITSYMTNRGFFEDK KATFAPSFLMNIKGNKTSVVKNSSILEQG QLTVN
2269	10320	A	3203	1	3987	
2270	10321	A	3204	2	247	QGAGFSSSLRMASIFSISVGTDLRLS TILSPLYNTVAPGAN*CRELKLVLDDADD VLSTEVKRVITSSASNITPAFFCS
2271	10322	A	3205	1099	2224	DGQQIALHRLALRELQQAVHAGLPQQ AKILFDGGSE/TRQNPLQQLVHMGLPRPL DKKNFQEP
2272	10323	A	3206	1366	2673	
2273	10324	A	3207	1	7035	
2274	10325	A	3208	1	2328	
2275	10326	A	3209	1	2328	

2276	10327	A	321	819	1242	KAYASLSLWQAPSGESRPAPAAADLRGS SG/RPP*TFNPPCGPHTGCPAGSFPISFQ PRCLLVAKSKPGMPVSDAAAYESPWKG GAGAPALGLLGALSSEVADRALQAAPA WAPRDAGRGLPGQDRPQGAGASLGP SRS
2277	10328	B	3210	1	2541	MPRQVGS GPGPLLGVAGQAAVGTGGKK SLCQYRKPDGSGIVSLKIDWIIERYQLPQ SYQHRKAGECLLHEYEDLVPIRDTLRLF PGGRYLPRAKHVAPSEPDPQDEQKLRLD FADFGTTIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTLAPNTQT ASPRALADSLMQLARQVSRLESGQDFA DFGTTIKQDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGQDFADFG TTIKQDFRLLGQTSVDRLLQLSQGQAVK GNQLLPVSLVKRKTTLAPNTQTASPRAL ADSLMQLARQVSRLESGQDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQDFADFGTTIKQDF RLLGQTSVDRLLQLSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRALADSLMQ LARQVSRLESGQDFADFGTTIKQDFRLL GQTSVDRLLQLSQGQAVKGNQLLPVSL VKRKTTLAPNTQTASPRALADSLMQLA RQVSRLESGQDFADFGTTIKQDFRLLGQ TSVDRLLQLSQGQAVKGNQLLPVSLDD VTYAIKPTCWPGLAIIPSCALHRIETELM GKFDEGKLPTDPHMLRLAIETVAHDYD VIVIDSAPNLGIGTINVVCAADVLIPTPA ELFDYTSALQFFDMLRDLKNDLKGFE PDVRILLTKYSNSNGSQSPWMEEQIRDA WGSMVLKNVVRETDEVGKGQIRMRTVF EQAIDQRSSTGAWRNALSIWEPVCNEIFD RLIKPRWEIR*
2278	10329	A	3211	1	3849	
2279	10330	B	3212	1	6724	MDNFFAPVFTMGKYYTQGDKVLMPALAI QVHHAVCDGFHVGRMLNELQQYCDEW QGGADFADFGTTIKQDFRLLGQTSVDRLL LQLSQGQAVKGNQLLPVSLRKQNTSRPP SMHVDDFVAAESKEVVPQDGIPPKRPL KVSQKISSRVENLNTLNLKELMLCHHQ EEGAGEDLDRVYDLMIFFVRENRTQVD HHLCMWMTLLLLKVKKWFLKMEYLHQ NGHSKYHRRFLPVVGFQAIEEDGVLSTV RIGFSHLL
2280	10331	A	3213	532	1232	
2281	10332	A	3214	8749	11698	CSWHDRFPDWKAGRILPISEPPSNRIFAC WGKPAWTGLLQLSQGQAVKGNQLLPVS LGFRGPPASNPGGAPGSASVAAAAAVA AKAAAAAPPVDNAAPHSAAKLEERRK PDPRRDFADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKTTLAPNT QTASPR
2282	10333	A	3215	3	452	
2283	10334	A	3216	24	609	GIPQTQREPTMVLSPADKTNVKAAWGK VGAHAGUEYGAEALERMFLSFPTTKTYF PHFDLSHGFCPLRATGKKVADALTNA VAHVDDMPNALSALSDLHAHKLRVGP GSTFKLLSHLPCW*TLGRPPSPAEFQPLA VARLPWEKFPGLFVEAPLLDLQITFKVG SFGWPLFFCPFGPPSPSSPFLHPYRGL

2284	10335	A	3217	3	583	EPRLRKAGGLLSRSRQNDQEGREGAQQ WPAYGPARGVVPQPWVQTGTWQGN TG QRVPQLPPHPPPIHLVSRHRGKLRHGFLR PMPEPRGLESKGT/GQCSGSCSMYVTMR AKRPWEGGHDTLTQQGGCRSSVCGRRA HEALRPVWCGEGPQWTWCAVCPNRS APGAGLAD\RQHPGESRAWGETRLGEAG GAE
2285	10336	A	3218	3	398	
2286	10337	A	3219	1766	3896	NTKLDQAQQAPEDHYPIISLLPSHMAIG LLMAQEGHCKDSSAMGEEAHHPLTPAT PPFPPLSPDWGHMQPDDFFVPVAVPAVFR GPPQLQCHGRRLFLNSPCAQKSSSGLVV EPGLSRTLLEMVKLTSMRGQFLEAQIPT GISLTLQYQLYQKQTNKNMSYSFVFLK WVALGQRRAGYPSLEDADSRFNGSR SFLITVIGITLTVEIVTSGMMKGTRVRWS GAGNEGMMGLEEGRNERSVKEAPRRA VEAQPKDRTWDVGKGQGTEGEGRGLEV EGQQHQGSEPGTIPFSVSWGVLLLAGLC CLVPSSLVEDPQEDAAQKTDTSHTDQG DWEDLACQKISYNVTDLAFDLYK\SWLI YHNQHVLTPTSVAMAFAMLSLGTKA DTRTEILEGLNVNLTETPEAKIHECFQQV LQALSRPDTRLQLTTGSSLFVNKSMKLV DTFLEDTKKLYHSEASSINFRDTEEAKEQ INNYVEKRTGRKVVDLVKHLKKDTSLA LVDIYSFHGKWKDKFAERIMVEGFHV DDKTIIRVPMINHLGRFDIHRDRELSSV LAQHYVGNATAFFILPDPKMWQLEEK LTYSHLENIQRAFDIRSINLHFPKLSISGT YKLKRVPRNLGITKIFSNEADLSGVSEAE PLKLSKAVHVAVLTIDEKGTEATGAPHL EEKAWSKYQTMFNRPFVIIKEYITNFP LFIGKVVNPTQK
2287	10338	A	322	2	373	PRVRVRVDLVSGWGGKMVDLFLVTV KRVIDYAVKILVKPDWTGVVSDGVKHS LNPFCDIADVDEAVLLKEKKLVKEGIAVC CGPAQCQETNRTALGMGAHRGIHVEVS P**AQRCLPLQVARG
2288	10339	A	3220	3	1226	MRRNKPRQRGVREARPAGGAGPGWRG ARCSGAGEGGGGERRGSPPAALALAPAS GPRRNFPDARCLIQIHHQGAFLLAGSA SLSAVTGVPEGEARFTEDYCPEEKMFGE HKPKMYRSIEGC\CISGAKSSSSRFTDSKR YEK\DFQSCFGLHETRSGD\CNACVLLV KRWKKLAPAGSKKNWNHVV DARAGPS\ LKTTFEPK\KVKTLSG\NRK\ISTQISKLOK EFK\RSNSDAHSTTSSASPAQSPCYSNQS DDGSDTEMASGSNRTPVFSFLDLTYWK RQKICCGIYKGRFGEVLIDTHLFKPCCS NKKAAAEKPEEQGPEPLISTQEWTECP DLSLVVSWRPPLSSLPAGCSLHGLAADW TTDMITVTTSKCREPSCQEGSFQRRKA FPKRLPKMAEVQVLLL
2289	10340	A	3221	1	269	
2290	10341	A	3222	240	377	SNTHRVPTFTDAWEVEMVTSLSLQSFL LPHIHCLKLQ*DPLHSP
2291	10342	A	3223	47	263	
2292	10343	A	3224	416	498	KRLSLQSFLLLPHIHCLKLQ*DPLHSP
2293	10344	A	3225	1	305	RTRGRTRGGDGGGHLGSGRNGGGS MN APPAFESFLPLRG/QRITINKDTKVPNAC LFTMNKEDHTLGNIKSRACFPFAFCRD CQFPEASPATLPVQPAEL

2294	10345	A	3226	74	562	GSGGGGGHLSGRNGGSMNAPPAFE SFLLEGEKK/ISDAGCGPRITINKDTKV PNACFLTINKEDHTLGNIKSQRDLKDPQ ALFAGYKVPHPLAEHKIIIRVQTPDYSPQ RAFTNRQSPDLAISELSLLGGSAFRGGHK KTSQERNLSRGARGGLCSGL
2295	10346	A	3229	1	2661	
2296	10347	C	323	303	395	
2297	10348	A	3230	1	1454	
2298	10349	A	3231	1	2364	
2299	10350	A	3232	1	1368	
2300	10351	A	3233	114	1473	VKGDRFGALRFNDPCAGIKLPMTFFTEL EKTTLKFIWNQKRARIAKSILSQKNKAG GSTLPDFKLYYKATVTKTAWYQNR DIDQWNRTGPSEITPHTYNYLIFDKPEKN KQWGNDSLFNKWCWENWLAICRKLKL DPFLTPYTRINSRWIKDLNVRPKTIKLE ENLGITIQDIGMGKDFMSKTPKAMATKD KIDKWDLIKLSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAAKRH MKKCSSLAIEMQIKTTMRYHLTPVRM AIKKSGNNRCWRGCGEIGTLLHCWWD WKL VQPLWKS VWRFLRDLEIPFDPAI PLLG IYPNDYKSCCYKDTCTRMFIVALFT IAKTWNQPKCPTMIDWIKMWHIYTIME YYAAIKNDEFM/SFVGTWMKLEIILSKL LQEQKTK
2301	10352	B	3234	1	1890	MDKFLDITYTLPRLNQEEVESLNRPIITGSE IVAIINSLPTKKSPGPDGFTAIFYQRYKEE LVPFLKLQFQIEKEGILPNSFYEASIIIP KPGRDTTKIENFRPISLMNIDAKILNKILA NRIQQHIKKLIHHDQVGFTPGMQGWFNI CKSINIQHINRTKDKNHMISIDAFAFD KIQQHFMKLTNLKLGIDGTYLKMIRTIY DKPTANIILNGQKLEAFPLKTGTRQGCPL SPLLFNIVMELLARAIQEKEIKGIQLGKE EVKLSLFADDMIRIKYLG IQLIRDMKDLF KENYKPLLNEIKEDTNKWKNI PCSWVGR INIVKMAILPKVIYRFNAIPIKLPMTFFTE LEKTTLNFIWNQKRARTAKSILSQKNKA RGIMLPDFKLYYKATVTKTAWCWYQNR DIDQWNRTPESEITPHIYNYLIFDKPDKN KQWGKDSLFNKWCWENWLAICRKLKL HPFLTPYTTINSRWIKDLNVRPKTIKLEE NLGNTIQDIGMGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTISVNRQPTK WEKIFATYSSDTGLISRIYNELKQIYKKK TNNPINKWAKDMNRHFSKEDIYAAQKH MKNAHHHPSEKCKSKHNEIPSHTS*

2302	10353	A	3235	1	2676	MKAEIKMFFEINENKDTTYQNLWDAFK AVCRGKFIALNAHNRKQERP KIDTLTSQ LKELEKQEQT HSKASRRQEMTKIRAE LK EIEIQKTLQKINESRSWFFERINKIDRPLA RLIKKKREKNQIDA IKNDKGDITTDPT EI QTTIREYYKHLYANKLENLEEMDKFLDT YTLPRLNQEEVESLNR PITGPEIVAIINSLP TKRSPGPDGFTA EIFYORYKEELVPFLLK LFQSIEKEGILPNSFYEA SIIIPKPGRD TT KKENFRPISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGW FNIKRSINVV QHINRTKHKNHMIISIDA EKA FDKIQQPF MLKTLNKL SIDGTYLK IIRATYDKPTANII LNGQNLEAFPLKTGT RQGHPLSPLLFNIV LEVLAIRQEKEIKAQ NLLKLISNFRKV SVYKINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDV KDLFKENY KPLLNEIKEDTNK WKNIPCSWIGRINIVK MAILPKVIYRFNAIPIKLPTTFFTELEKTIL KFIWNQKRAHIAKTILSQKNKAGGIMLP DFKLYYKATVTKTAWY WYQKRDIDQW NRIELSEIIPHIYNHLIFDKPDKNKKWGK DSVFNKRCWENWLAICRKLKLD TFLTPY TKINSRWIKDLHVRPKAIKTLEENLGITIQ DIGMGKDFTSKTPKAMATKAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKIFAIY SSDKGLISRIYKELKQIYKKKTNNPIKKW AKDMNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRKAIHKSGNN RCWRGCGEIGTLLHCWW DCKLVQPLW KTVWQFLRDLELEIPFYPAIPLLGIYPKD Y
2303	10354	A	3236	1	3045	MDKFLNTYTLPRLKQEEVESLNR PITGS DIEAIINSLPTKKISPGPDGFTA EFCQRYK EE/LEKEGILPNSFYEA SIIIPKPSD TT KENFRPISLMNINAKILNKILAKI RQHIK KLIHHDQVGFIPGMHGLFNICKSVNIIQHI NRTNDKNHMIISIDA EKPFDKIQQH FML KTLNKL AQNLLKLIGNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMNEFPFTIASKR IKYLGIQLTRDV KDLFKENYK
2304	10355	A	3237	1	2142	
2305	10356	A	3238	1	1551	MRFKEKIHLHNIKEPSEAASADGGAVAS YPD LAKIVDEGRYKAEVMQLRCGWRAP ASDCVHSVAVVGVD SVLEVLAIRQE KEIKGIQLGKEEVKLSLFADD MIVYLENP TVSAQNLLKLISNFSRVSGYKINVQKSQ AFLYTNNKQTESQIMSELPFTIASKTIKYL GIQLTRDV KDLFKENYKPLL NKIKEDTN KWKNIPCSWIGRINIVKMAILPKVIYRFN AIIHKLPM TFFTELEKTTLKFIWNQKGVH IAKSILSKKNKAGGIMLP HFKLYYKATV TKTAWY WYQNRYTDQCN RTEPSEIIPHI YNHLMFDKPDKNKKWGKDSL FNKWCW ENWLAICRKLKLD PFLTPYTKINSRWIKD LNV RP KPIKTLEENLGITIQDIGMGKDFM SKTPKAIATKAKIDKWDLIKLSFCTAKE TTIGVNRQPT ELEKIFAIYSSDKGLISRIY KELKQIYKKKNPIKKWVKDMNRHFSK EDIYAVNRHMKKCSSSLVIREMQIKTTM RYYLTPV

2306	10357	A	3239	1	1458	GLSGDLLGAHQLPDVLGCVQPLPDLLP PQNLLALQSLQDDLLWALDPAAPWA MDRGAATQWAVGPVVS DPWVMEAVAS LPSAMDLDSAAQPTWLLGAASLLVTDQ PMDQPSADQLAEFPDLLSKVSQSLRIKY LGIKLTRNVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVIYRFN AIPKLPMTFFTELENTTLKFIWNQKRACI AKSILSQKNKAGSIMLPDFKLYHKATVT KTAWYQYQNRDIDQWNGTEPSEIMSHIY NYLIFDKPEKNKQRGKDSLFSKWCWEN WLAICRKLKLDPFLTPYTKINSRWIKDLN VRPKIKTLEENLVNTIQDIGMGKDFMSK TPKAMATKAKIDKWDLIKQKSFCTAKET TIRVNRQPTWEKIFAIYSSDKGLISRIYK ELQQIYRKKTNPIKKWAKDMNRHFSK EDIYAANRHMKKCSSSLAIREMQIKTTM RYHLTPV
2307	10358	A	324	268	393	DGRRKEKWHKVERRHRPYLLSSLSQHR W*TVTNFGEISGTIAIEVDEGTIHALNN GLFTLGAPHK/ERIALKPGYGKYLNSND ELVV/GRSDAIGPREQWEPVFQONQEVNR GGPAEMGEEKRNGTKWREDTDHTSFPL FPSTGGQPKAHSNWRKVCH
2308	10359	A	3240	1	2028	
2309	10360	A	3241	2	1547	
2310	10361	A	3242	3	1945	
2311	10362	A	3243	1	2124	
2312	10363	A	3244	1	2250	
2313	10364	A	3245	2	2483	GKYYKLSSGTAPTCVSLGWGLARGDSA APALGSRTSACAPCSHGTWKL SLEPSDR LSPCDRSSEEATHAPHRLALVASLPW SRLPLLAPQSHSEAEATSQPTGVENHHQ KTRYVKAGGPVICRSLPESRGFLWASEG RKCMLIGSWAAMGRLRKSTISSRFGPQT LAGTGRPQAIPVLKKHSDAVLLGVCFLK LLHQHHQELGENADSQTLPTQTHWEFILS EDYNKMTPVKNYQVLEVLARAMRQEK QIKSIQLGKEEVKLSVFADDMIVYLENPI VSAQNLLKLISNFSKVS GYKINVQKSQA FLYTNNRQTESQIISLPFTIPSKRIKYLGI QLTRDVKDLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPRVIYIFNAIS IKLPMTFFTELEKTTLKFIWNQKRARIAK TILSQKNKAGGITLPDFKLYYKATVTKT AWYWYQNRGVDQWNRIEPSEIIPHIHNH LIFDKPDKNKKWGKDSLFTKWCWENW LAICRKLKLDPFLTPYTKINSTWIKDLNV RPKTIKTLEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLKSFTAKETT IRVNRQPTWEKIFTIYPSDKGLIPRIYKE LKQIYKKSNNPIKKWAKDINRHFSKED IYAANRHMKKCSSLVIREMQNKITIR/Y HLTPVRMAIHKSGNNRDMDEAGNHHS EQTIARTENQAPYLLTHR WELNNENTWT QVEEHHTLGPIVGVICRKVFPNGSGPSKP SGLHFSQPLPQVTSVVAKITIVPWEMKLI AMGVQDELNIAFHKNHLLMNDTTIHMT PYIQPAPKS
2314	10365	A	3246	1	2622	

2315	10366	A	3247	853	2831	YPESTMNSNKFTRKKQTPPSKSG*RI*TD TSQKKTFMQPKDT*KNAQHWSLEKCK SKPQ*DTISHQLEWRSLSQDRKD*QSTL LAILIKKKGQKNQIDT/IKNDKEGITTDP EIQTIREYYKHLYTNKVENLEEMDKFL DTYTLPTLKQKKEVKTLNRPITGSEIEAI NSLPT/KKSPGPDRFTAIFYR/DIRSSGQG NQARERNKGYSIRKRGSOIVPCR*HHCI FRKPHHLSPKSS*ADKQLQQLRIQNSA KITSIPHQ*QTNREPHE*TPIHNCFKEN KMPRNPTYKGCEGSLQGELOTTAQ*NK RGHKRMEEHSMMLDRKNQYRENGHTA QGNL*IQCHPHQATNDFHRIKKNYFKV HMEPKKSPHRQVNPKEQSWRHHTT* LQTILOGYSNQNSMVLVPKQRHRPMEQ NRAPGNNTIHLQLSDL*QI*QKQEMGKG FPI**MVLGKLANHM*KAETGSLPHILYK N*FKMD*RLKC*T*NHKNPRRKPRQYHS GHRHGQGLHD*NTKSNGNKSQN*QMGS N*TKELLHSTRNYHQSEQATYRMGENFC NLLI*QRANIQNLQRT*TNLQDKNKQPH QKVGKGYEQTLLKRRHLCSQKTHEKML IITGHQRNANQNHNEIPSHTS*NGDH/SN QVRKQOVLERMWRN
2316	10367	A	3248	1	4954	MVFSIDAQKAFDKIQRHFMKLTNLKGI DGTYLKIIRAIYNKPTGNIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDIIVYLENP IVSAQNLLKLIGNFSKVSQYKINVQKSQA FLYTNNRQTESQIMSELPFTIASKRIKYL GIQLTRDVKNLFKENYKPLLNEIKEDTD KWKNIPCSWIGRIHIVKMATLPKVIYRLH AIHIKLPMTFFTELEKTTLKFIW
2317	10368	A	3249	25	527	EFHRLRENPPMVAVSCPTKTNVKAIAWG KVGAAHVRSMCAEALERMFLSFPTTKT YFPHFDL\SHG\SAQVKGATGKKVADAL TNAVANVDDMPNVAVRPEATLHAHKL RVDPVNFKLLKPLACLVDPGPAHLPRP SFTPGGATSSLGQSFLGFLKHRCLNLPN YR
2318	10369	A	325	1	67	
2319	10370	A	3250	97	1360	SACAWRLPSPGPSAMWPLWRLVSLAL SQALPFEQRGFWDFLDDGPMMNDEE ASGADTSGVLHPDSVTPTYSAMCFFGC HCHLRVVQCSDLGLKSVKESPDITLL DLQNDISELRKDDFKGLQHLYALVLV NNKISKIHEKAFSPLRKLQKLYISKNLV EIPPNL\SSL\VELRIHDNRIRKVPKGVFS GLRNMNCIEWMGGNPLENSGFEPGAFDG LKLNYLRISEAKLTGIPKDLPETLNELHL DHNKIQAIELEDLLRYSKLYRLGLGHNQ IRMIENG\SLFPLTLREVHLADNNKLAR VPSGFPLDKLLQVV/YILHSNNIHQSGVF NEFLFPWFGGGEAGPYYNH/ISLFNNPV PYWEVQPATFRVVTDRLAIQFGQLQKV EAAAATLVSQWGLGNRARHPDGEAEP GS
2320	10371	A	3251	1	2535	

2321	10372	A	3252	5	2333	NPILWLETQMASNERDAISWYQKKIGAY DQQIWEKSIEQTQIKGLKNPKKMGHIK PDLIDVDLIRGSTFAKAKPEIPWTSLTRK GLVRVVFPLFSNWWIQVTSRIFVWLL LLYFMQVIAIVLYLMMPIVNISEVLGPLC LMLLMGTVHCQIVSTQITRPSGNNGNRR RRKLRKTVNGDGSRENGNNSDKVRGIE TLESVPIIGGFWETIFGNRIKRVKLISNKG TETDNDPSCVHPIKRRQCRPEIRMCQTR EKPKFSDGEKCRREAFRRLGNGVSDDL SEEDGEARTQMILLRRSVEGASSDNGCE VKNRKSILSRHLNSQVKKTTTRWCHIVR DSDSLAESEFESAASFQGSRSVSGGSRS LNMSRRDSESTRHDSITEDMLWDDLH GPECRSSVTSDEGAHVNTLHSGTKRDP KEDVFQQNHFLFWLQNSSPSSDRVSJIIW EGNECKKMDMSVLEISGIIMSRVNAYQQ GVGYQMLGNVVTIGLAFFPFLHRLFREK SLDQLKSSISAEIILTFCGAPPVTPIIVLSI INFFERLCLTWMFFMCMVAERTYKQIR FLFAKLFSHIYFCQKGLGKYEIPHFRLKK VENIKIWLRLSYLKRGRQPSVDVWVS SVFLLTSLIAFICCAQVLQGHKTSWDA YNWGVFDLGETALLFLRLASLGSETN KKYSNVSILLTEQINLYLKMEKKPNKKE QLTLVNNVLKLSTKLLKELDTPFRLAYGL TMNPLIYNITRVVILSAVSGVISDLLGFNI RLWKIKS
2322	10373	B	3253	73	358	XVPGSRGPETKLWDDFSMSQATKRKHV VKEVLGEHIVPSDQQQIVRVLRTPGNNL HEVETAQQQRFLVSMPSKYRKNIWIKRG DFLIVDPIEEGEK*
2323	10374	A	3254	80	201	
2324	10375	A	3255	498	748	FLPRRGDNDSTYPQ/WTACCCRRRRTCW* T*TWIRSGQRKMWSCGRRSLTTCMP RTRTAARLMACGSGSWRRSGPSCGCR LSP
2325	10376	A	3256	1	1764	MTTSQKHRDFVAEPMGEKPVGSLAGIGE VLGKLEERGFDKAYVVLGQFLVLKDD EDLFREWLKDTCGANAKQSRDCFGCLR E/WCAKSRPAAEVSELKADSKEGPQAQG PEQERTGL
2326	10377	A	3257	842	1186	FLPRRGDNDSTYPQ/WTACCCRRRRTCW* T*TWIRSGQRKMWSCGRRSLTTCMP RTRAWTWRSKNLALSCPSMTKSLKGS GHIPSAWSRAARLMACGSGSWRRSGPS CGCRLSP
2327	10378	A	3258	526	1158	SCGLSLIKMTTSQKHRDFVAEPMGEKPV GSLAGIGEVLGKLEERGFDKGL/YVVL GQFLADIEKMKTSFREWLKDTCGANAK QSRDCFRMPFEKWCEALLVDALLGKFSI PPAPQSRSLASRSDSSPCPSYEGKDICY C\RTHLARRYFRGSFGEFSPLNHFQLF FI LRSWHAFPRPFFPWPVSWVTVYQLFLE WDFPGPIPHPHPHFQSV
2328	10379	A	3259	35	407	
2329	10380	A	326	163	552	AGFSLSAQKSPGAMA*YSYVKSSKLVLK GT\SKKKKSKDKKRKREDEETQLD/IVGI W*TVTNFGEISGTIAIGMDEGTIHALDN GLFTLGAPHK/ERIALKSGYGKYLGINSD ELVGHSDAIGPREQWEH
2330	10381	A	3260	3859	4052	ASCPNPKEFAPPRAGPPWFWGPPPLARVN PGLGGPFSGTRPTPPQPLPEQRVTLTSTN PWLAAVS
2331	10382	A	3261	493	712	AHGRQLRKYSQQQGCWRLPFCGCHAV SGGGCGKCC\SPANGPCGAA\CLGFQPH NFPDPCETC/CGCHAVSGGGCGKCCISSK WSLWCSPA WVSSHTTSRIPVKLAGLPSP SFLPG

2332	10383	A	3262	51	539	
2333	10384	A	3263	742	4858	
2334	10385	A	3264	2	658	AFLRMLFPESWMETRREGAPAPPAPRSET SHDLVATLMRCTPHYIR*SNPTRPRGPET GRRTA*TRSPQVPHLQHLPTPRLVTPHP EGTQPTLPTRSSSTRWNTWA*RRTSGCES RLRLPPPVRQIPAEYAILTPETWPRWRGD EPRASSTCFGRSTWSPTRPDGEHQGLCQ EPRVAFPPGGGAKRKFDGFARTIQKAWR RTWLSGSTRRCGRKLPTSC
2335	10386	A	3265	1	4095	
2336	10387	A	3266	26	173	
2337	10388	A	3267	387	1443	PHRKQAEPPRHHERLGRRVRHHARHGR GSRPDTAAEAAGGCGDPRAFQQLERRL RHPPLRWQGLLRQRLLEEPRLSLRP HRADAVQ*PGLPPDALPREAGWRQEGA PQHRLQDYETCQLTWPH**GAHPTTS AALNPTRPRGPETGRRTESSTRWNTWA* RRTSGCAEPASPTA/SQFAFLQRYAILTP ETWPRWRGDERHGVQHLLRAVNMEPD QYQMGSTKVFKNP/VVAFPPGGGARA KVRWLCPNHPEGLAAPRGCEVRGDA/R RKLPSTC*TRRSGGATASIGTSSGTTWG WRSGPSCVSSWARRSGWTSPRSPSTTA ASSPSSGT*S*RPSVCM*LGERR
2338	10389	A	3268	1	4496	MEGNVNAHRASGAQIRTCRAPPGATGC TALFKANSPEFTGLKSAQRGPVVGAP RKRFSGLRGHREAERRTLGWGSQAPPPA AQAHTPAAGDSTLLRSAPVGTCLLYAP HPQDFPPAGFLREQWWPRLLTLQVFLHL RTGGRVGPVDWVLLGGGRLLGGHRMP GPCNLAEAVLLREARWPWGEAGGSEEG EPSGGSVGGNCQRRARPLPSAHPEAQQGV GLEVGRGMVAPAASYFADEGRPNGDHP ARQPRLGP
2339	10390	A	3269	911	2827	ERKHLGWMEFSIKQSPLSVQSVVKCIKM KQAPEILAGSANGKTPSCEVNRECSVFLS KAQLSSSLQEGVMQKFNGHDALPFIPAD KLKDLTSRVFNGEPGAHDALRFESQE MKGIGTPPNTTPIKNGSPEIKLKITKTYM NGKPLFESSICGDSAADVQSEENGQKPE NKARRNRKRSIKYDSLLEQGLVEAALVS KISSPSDKKIPAKKESCPNTGRDKDHLK YNVGDLVWSKVSGYPWWPCMVSAADPL LHSYTKLKGQKKSARQYHVQFFGDAPE RAWIFEKSLVAFEGEGQFEKLCQESAKQ APTKAEEKIKLLKPISGKLRAQWEMGIVQ AEEAASMSVEERKAKFTFLYVGDQLHL NPQVAKEAGIAAESLGEMAESSGVSEEA AENPKSVREECIPMKRRRRRAKLCSSAET LESHPDIGKSTPQKTAADP/RRRGVGSF PGRKKTTVSMPSRKGDAAASQFLVFCQ KHRDEVVAEHPDASGEEIEELLRSQWSL LSEKQRARYNTKFALVAPVQAEEDSGN VNGKKRNHTKRIQDPSENADLEDTPRK GLRTDKHSLRKRDTITDKTARTSSYKAM EAASSLKSQAATKNLSDACKPLKKRNR ASTAASSALGFSKSSSPASLTENEVK
2340	10391	A	327	289	818	EPSRGVWPHEARINGSKKKKSKDKKR KREDEETQFD/IVGIW*TVTNFDEISGTI AIEMDEGTYIHALDNGLFTLGAPHK/ERI ALKPGYGKYLINSDELVV/GRSDAIGPR EQWEPVFQNGACAAVFTVIGSEKQSECS LLRESRAKYHGCTHGQISSSLKQHPRWM YSHQEDLKV
2341	10392	A	3270	3	114	
2342	10393	A	3271	328	471	
2343	10394	A	3272	1	190	

2344	10395	A	3273	2	479	SGLGRLPGPWQEAQSSRGPSGDMAGV KALVALSFSGAIGLTF/LHMLGCALEDYG VYWPLFVLFFHAISPIPHFIKRVTYDSD ATSSACRELAYFFTTGIVVSCLWISPVIL ARVALIK\WGACAFVLAAGNAVIFPYN RGFSLYLGRGDDFSWEQW
2345	10396	A	3274	3	586	ARAMGISRDNLHKRRKTGGKRKPYHKK RKYELGRPAANTKIGPRRIHTVRVRGGN KKYRALRLDVGNFSWGSECCTRKTRIIDI VYNASNELVRTKTLVKNCIVLIDSTPY RQ/WTPEEEIILNKKRSKKIQKKYDERKK NAKISSLLEEQQQKLLACIASRPGQCG RADGYVLEGKELEFYLRKIKARKGK
2346	10397	A	3275	2	727	LFPASAEQMGISRDNWHKPRKTGGPRE SPYQQEAKSMSLGRPAA\NTKILAPRIQ HSPVCRGG*QVNTVPLRFD\VGNSWG/S KECCTRKTRUIDVVYNAI**PSWVRYPRP LVERICIVLIDEQHPYRQWVRSPTYALP LGPQRKGAKLDSLRKEIFKPKTDLK*IQ KKYD*/ERKKNCQNSASLPGRSSFQQGK ASLRCAFK/RPGQC\GRA\GYMTRGHR VRSYYLRKIKARQSKINT
2347	10398	B	3276	48	209	XKNQCETRTMQENGYSSHAVDGTGPAG GAGRPAGSTGAQVSVQPNFQQDKFLGR X*
2348	10399	A	3277	2	353	
2349	10400	A	3278	3	676	SAVEFPPLSHTTGTRPRTPIILLQQENGY FIHTLWMGLALLGVLGDLSGQHRPRSP CQPNFQQDKFLGRWFKRGLASNSSWL EKKAALSMCKSVVAPATDGGFNLSTF LQEKTSVETRTMLLQPRGVPSASLQLTG VPHWGQA/HYSVSVVETDYDQYALLYT RASKGPGEDFRMATLYSRTQTPRAELK EKFTAFCQAQGFTEDTIVFLPQTDKCM EQ
2350	10401	A	3279	154	522	HVACGLLWIYVSPSAHLNLDGTITTK/EN LGTVNEILLGSNPTEAELQDMINEVMSD GNGTIDFP\EFLTMMARKMK\DTDSEGR KLEEAFAFRVFGRLRVGNGLYLACRNFH VDGQTLGGGSLPD
2351	10402	A	328	213	905	YVQSLKQILS/GCI*ESIAIKKKKNKDKKR KREDEETQLDIVGIWWTVTNFGESGTI AIEMDKGT\YIHALDNGLFTLGAPHKEVD EGPSPPEQFTA\VKLSDSRIALKSGYGKY LGINSDDL\VVGRSDAIGPREQWEPVFK\ MGKMALSTSNSCFIR\HEAEDIEAKSKT AGEEEMI/KGSPNLCQTFMTLPYLPEH RSLLLKIRSCAERETKKKDDIPEEDKGN KQCE
2352	10403	A	3280	1	1446	
2353	10404	A	3281	774	3564	VLSKGNERSQPRSLRLLAPQLKAEAAA DKGLAPVPPPFSSGHSGPCERELEGQRG RGRSRRGAHLELKPSPLRAGAPTDRGR GGPAEVAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAGEDNPA GAGGAAVAGAAGGARRFLCGVVEEQ MTLISAAREYEIEFIY\AISPGLDITFSNPKE VSTLKRKLDQVSQFGCRSFALLFDDIDH NMCAADKEVFSSFAHAQVSITNEIYQYL G
2354	10405	A	3282	51	672	VLSKGNERSQPRSLRLLAPQLKAEAAA DKGLAPVPPPFSSGHSGPCERELEGQRG RGRSRRGAHLELKPSPLRAGAPTDRGR GGPAEVAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAGEDNPA GAGGAAVAGAAGGARRFLCGVVEEQ MTLISAAREYEIEFIY\AISPGLDITFSNPKE VSTLKRKLDQ

2355	10406	B	3283	506	2416	MNPSAPSYPMASLYVGDLPDVTEAML YEKFSAPGILSIRVCRDMITRSLGYAY VNFQQPADAERALDTMNFVKGKPVRI MWSQRDPSLRKSGVGNIFKNLDSIDN KALYDTFSAFGNLSCKVVCDENGSKGY GFVHFETQEAARAIEKMNGMLLNDK VFVGRFKSRKEREAEKGARAKEFTNVI KNFGEDMDDERLKDIFGKFGPALSVMV MTDESGKSGFGFVSFERHEDAQKAVD EMNGKELNGKQIYVGRAQKKVERQTEL KRKFEQMKQDRITRYQGVNLYVKNLDD GIDDERLRKEFSFGTITSKVMMEGGR SKGFGFVCFSSPEEATKAVTEMNGRIVA TKPLYVALAQRKEERQAHLTNQYMQR MASVRAVPNPVINPYQPAPPSGYFMAAI PQTQNRAAAYPPSQIAQLRPSRWTAQG ARPHPFQNMFGAIRPAAPRPFSTMRPAS SQVPRVMSTQRVANTSTQTMGPRPAAA AAAATPAVRTVPQYKYAAGVRNPQQHL NAQPQVTMQQPAVHVQGEPLTASMLA SAPPQEQKQMLGERLFLIQAMHPTLAG KITGMLLEIDNSELHMLSPESLSKVD EAVAVLQAHAKEAAQKAVNSATGVPT V*
2356	10407	A	3284	183	3080	PRRCSTGNSGRPKIIRRAAEANEDRTL RLLPGNERSQPRSLRLLAPQLKAAEAV DKGLARVPPFSSGHSFGPCEREGERG RGRSRGAHLELKPFGSLRAGAPTRD RGGPAEVAAAGGRRMVQKESQATLEER ESELSSNPAASAGASLEPPAAPAGEDNP AGAGGAAGVAGAAGGARRFLCGVVEGF YGRPWWMEQRKELFRRLQKWELNTYLY APKDDYKHRMFWRMYSVEAEQLMT LISA
2357	10408	A	3285	3	452	
2358	10409	A	3286	26	526	NSTDSETHPWLLSPADKTTVK/APAWG KVGAGAGEYGSEALERMFLSFPTTKTY FPHFDLSHGFCPLRATGKKVADALTKR RGAPLDDMPNALVRPLASDLHAHLARV GPGSTFKLLKPLACLTLGPAHLPRPSFT PGGCKASLGQSFLGFLKHRCLNLPNYR
2359	10410	C	3287	410	484	
2360	10411	A	3288	3	170	IRGSVVLSLNFLLNTFFTP*RSFISTSVMF* KPFIFSFLMLLL*VFIFSLKILSY
2361	10412	A	3289	831	1559	IAWAFKINWLPILFISVLFYPIFGFIFFYL LYFSNTCLSLFFHFLSETLDNIFIFLYVSIF QFSSKFVHFAISFMFPLSFFFCFILSRKF IFFSSKKYVFIFLISLSFIFF
2362	10413	A	329	133	480	GYGRRSVKVRARCTGFSPKTPNPWV NSQHFGRRLWADHLRSGVRDQPGQHGE TSLLLKIQKLPCCGGRCL*FQLFGRRLRQE N*/RLNPGGGGCSELRSHHCTPAWVTEQ DSVSK
2363	10414	A	3290	253	414	
2364	10415	A	3291	3	225	
2365	10416	A	3292	218	602	SFLLLPRCTAEQQRWGHQQLYWSHP KFGQGSRSICRVCSNNRHGLIRKYGLN MCRQCFRQYAKDIRFHLSTKCSSFRGL SGASTSMKKPWINSFVYIIHFKEATEKK RKKNEIKRGPFCKGPL
2366	10417	A	3293	33	494	
2367	10418	A	3294	1	609	PLKRSDGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVNVD VGGEALGRLLVVPWTQRFESFGDLST PDAVMGNPKVKAHSKKGLRGAFSDDL AHLNLDLKGTFATLASELHCDKAAPWIPE ELQAPWATCLVCVAWPITFGKRISTPPV AGLPNQENWLAWCWLNALGPTSNHLSL

						AFLAGPISN
2368	10419	A	3295	8	519	SAQMAVTTADPRVRPRVRTQLCSLASLI QTLLVHLTPEEKSAVTALWGKVNVDV VGGKALGRLLVVYPWTQRFLAESFGDLS TPDAVMGNPKVKAHSKKVLGAFSGGP GCTWDNLKGTFAHTEVSLHCDK\LRHGS LKNFRLLGQRAWVSVAGPIHFWQKNFN PTSCRLA
2369	10420	A	3296	3	333	
2370	10421	A	3297	35	717	RRSSPSLLPLAERGGARARGRPERAPHP TPATRTAPPPWARRMMKLKSNQTRTYD GDGYKKRAACLCFRSESEEEVLLVSIS R\HPDRWIVPWKEGMEARRKEAKCGKQ VREVCGR LGVKGTLGR LVGIFENQER KHRTYV\YVLIVTE\LEDWEDSVNIGR KREWFKIEDAIKVLQYHKPVQASYFETL RQGYSANNGTPV\ATTYSVSGFRASMF RAFRWT
2371	10422	A	3298	81	426	PSFHYAVLPLHNC LGFFPSLRHRWLHSM TDDPPTTKPLTARKFIWTNHKFNVTGPQ NNMYLILPLERRFRSGSHLQHLTSKDNE EQLKHAKYGAFHVITLLFTIHYNSQLKL CD
2372	10423	A	3299	180	484	RQQAIFWHRWLHSM TDDPPTTKPLTAR KFIWTNHKFNVTGPQNNMYLILPLERRF RSGSHLQHLTSKDNEEQLKHAKYGAFH VITLLFTIHYNSQLKLCD
2373	10424	A	33	200	559	KNFFFLEMEF/SVLLPRLECNGVISAHRR LRLPLSSYSPASSSQVAGDYRACTTAG* ILYF**ETGFLHVG\QAGLEFPTSGDQPAL ASQSAGITGVSHCPQLKKSILHETPKGLT GVTS
2374	10425	A	330	27	201	LQE*SRRPSRSEAADLHGECYSS*GSTSG VVCSSRWARGLAGLRSEAADLRSEYYSS
2375	10426	A	3300	591	942	MAKTHFWDVDGSMVPPEWHRWLHSM TDDPPTTKPLTARKFIWDGTIKFQRGLG HPRNNMYLILPLERRFRSGSHLQHLTSK DNEEQLKHAKYGAFHVITLLFTIHYNS QLKLCD
2376	10427	A	3301	1	508	NFALEAKNSARAISYVQTPMGHFTRG PRLTITSLWGK\VNVEDAGGETPGKGS VVYP\WTQRFFDSFGNLSSAFCPSWPT KVKAHGK\KVLTS LGDAHKSTWDDLKG HLLPKPEVNCTVDK PAMWDPENFKAPG EMLLVTRFGQSLFRQKNFTPEGCRASLG KKDG
2377	10428	A	3302	3	452	
2378	10429	A	3303	1	627	TLLVPQDSERTHPWLLSPADK\TNVKA WGKVGAHAVRSMCAEALERMFLSFPTT KTYFFPHFDLSHGSAQVKGATGKKVAD ALTKRRGAPLDDMPNAL/SSALEATLHA HKL RVGPGSTSKLLKPLACLVDPGAHL PRPSSTPGGCNVFPGTKFPGFVEAPLLE PSKLPLKLGSLRLAIVFLPWGFPAPPL SCTRTPVVFEIKS
2379	10430	A	3304	131	406	EAMGILKLQVFLIVLSVALNHLKATPIES HQVEKRKCNTATCATQRLANFLVHSSN NLGGILSSTNVGSNTYGKRNAVEVLKRE PLNYLPL

2380	10431	A	3305	154	1702	IGHRDPARGRSCRCSGYYSRMVCEKLAP QSEMASAG\VSLRATILCLLAWAGLAAG DRVYIHPFHLVIHNESTCEQLAEANAGK PKDPTFIPAPIQAKTSPVDEKALQDQLVL VAAKLDTEKDLRAAMVAGMLANFLGFP YYMGMHSELWGVVHG\ATVLSPTAVF GTLASLYLGALDHTADRLQAILGVPWK DKNCTSRDLAHKVL\SAIQAVTGLLVAP GRADKQA\QLLLSTVVGVFTAPGLHLK QPFVQGLALYTPVVLPRSLDFTELDVA ETIDRLMQAVTGWKTGCSLTGAKADST LAFNTYVHFQGMKGFSLLAEPQEFWV DNSTSVSPMLSGMGT\QFHWSDIQ\DNF SVTQVPFTD\SAFLLLIQPHYASDLADKVE GLTFQQN\SFNWMRKLF\PRTHLTMPQL VLQGSYDLQDLLRPGSSCPFLHTELNL GRISGNDRIRVGEVLNSIFFEADERE TESTQQLNKP\EVLEIVPLTRPFLFAVYD QGATALALSWGRVGKPA
2381	10432	C	3306	223	417	
2382	10433	A	3307	3	742	HEASCRSERRRQMAFDITYDDRAYSSF GGGRSGRGSAGGHGSR\QKELPTEPPYT AYVGNL\PFNTVQGDID\AIFKDLIRS LVRDKD\TDKFKGFCYVEFDEVDSLKEA LTYD\GALLGDRSLARVDIAEGRKQDKGG F\GFRKGGPDDR\GFRDDFLGGRG/GLSR PGDRRTGPPMGS\FRDGPPLRG\SNMDF REPTTEERAQRTTTPALKPRTVATPLNQ VANPNSSIFGGARPREEVVQKEQE
2383	10434	A	3308	1	861	
2384	10435	A	3309	1	2076	
2385	10436	B	331	396	809	MAGCRSRALPHGEAAKAQRKVTAAGP GAKHLTAWGWQQLATPSVGPAEPTHT QNSHWPASAVCSPSSRLRLSLHTYPQAE GAGSGLGQPRKGLPQCSSLKGSSSAAK VGAQAEEVPRASEACEGCQHAVTSHKY *
2386	10437	A	3310	34	657	SDGRCGRCCAPRAPRAMHMSFAIS/RCA FYQLLLAALMLVAMLQLLYLSLLSGLH GQEEQDQYFEFFPPSPRSDQVKAHVRT ALASGGVLDVSGD\YRV\YRGLLKTTMD PNDVIL\ATHASVEQTCLHL\SGLL\ERW EGPAVPCSVFAA\TKEEAQLATVLAYAL SSHCPDMPAR\VAMHLVCP\RYEAAVPD PREPGEFALLRSCQEVFDKLARVAQPGI NYALGTNVSYPNNLLRN\AREGANYAL VIDVDMVPTEGLWRGLREMLDQSNQW GGTALVVP\AFEIRARRMPMNKNE\LVQ LYQVGEVRPFYYGLCTPCQAPTNYSRW FNLPEESLLRPAYVVPWQDPWEPFYVAG GKVPNFRRSGFRQYGFNRISQACELHVG GFD\FEVLNEGFLVHKGFKEALKFHPQK EAENQHNKILYRQFKQE\LKAKYPNSPR RRAQLATVLAYALSSHCPDMPARGRHA PRVPLALRGSRARPPGAGGVCPAAVLPG GL
2387	10438	A	3311	160	441	
2388	10439	A	3312	107	691	RTAILSRMKIFLPVLLAALLGVERASSL MCFSCLNQKSNLY\CLKPTICSDQDNYC VTVSASAGIGNLVTFG\HSLASKTCFPCL APFPEGRSMLGV\ASMGHSAFCQSFLVAI FSCGPMAGLRGKRSPLLGARACCLSLAG RALLARFGPLDRPEPCSPDPPAQEGKPSPF WIPQCMGAPDSSRALICALGPRSG
2389	10440	A	3313	388	525	

2390	10441	A	3314	194	1131	PQHGGHFPRKIKSCSWQARPLEDEATLG QCGVEALTTLEVTRPACLEVKSMVPWP VLEKVRGQTPKVAKHGEKKKKKTGRAK RRMQYNRRFVNVVPTFGKKKGTTFTKIF VGGLPYHTTDASLRKYFEGFGDIEEAVVI TDRQTGKSRGYGFVTMADRAAAERACK DPNPIIDGRKANVNLAYLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMYPPI VQATVVIPAAPVPSLSSPYIEYTPASPAY AQYPPATYDQYPYAASPATVRSFVGYS YPAAVPQALSAAAPAGTTFLQYQAPHV QPD RMH
2391	10442	A	3315	1	407	DAERQEALGIVRRIGTDTEAATEPAGAT VPA AAAAARIGTVGPQPAMP RRKRNA GSSSDGTEDSDFSTDLEHTDSSES DGT SR RSARVTRSSARLSQSSSRISRSCKSGSLL ALRSLLTLPEE*PVVSSSLPQ
2392	10443	B	3316	78	316	XS YLLGQWPRDADGAFTCCTNDKATQT PLSWQELEGERASSCAHKRSASWGSTD HRKEISK LKQQLQRTKLSRSGKEKERX*
2393	10444	A	3317	1	2319	GHPAFLEDGSPSPVLAFASPRPNHSYIF KREPPEGCEKVRVFEEATTRGKYGEGAK QETFTFALTLVFIQCVINAVFAKILIOFFD TARVDRTRSWLYAACSISYLGAMVSSNS ALQFVNYPTQVLGKCKPIPVMLLGVTL LKKKYPLAKYLCVLLIVAGVALFMYKP KKVVGIEEHTVGYGELLLLLSLTLDGLT GVSQDHMRAHYQTGSNHMMLNINLWS TLLLGMAVSCPDQGP ELVPRCPFVQALE KPS
2394	10445	A	3318	845	1343	LSLGDSAQCLLPHASWCQVAGHPAFLE DGSPSPVLAFASPRPNHSYIFKREPPEG CEKVRVFEEATS/RRVLTGPFLTSCPDKN KVHFQPTGSAFCPVNLMKPLFPGMGFIF RNCPSNPGISSSPGQPQATTSEGGSLQG LPTAIRAMAVAPHLQMSLCFSRAP
2395	10446	A	3319	44	498	
2396	10447	A	332	130	249	
2397	10448	A	3320	1	164	
2398	10449	A	3321	2	438	ARAARVFLHRSSLNLSNGETESVKTMIV HDDVESEPAMTPSKEGLIVRQTQSASST LQKHKSSSFTPFIDPRLLQISPSSGTTVTS VVGFS CDGMRPEAIRQDPTRKGSVNV NPTNIRPQSDPPEIRKSGKG*L*ILGAGLW
2399	10450	A	3322	3	174	
2400	10451	A	3323	2	4978	RRTSAVSRGLLFMSFVQPLLQPPVHLLT ARVRVPGYLQIDGVKIKEHNGKLMNCF KTKMTYYSFMKCVGLPAQLTIGFSGPSR ETGSDPRAARRGEDPQSKDRGDLSEQT EAQRSGVHCPRSQLVGELAGQSPRTIPA ALRVCLYLLCITSYNHTSKDESSKDEEEE IKLEINMLKKYSHRNATYYGAFIKKSP PGHDDQLWLVMEFCGAGSITDLVKNTK GNTLKEDWIAYISREILRGLAHLHHHVI HR
2401	10452	A	3324	197	332	
2402	10453	A	3325	1	1788	
2403	10454	A	3326	3	111	
2404	10455	A	3327	220	423	HEELKSGPYLLTFRDCFLHFWALVSKR /LALNFM*TSAPT*KALSKRNICLVNKNR NIKIPYPK KKKK
2405	10456	A	3328	273	499	RSGVRDQPGQHGKITSLLKIQKLARRGG ACL*SQLLRRLRQENRLNPGGGGCSEPR SCHCTPAWETEQDSISKIK
2406	10457	A	3329	1	1176	
2407	10458	A	333	1	3408	

2408	10459	A	3330	245	394	
2409	10460	A	3331	458	701	GPAPTRRGPAHPGAHTR**PAGTARAAC GSA*SAGTASPAHKGKGHHPGSRASGTG PGPCQRRRRSDHSSAGKWPLREASL
2410	10461	A	3332	365	814	AALRSSSENSRHRSLVKMSDKKAKDPV NKSGGQGPKRKNWSKGKSSGTSFNNL VLFDKATYDKLCKEVPNYNLITPAVGSE RLKIRGSLGQGPQFQELLSKGFIPNWFS KHRASSYFTPGITKGG\DAPSLLEDGCMN RSNPPVHLEK
2411	10462	A	3333	41	565	APSPRRPWGHFTEEDKATIKNLWGKGE MWKDAGGKNPWERLPWLSYPMGPQRF FDQLLANLSLCPIMPGNPPKVKGTWPR KVLTSLSAHSKSTWDDLKGHLLPKPEV NLHC\DKPAMWDPENFKAPGEMLLVTR FGQSHFRQKNFTPGGCRASWGRKMGDL ELASALVPSRYH
2412	10463	A	3334	399	592	KCIHFPGPTPKFVCVIVVTAVP/TFGM* TVYV**LPFSILAQNVG*RDDCDPGWKL NLFYAKKKK
2413	10464	A	3335	28	312	
2414	10465	A	3336	26	417	
2415	10466	A	3337	16	3567	
2416	10467	A	3338	6385	6599	
2417	10468	A	3339	2	758	
2418	10469	A	334	3	443	SFQGGLEGEAWAGTGAAPGACGPARPV GGRRLRGPRTRPAGPTGPGQ*G/VLAPGP AAAVL/RFLTGP*LPSRSRARDREGLQLH S*SQRDHEPTGRN/GTTPDAPP*EL*HSPR RSAASLCPQAPEVSPQGSQVPALSGNSP QRLLPT
2419	10470	A	3340	116	627	
2420	10471	A	3341	1830	2259	
2421	10472	A	3342	1	619	
2422	10473	A	3343	1830	2258	
2423	10474	A	3344	290	1377	RSFRAIGEVSIRGWGGGYAAQLQSPSR LPVLGGGKKGGSRGVGGQSSRAEVGLG SQRERSGTCGAEEEEAAQLIAGTGSSL PYQGGPQNQTAIAPTCAPLSPCKAAAVI MGNIFGNLLKSLIGKKEMRILMVGLDAA GKTTILYKLLGEIVTTIPTIGFNVETVEY KNISFTVWGC GVARDK\IRPL\WRH\YFQ NTQGF\DLWSDSN\DR\ERVNEA\REEL\ MKNAGAETSLRDAVLLVFGQTNRICPN AMNAAG\IQDKLGLHSLRHRNWY\QAT CATRGN\GLYEG\HLWLANSVPKQEVESR TALTKHSTSPLTYLLSPCPQFLPLLSMQG LARAWGIMSTLPSRTLPLTSLPFSCPI
2424	10475	A	3345	292	574	VTTENSGGQTQCGKQDRIQVPRHPARRG PPGSQY/PVTPPVPPGPLHATQLPPGPIPL GKRKAGQERRLDPRPTTCQAAAPTRSSP FCPPQKVR
2425	10476	A	3346	3	142	TISSIIRKARKP\QDLLNNYTPRSSPLRSSG RTRMYKGNVRPGNSS

2426	10477	A	3347	1	1418	MAAALFVLLGFALLGTHGASGAGEERA RKQPCGKSRFQGHSEALATRFSAAGNTG FVQAPLSQQRWVGGSVELHCEAVGSPV PEIQWWFEGQGPNDTCSQLWDGARLDR VHIHATYHQHAASITIDTLVEEDTGTYE CRASNDPDRNHLTRAPRVKVVRAQAV VLVLEPGTVFTTVEDLGSKILLTCSLND ATEVTGHRWLKGGVVLKEDALPGQKTE FKVDSDDQWGEYSCVFLPEPMGTANIQL HGPPK\VKAVKSSEHINEGETAMLVCK ESVPPVTDWAWYKITDSEDKALMNGSE SRFFVSSSQGRSELHIENLNMEADPGQY RCNGTSSKGSQDQAIITLRVRSHLAALWPF LGIVAEVLVLVTIIFIYEKRRKPEDVLDAL RRCTWPGLMSCPEPLGVTEGRAGSTDA PARGLSGASADRLSSRPLFHGGGPSSDD DAGSAPLKSSGQHQNCKGKNVRQRNSS
2427	10478	A	3348	3	896	SCRGRRRQRLEVVRGFRRGIGIMAAALF VLLGFALLGTHGASGAAGTVFTTVEDL GSKILLTCSLNDSEVTGHRWLKGGV VLKEDALPGQKTEFKVDSDDQWGEYS CVFLPEPMGTANIQLHGPPRVKAVKSS EHINEGETAMLVCK\SEFVPPVTDWAW YKITDSEDKALMNGSESRFFVNSSQGR SELHIENLNMEADPGQEQRCNGTSSKGL RPRPLQFLRVRSHLAALWFLGIVGVEVL VLVTIIFIYEKRRKPEDVLDLDDDDAGSAPL KSSGQHQNCKGKNVRQRNSS
2428	10479	A	3349	870	997	KWASNTYVISSNEESMIS*LSGRQ*NLRV WRLRKTWWLNWTL
2429	10480	A	335	2	306	
2430	10481	A	3350	2	225	GILKGLYYPLATNSFPATCWRL*VSPAHS KDPRNAATVHLSFFSPSGGPRYLLGHTT WQQGLGKRGRRTQHS
2431	10482	A	3351	1	336	
2432	10483	A	3352	1193	2524	SKPPAASFAPRRPPATSRTLAAACAFRRS CRLAACSFVRPLPHTDTNMNGQLNGFH EAFIEEGTFLFTSESVGEGHPDK\CDQIS DAVLDAHLQQDPDAKVACETVAKTGMI LLAGEITSRAAVDYQKVREAVKHIGYD DSSKGFYKTCNVLVALEQQSPDIAQGV HLDRNEEDIGAGDQGLMFGYATDETEE CMPLTIVLAHKLNAKLAELRRNGTLPWL RPDSKTQVTQYMQDRGAVLPVRVHTIV ISVQHDEEVCLDEMARDALKEKVIKAVVP AKYLDDVTIYHLQPSGRFVIGGPQGDAG LTGRKIIVDTYGGWGAHGGGAFSGKDY TKVDRSAAAYARWVAKSLVKGLCRR VLVQVSYAIGVSHPLSISIFHYGTSRKSE RELLEIVKKNFDLRPGVIVRDLDLKKPIY ORTAAYGHFGRDSFPWEVPKKLKY
2433	10484	A	3353	346	461	

2434	10485	A	3354	3	1632	MTEQLEPILMQAFIKSTAGLEARKLKAY RTMEYMAKSTDRSPGHILCCECGVPISP NPNANICVACLRSKEDISQGIKQVVISFCK QCQRYFQPPGTWQCALESRGTFLLWCL EKNPKPLWSKVRLVDAGFVWTEPHFK RLKVKLTIQKEVMNGAILQQVFVVDYV VQSQMGCDGHESEKLKDFWKAIVQVR QKTLHKKTFFYYLEQLILKYGMHQNTLRI KEIHDGLDFYYSSKQHAQKMVEFLOCT VPCRYKASQRLISQDIHSNTYNYKSTFSV EIVPICKDNVCLSPKLAQSLGNMNQIC VCIRVTSAILHIDPNTLQVADIDGSTFWS HPFNSLCHPKQLEEFIVMECSIVQDIKRA AGAGWMISKKHTLGAEVWGTEGHLEMN RIKQYFCRTHLGTSCLNPGDARVLGFDL ANCNLNDEHVNMNSDRVPDVVLIKKS YDRTRKQRRRNWKLKELARERENMDT DDERQYQDFLEDLEDEAIRKNVNIYRD SAIPVESDTEDEGAPRISLAEMLEDLHFS PGCPLVKEGASMLT
2435	10486	A	3358	231	877	PKPGGYSQCRTTSSRATERNRIDYVSSA VPYLTTTPDLRPEVVFIGRSNVGKSSL IKALFSLAPEVEVRVSKKPGHTKKMNFF KVGKHFTVVDMPGYGFRAPEDFVDMVE TYLKERNLKRFTLLVDSVVGIQKTDNI AIEMCEEFALPYVIVLTKIDKSSKGHLLK QVLHIQKFVNMKTQGCFFLPVSAVTF SGIHLRLCFIASVTGSLD
2436	10487	A	3359	3	234	
2437	10488	A	336	243	748	PCQSFQPSGFGKDRPTSLEQRSQRERQA AIFAVSQPSLVIPPGTGKSEVNADRSRPP AYCSNLGRYSGPGPSLVIPPGTGKSEVN ADRSGPPAYCSNHFPSALP**RSSMRSLS LQQTSAWTCRHFHTSFEIQ/RGGSQILTL AFCAPAGPTPRGSHVLGLAPSEALT
2438	10489	A	3360	25	546	QSGDLGGRLSRSENCQSRVVRHRVVG VMAGVLKKTGVLVGLAVCNTPHERLR ILYTKNLDVLEEIPKNAAYRYTEQITN EKLAMVKAEPDVKKLEDQLQGGQL VILAQAHEHNLAKKK*GEWKLWEP EPPADQWKWANIHKLTLVVFMGKLD VIKIFYI
2439	10490	A	3361	2	367	YAGFSLSAQKCPGAMAE*SYAKSTKLVL KGTKTKSKKKKSKEKKRKREDEETQF D/IVGTIAIEMDEGTIYHALDNGLFTLGAP HKEGKMALLASNGCFIRCNEAGDIEAK SKTAGEEEMIT
2440	10491	A	3362	268	393	DGRRKEKWHKVERRHRPYLLSSLSQHR W*TVTNFGEISGTIAIEVDEGTIYHALNN GLFTLGAPHK/ERIALKPGYGKYLINSND ELVV/GRSDAIGPREQWEPVFQNEVRN GGPAEMGEEKRNGTKWREDTDHTSFPL FPSTGGQPKAHSNWRKVCH
2441	10492	A	3363	6	223	TVTNFGEISGTIAIEMDEGTIYHALDNGL FTLGAPHK/ERIALKSGYGKYLGINDEL VGHSDAIGPREQWEH
2442	10493	A	3364	329	877	RPWKQDRRAGDPWPRTHEFRSSEASLQ ASACKKKKSKEKKRKREDEETQFDMF GIW*TVTNFDEISGTIAIEMDEGTIYHALD NGLFTLGSSTQRRIALKSGYGKYLGINSD ELVV/GRSDAIGPREQWEPVFQNGACAA VFTVIGSEKQSECSLLRESRAKYHGCTH GOISSSLKQHPRWY

2443	10494	A	3365	97	704	AGFSLSAQKCPGAMAE*SYAKSTKLVLK GKTKSKKKKSKEKKRKREDEETQFD/ VGIW*TVTNFDEISGTIAIEMDEGTIHAL DDGLFTLGAPHKEGKMALLASNGCFIR CNEAGDIEAKSKTAGEEEMIKIRSCAERE TKKKDDFLEEDKGNVKKQCEINYVKKFQ SFQEHKLKISKEDSKILKKAQKDGFLHET LLDR
2444	10495	A	3366	24	981	AIQRLGEDGGGFYRDVGCQGVFISRPLL FLRAPVLPRLTYSSRTGLSLSAQKLPGA MAEYSYVKSTKLVLKGTGKTKSKKKKSK DKKRKREDEETQLDIVGIWWTVTNFG ISGTIAIEMDKGTIHALDNGLFTLGAP HKE\SDGSPPEQFTA\VKLSDSRIAL\KS GYGKYLGIIRDGLVVG\RSDA\GPREQW EPVFK\MGKMALSTSNCFIR\HEAEDIE AKSKTAGEEEMIKIRSCAERETKKKDDIP EEDKGNVKNCEINYVKKFQSFQDHKLKI SKEDSKILKKARKDGFLHETL\LDRAK LEADRYCK
2445	10496	A	3367	1	555	PLKRS DGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVNVD EVGGKALGRLL\VVYPW\TQRFESFGD LSTPDAV\MGNPKVK\AHGKKVLGAFS GGPGCTWDNLKGTFAHTEVSLHCDK\H RGS LKNFRLLG\NV LGLCCLAHSLLGKEF QPHQLQACLIKKIGWLVGVG
2446	10497	A	3368	1	390	WEEIQELNEVARHRPSTLVMGIQOENR QIRELQOENKELRTSLEEHQSALELIMSK YREQMFRLLMASKKDDPGIIMKLKEQHS KELQAHVDQITEMAAVMRK\PLKLTNR VARNKNEYFNLNKKTKA
2447	10498	A	3369	769	912	FPTPIPLFQELQAHVDQITEMAAVMRK\PL LKLTNSNRVARNKNEYFNLK
2448	10499	A	337	514	967	APACCPAAVSPFLCEPTLIHPPHPPDLKE DTGQKHARGAQSHPTLAGAGLAGRSSKQ PSPSAISIWHSD\GTSSCDRROQCDRLPS ALLSPHLRCSQPATRQLESS*TPPGTADL FLASSGPNPRAFSNARSVRKCKATSEKS KPKSYQGS
2449	10500	A	3370	1	463	MKKNIAFLASMFVFSIATNAYADIQMT QSPSSLSASVGDRTITCRSSQSLVHGIG NTYLHWYQQKPGKAPKLLIYKVSNRFS GVPSRFSGSGSGTDFLTISGLQPEDFAT YYCQHYDSLPTYTFGQGTKLE\KRTVAA PSVFIFPAHLMSS
2450	10501	A	3371	2	166	
2451	10502	A	3372	39	1200	FCGVAAMQLEIQVALNFIISYLYNKLPRR RVNIFGEELERLLKKKYEGHWYPEKPY KGSGFR\CIHIGEKVDPVIEQASKESGLDI DDVRGNLP\QDLESFRIDPFEVSYQIGEK GPVKVLYVDDNNENGCELDKEIKNSFN PEA\QVFMPISDPASSVSSSPSPFGHSAVA VSPTFMPRSTQPLTFTTATFAATKFGST KMKNSG/RGSSRFARTSPINRLGMWN DLLEGRKAISSSMHSLYGLGLGSQQQP QQQQQPAQPPPPPPPPQQQQQKITSALS PNAKEFIFPNMQGQGSSTNGMFP\GDSP LNLSPQYSNAFDVFA\TYGGLNEKSFV DGLNF\SLNNMQYSNQFQPCYGLTKKK KMYRTKLKCTGPRGIFFFSP
2452	10503	A	3373	1	1197	
2453	10504	A	3374	66	632	RRDPRTPANMALRVVRSVRALLCTLRA VPLPA\APCPPRPWQLGVGAVRTLRTGP\ ALLSVRKFTKQESGNNQEKSMNQLGS GNFAQEA LGDVVYCSLPEVGTCLNKQ\ DE\FGALESVKAASELYSPL\SGEVTEINE AL\AENPGTCKTNFCYEDGWLIKMTLSN P\SEL\DELMSEEA\YEKYIK\SIEE

2454	10505	A	3375	162	552	VASEHSPKIGASQGLDYEPLLVVAKVWVY LTRPTGTKAGSVFSQYLPFLEPGILGPAS LPWLRQTLTGKEIEIDIEPTDKVERIKER VEEKEGUPPQQQLHLQVAKQMNDK TASWITKILRWVQSQT
2455	10506	A	3376	77	427	GRDKEGEYPPAPSSGWGKSVGIMLTELE KALNSIIDVYHKYSLIKGNFHAVYRDDL KKLLETECPQYIRKKGADVWFKELDINT DGA VNFQEFLILVIKMGWQPTKKAMKK ATKSS
2456	10507	A	3377	1	143	
2457	10508	A	3378	200	899	GKSTGPVVCVHMSLCEWTL SLATRVSLSS HPSHQSHSHLLVWLFGESRPGQGLRLGH ESSAYCPGQM QIPCHGIPQKVLFFRWGK SVGIMLTELEKALNSIIDVYHKYSLIKGN FHAVYRDDLKKLLETECPQYIRVRRLG WRGLSAWSWGCPGPAVL PATLHRWLCL GSL*DL*TLASSSILT KKGADVWFKEL DINTDGA VNFQEFLILVIKMGWQPTKKA MKKATKSS
2458	10509	A	3379	99	497	RESGGKRLNIYHQT VYHKYSLIKGNFVH AVYRDDLKKLLETECPQYIRKKGADV WFKELDINTDGA VNFQEFLILVIKMGW QPTKKAMKESHKGVSLSLGPKGWAL GGHVTCTRIK VINTSKKKKKVDAA
2459	10510	B	338	1	456	MKLRTLAVSATA LKVARLEFPFDVRM CSEFLSSGVKLQTF AVSVTALNARLELF VPPGGLMVSLASGVKLQIFTVSVAHKS SVDPKTLGWSMGLGAVEQGAALIGEAW AAQEPMEGVGGSGMAGCRSRALPRGKA AKARREIERSAGH*
2460	10511	A	3380	1	282	PLKRSDGCNDGRPTRPPTRPDTTVFTSNL KQTRMVHLTPEEKSAVTALWGKVNVD EVGGKALGRLLVVLPLGPPKGPLKSFG GICPNSLNAG
2461	10512	A	3381	24	452	APSPDAMG/HSLWGKVNVEDAGGETLG RLLVVYPWTQRFFDSFGNLSSASAIMGN PKVKAHGKKVLTSLGDAIKHLDDLKGTF AQLSELHCDKLHVDPENFKLLGNVLTV LAIHFGKEFTPEVQASWQKMTGVASA LSSRYH
2462	10513	A	3382	3	549	FCPRGQEFEGENKLLVPDA MGHFTEED KATITSLWGKVNVEDAGGETLGRLL VVYPWTQRFFDSFGNLSSASAIMGNP KVKAHGKKVLTFLGRCQQSTLDDLKGH LLPKPEVNCTVDKPA MWDPENFKAPGE MLLVTRFGQSHFRQKNSPPGGCKASWA ERWVTGVASALVPSRYH
2463	10514	A	3383	347	716	REPCVSRSTCCPLPWMEPRAMCPPVGA MRGSRDPASSSLSPDH LAQLQPGAGFL FCSAPALSGSFPRPSPQGH LATAGSWL/ CPPVQAQPA PALCGPRRGVAWVGIAW EDSGKSVGEVAS
2464	10515	A	3384	1	1362	
2465	10516	A	3385	284	540	KLFQKKNKKSSCISDNFFFLAIMVNLLQ IVRDHWVHVLVPMGFVIGCYLDRKSD ERLTAFRNKSM LFKSFPHRELQPSEEV WK
2466	10517	A	3386	194	353	
2467	10518	A	3387	57	880	DPHSVSSTGGPLPIWFWPLSSGPGAVAA DPAPQSGSPTVDAGVPIPHIRARDSARLP LCPWHASALELGIATPGTVTTQAPGSYP AWRSRCLLYQSPVLLASLGVLVTLG LAVGSYLVRSSRRPQVTLDPSEKYLLR LLDKTVSWGRKGQEGGDQSAPGM*GT APT VVGMSKGRGSARRAW*NTCVLHPP TVSHNTKRFRFALPTAHHTLGLPVGKES VEWAPFPGYPQKVTPLLGSHE TRCFNRF APHTISPSPTWLCILQAVRCHWA

2468	10519	A	3388	430	483	NQPCLTLPTRKSECTD TVISWSLSFGFLF TRWVTGMAVLLRLSLRQAEYTHSQLLL PLDT*RLGNVVKFRGPISGLLSYTGKGFH NIQPNKKSPPEPRVAKKLGMIAGGTGITP MLQLIRAILKVPEDPTQCFLLFATQTEKD IILREDLEELQARYPNRFLWFTLDHPPK GILPISGHPTIPSSSKSKPCPFVNSGFIEINL ASHCQLGSLSAQTQ
2469	10520	A	3389	3	1007	HACAHASAHASGRLVVRWGRKRSSVMGI QTSPVLLASLGVLVTLGLAAGSYLVR RSRRPQVTLDPNEKYLLRLLNKTTVSH NTRKRFALPTAHHTLGLPVGKHIYLS RIDGRVRKPYTPVTSDEDDQGYVDLVIK VYLKGVQPKFSEGKMSQYLDLKVVG DVVEFRGPSGLLTYTGKGFHNIQPNKK SPPEPRVAKKLGMIAGGTGITPMLQLIR AILKVPEDPTQCFLLFANQTEKDIFAGG LKRNLQARYPNRFLWFTLDHPPKDW YSKGFVTADMIREHLPAPGDDVLVLLCG PPPMVQLACHPNLGQTGVTSQKMAISP Y
2470	10521	A	339	1	1519	MAPELSSKEQPGSEWKKACQMEGTVC KAQRDLLDGFQDQADDDMDNEIQAE VSDGDEELVGNWSKEPTTLGAATMGLG TEKQLGMGWAGRKGPIEDLEPLQAAC KLHAVAHTTWEEAVQCGSLPRRNSNLL LEQGVLEETRNLQEHGGEIDLEKKRWL GTVAHTCNASTLGGRGVKLQFTVTSITA PKAARLELFVPPGGLVLLASGVKLQIF AVSVTAHKSSVDPKTLGWSMGLGAVEQ EVVLVGEAPAAQEPMEWVGSGMGAA GPGALPRGKAAKARREIEHSAGLYKLLP HSEYSRPNRVFNSQGSNPVRVSFVNLN DQSGNGDRLCFNVGRELYFYIKGVRK TIP*GICRTEILISVLTEAADLSKPIDKRIY KGTQPTCHDFNHLTATAESVLLVGFS AQVQLIDPIKKETSKLFNEEAFEGRYATF FTI/WYECSHGKLHISSALGLVFFGGDISY SLSSQPAPLEGASRDSGSRGHELWSESSR KRNNKRH
2471	10522	A	3390	2568	2781	RSPGRPPHDPNAPV/RRPASCHS/AAESQ HGGWKKSKISASRKLQKLTLLQIAKQE/ LEREAERRGEKGRAL
2472	10523	A	3391	2	409	
2473	10524	A	3392	3	490	SSPEETVGPWDPEGHPGGPLTDPPNAPV LALPPAIPGLSLIMADGSSDAVRAAG*GV AGTPRARAREPRPAPAPIRRRSSNYRAY ATEPHAHKKSKISASRKLQKLTLLQIAK QELEREAERRGEKGRALSTRCPLELA GLGFAELQDLCRQLHARVDK
2474	10525	A	3393	2023	2613	
2475	10526	A	3394	150	848	VSAWRNGSSDAAREPRPAPAPIRRRSSN YRAYATEPHAHKKSKISASRKLQKLTLL LQIAKQELEREAERRGREGARSLAPRC VQPLELAGLGFADLPGLCCRQFHARVD KVDEERYDIEAKVSKNITEIANLTQKIF DLRSKFKRPTLRRVRISADAMMQALLG ARAKESLDLRAHLKQVKKEDPEKENRE VGDWRKNIDALSGMEGRMKKWRELSLP AYCPCPEEGH
2476	10527	A	3395	1	2880	

2477	10528	B	3396	61	5070	MGPTSGPSLLLLLTHLPLALGSPMYSIIT PNILRLESEETMVLEAHDAQGDVPVTVT VHDFPGKKLVLSSEKTVLTPATNHMGN VTFTIPANREFKSEKGRNKFVTVQATFG TQVVEKVVLVSLQSGYLFQTDKTIYTPG STVLYRIFTVNHKLLPVGRTVMVNENPE GIPVKQDSLSSQNQLGVLPLSWDIPELVN MGQWKIRAYYENSPQQVFSTEFVKEY VLPSFEVIVEPTEKFYIYNEKGLEVTI
2478	10529	A	3397	3	560	EGKGQGTLSVVTMYHAKAKDQLTCNKF DLCLPGSRQKVEVFLGPCLOPGTFLWSR NRRVLGFPSMNGEDMGLLFLCSEWERS EGWLCNREGGSGHSIEPHCCTFLHLTHR SLAFSLLAGVSCTCASSCKCKEICKCTSC KKSECGAISRNGLWLKVGREP KAVEV RASGEP AFLCPCRLSLPV
2479	10530	A	3398	3	1584	SNQPLRREAFPETPKGLRQGIPGEPEND RSHFFSFDVTAVMILYKESQALTGNLPG PQLPRRLRAAGRGHPSVPAPSRRGALS RFPASGRSAVPTIGWLCRSHYPHSIRGAN GWDRQELVRASHTMSATAQTNHRAEK AGRELSQANNDRTGRLAHPAPPSQARQ VPRLEHLASPRCRWPAVISRPFWSHCIL EIRFRKGKLGGRASPENEGAGEIRVKVP KDRDWLTAKLQGDLLTVSQTAKLED MV LQTAKSTQDFLTPTARSYSPTTKLKGV NTKSPTLLTPTARGRHYLLGAPIASWRC HTSTIRYHTVVVMSMTLSEHQAGSVD MSANDYAHYSGASGDNEMCVVIACPTP LFLSPRAWKPCDAGSKVKNWGIENGL VHTVLSSTQHGDPHEVHAPFGMEAEYA HPLETLILGTGFFIGIVLLCDHVILLWAW VTIRLETIDVHSGYDIPLNPLNIPFYAG SRHHDFFHMFIGNYGFQHFTRWDW NFLGTDSQYNAYNEKRKKFEKTE
2480	10531	A	3399	2	873	GRVGEMSQGRGKYDFYIGLGLAMSSSIF IGGSFILKKKGLRLARKGSMRAGQGGH AYLKEWLWRAGLLSMGAGEVANFAAY AVAPATLVTPLGALSVLVRAILSSYFLNE RLNLHGKIGCLSILGSVVMVIHAPKEEEI ETLNEMSHKLGDPGFVVFATLVVIVALIL IFVVGPRHGQTNILVYITICSVIGAFSVSC VKGLGIAIKELFAGKPVLA GIPWAWILL LIVCVSTQINYLNRPDIFNTSIVTPIYY VFFTSVLTC SAILFKGVGKDMFVGRCP LVL
2481	10532	A	34	2583	3580	DRVSLLLPRLECNGAILAHCNCLSGSSD SPASASQVTGITGKCHHTQLIFVFLVEMG FHHIAQAGLELLTSDSPTLASQSAGITGV NHHAWLFFFCSDRTVSLCYPGWSRVA* SRITATSAPGLK*FACFSLPSSRDYRHVP PHPGNFCIFGRDEVSPCWPGWF*TPDLR YPPASASQSAEII GVSHHTWPQEVFLFN LFIYLRWSL/DSVAQARVQRRDLGSLQA PPPRFKPFSCSLPSSWDYRRPPHPANFF VFLVETGFITVLARRVLIS*PRDLPASASQ SAGITGVSHHTR/LIF/NFFETGTHSVTWA AVQWYTI/GSLQPRTPELK*SSHLILTSN WDYRCTPPCPPNLFIYLFYFHRDEGLC CPGWS*TPELK
2482	10533	A	340	759	1034	
2483	10534	A	3400	90	458	HFSRGYLEAFSEISNIRFVPPHSVTVVVV FGACFLCILGIWPWACLPGPGGEGSGGF GEGRGSEAGRLGSVELTPATLPLQAPEA YPVFEPVPPVPEAAQGDTEDEGAPPLK RICPNAPDP

2484	10535	A	3401	3	787	PGSTISWRPGLARSLSPDGRRPRRGLGP GPSPASMAGR TVRAETRSRAKDDIKKV MATIEKVRRWEKRWVTV AATPFRILNW VAIVVDPQEEERRRAGGGAERSRGWRER RGRGASPDGGG/PLFILLDLNDENSQR FPLRKGS LQRGTE/PSPGGTPK/PNRP CVT LPDPPEGGPCTRAQPPT/RLGQEERSPGGI TVGSTDEPP/MLTKEEPVPELLEAEAPEA YYPVFEPVPPVPEAAQGDTEDFGSAPPLK RICPNAPDP
2485	10536	A	3402	1	172	
2486	10537	B	3403	1	5501	MVSKLSQLQTELLAALLESGLSKEALIQ ALGEPGPYLLAGEGPLDKGESCGGGRGE LAELPNGLGETRGSEDETDDGEDFTPI LKELENLSPEEAAHQKAVVETLLQEDPW RVAKMVKS YLQQHNIPQREVVD TTGLN QSHLSQHLNKGTPMKTQKRAALYT WYV RKQREVAQQFTHAGQGGLIEPTGDELP TKKGRRNRFKWGPASQQILFQAYERQK NPSKEEREAQGLGSLNLTVEVRVYNWFA NRRKEEAFRHKLAMDTYSGPPPGPGGP ALPAHSSPGLPPPALSPSKVHGVRYGQP ATSETAEVPSSSGGPLVTVSTPLHQVSPT GLEPSHSLSTEAKLVSAAGGPLPPVSTL TALHSLEQTSPLNQPPQNLIMASLPGV MTIGPGEPASLGPTFTNTGASTLVIGLAS TQAQSVPVINSMGSSLTTLQPVQFSQPLH PSYQQPLMPPVQSHVTQNPFMATMAQL QSPHALYSHKPEVAQYTHGTLLPQTMLI TDTTNLSALASLTPTKQVFTSDTEASSES GLHTPASQATTLHVPSQDPAGIQLQPA HRLSASPTVSSSSLVLYQSSDSSNGQSHL LPSNHSVIETFISTQMASSSQ*
2487	10538	A	3404	158	755	RGGRPAWPCGS RAMMVSKLSQLQTELLA ALLESGLSKEALIQALGEPGPYLLAGEGP LDKGESCGGGRGELAELPNGLGETRGSE DETDDGEDFTPIPKELLENLSPEEAAHQ KAVVETLLQEDPW RVAKMVKS YLQQH NIPQREVVD TTGLNQSHLSQH/HQQGHS HEDAEAGRPVHLVRPQAARGGA AVHPC RAGRAD
2488	10539	B	3405	133	2369	MVSKLSQLQTELLAALLESGLSKEALIQ ALGEPGPYLLAGEGPLDKGESCGGGRGE LAELPNGLGETRGSEDETDDGEDFTPI LKELENLSPEEAAHQKAVVETLLQEDPW RVAKMVKS YLQQHNIPQREVVD TTGLN QSHLSQHLNKGTPMKTQKRAALYT WYV RKQREVAQQFTHAGQGGLIEPTGDELP TKKGRRNRFKWGPASQQILFQAYERQK NPSKEERETLVEECNRAECIQRGVSPSQA QGLGSLNLTVEVRVYNWFANRRKEEAFR HKLAMDTKVHGVRYGQPATSETAEVPS SSGGPLVTVSTPLHQVSPTGLEPSHSLLS TEAKLVSAAGGPLPPVSTLTALHSLEQTS PGLNQPPQNLIMASLPGVMTIGPGEPAS LGPTFTNTGASTLVIVPTLDQSLCYISDT WVNQTDQNLSSSREAGTKHNTSILWY LRRPGLHAGTECAGHQHQGPDPHLQP VQFSQPLHPSYQQPLMPPVQSHVTQSPF MATMAQLQSPHX*

2489	10540	A	3406	1	2112	MMLKGKAHCSILDFGLDLQCSTNSAAE FIRSWEDPWVRVAKMVKSYLQQHNIPQR EVVDTTGLNQSHLSQHLNKGTPMKSQK RAALYTWYVRKQREVAQPHIPYPIPENS TGTEWLIELTWLDPHAKNDQEHRTDSP VNYGKKKGKENKNLKPPEVYVSLIKA CGGPGNFCPSFSELQRNFVKHRPTKLKS LLRLVKHWYQQWLQPHREWKEEVLDA VRTVEEFLRQEHFQGRGLDQDVRVLK VVKVGSFGNGTVLRSTREVELVAFLSCF HSFQEAACHHKDVLRLIWKTWWSQD LLDLGLEDLRMEQRPDALVFTIQTGT AEPITVTIVPAYRALGPSLPNSQPPPEVY VSLIKACGGPGNFCPSFSELQRNFVKHRP TKLKSLLRLVKHWYQQYVKARSPRANL PPLYALELLTYAWEMGTEEDENFMDLDE GFTTVMDLLLEYEVICIYWTKYTLHNA IIEDCVRKQLKKERPIILDPADPTLNVAEG YRWDIVAQRASQCLKQDCCYDNRENPI SWNVKRARDIHLTVEQRGYPDFNLIVN PYEPIRKVKEKIRRTRGYSGLQRLSFQVP GSEKQLLSSRCSLAKYGIFSHTHIYLET IPSEIQVFVKNPDDGGSYAYANPNNSFIL GLKQQIED\HQQGLPKK\QQQLEF\QQQVL QGLVGWVGFYGIQD\SDTL\NLS\KKKGE ALFPAS
2490	10541	A	3407	108	442	ALLSWEMSAACWEEPWGLPGGFAKRVL VTGGAGFIR*WRR*PSSGSPETPTFSRSS ACPSASHMIVSLVEDYPNYMIINLDKLD YCASLKNLETISNKQNYKFIQGDICDS
2491	10542	A	3408	115	1196	ALLSWEMSAACWEEPWGLPGGFAKRV LVTGGAGFISASHMIVSLVEDYPNYMI NLDKLDYCASLKNLETISNKQNYKFIQ DICDSHFVKLALFETEKIDIVLHFAAQTHV DLSFRTCPWSFTHVNV/YMGTHVLVSAA HEARVEKFIYVSTDEVYGGSLDKEFDES SPKQPTNPYASSKAAAE\CFVQSYWEQY KFPVVITRSSNVYGPHQYPEKVIPKFISLL QHNKCCIHGSGLQTRNPLYATDVVEAF LTVLKKGKPGIYNIGTNFEMSVVQLAK ELIQLIKETNSESEMENWVDYVNDRPTN DMRYPMKSEKIHGLRWRPKVPWKEGIK KTIEWYRENHFNWKNVEKALEPFPV
2492	10543	A	3409	359	532	IVMCHCLELVIGEPCHICGSVCVCVYA AVCVLCVCVHTCICFGACV/CVCVCRRV CPVCLCTYLYLLWGLCVVCYQRVNFWK
2493	10544	A	341	587	1097	QKIINKVVPITGRQCCFVRLSPLESKFQS KEEIRNTSHRANVTKRNSANRKTDAILA TPGPPPAQPHGA/PGGYAPRLPOHPAPGC FPKCGNPAPRPWYGPFSGPLLKEQKRN PRKGTG*MQGVSPVFPPT*NAGPLPGGS LGPPISGHFLVSHTWPPPPRSPTAPP
2494	10545	A	3410	27	1389	GQPRSQQAGSWGKRRQESYRAREGDG GSGSLTGLLRTAAGWLLPARASPRERAT RHPVRSPPQRRARRSLQRGPERPRDPPQ TAWAARMCTKMEQPFYHDDSYTATGY GRAPGGLSLHDYKLLKPSLAVNLADPYR SLKAPGARGPGPEGGGGGSYFSCQGS TGPSLKLASSELE\RLIVPNSKTA\TTTPT PPGQYFYPRGGSGGGAGGAWGGVTE EQEGFADGFVKALDDLHKMNHVTPPNV SLGATGGPPHGP/GIRASPEPPPVYTN LSSYSPASASSGGAGAAVGTGSSYPTTTI SYLPHAPPFAGGHPAQLGLGRGASTFKE EPQTVPEARS\DATPPVSPINMERPRAPS KLEPSGLRNRLAGHQSAKGRK\KRFAR LEDKV\KTLKA\ENAGPVEVPPGLPPGSR LAQAQTRKVIDPRVSNGLSSLLFGV\RGH AFLNVPCL

2495	10546	A	3411	1	3589	IRRPLDQQRGGIPLRKKPLEDLVCKLADISI NYVNERKSEQHLRFLSTLLDSFSSSRVFK MLLGDEKQSIVQAKPLEIAKL VQKNPAV QFLYQKLGWLNEDQ/RKDFGLVDILYS ALRCCDNDMERKKVLDDLT KVDLKWN SLLKIEKACPSSDKHALVTPWLKGDILG EKL VNLADCLCNEDLESRVSSSHFSE WTLLSLVLSQHVKN DYLG DVYVERIIV RLHETL FKT KKLSEAESSDSSVSFICDV
2496	10547	A	3412	112	828	PVFKTPLPSHRRRAHAAALDLLGASSSDP HADSGTGNWAEVDPGSAQHLPRPSSQLP HFLLSGGGPGQCRRGQRGELLPSGGTA TPCAPRGLGWGLRSCALRAAAAPPTAPQ TLRRAPRPARPRAGPLAPQPSISRDFL GQAACASGTMLRWLRDFVLPTAACQDA EQTRYETL FQALDRNGDGVVDIGELQE GLRNLGIPLGQDAEEVGRRRGAA*A*GG LRALGTLRGPRRAAA
2497	10548	A	3413	1	1413	RDARRYSGTTPHPSISRDLGQAVCASG TMLRWLRDFVLPTAACQDAEQTRYET LFQALDRNGDGVVDIGELQEGKLN LGIP LGQDAEEKIFTTGDVNKDGKLD FEEFMK HLKDHEKKMKLAFKSLDKNNDGKIEAS EIVQPLQTLGLTISEQQAEILQSIDVDGT MTVDWNEWRDYFLN PVTDIEEIRFWK HSTGIDIGDSL TIPDEFTEDKKSQWWR QLLAGGIAGAVSRTSTAPLDR LKIMMQV HGSKSDKMNI FGFRQMVKEGGIRSLW RGNGTNVIKIA PETAVKFWAYEQVMKT RLAVGKTGQYSGIYDCAKKILKHEGLGA FYKGYVPNLLGIPIYAGIDLAVYELLKSY WLDNFAKDSVNP GVMVLLGCGALSSTC GQLASYPLALVRTRMQAQA\MLEGSPQL NMVGLFRRIISKEGIPGLYRGITPNFMKG LPAVGISYVVYENMKQTLGVTQK
2498	10549	A	3414	1	222	
2499	10550	A	3415	2	528	SRVDPRVRHSARLTMCHSRV SCHPTMTIL QAPTPAPSTIPGPRRGSG\PEIFTDPLPEP AADP\AGRPSASRGHRKRSRRVLYPRVV RRQLP\VEEPNPAKRLLFLLLTIVFCQIL MAEEGVPA PLP\EDAP\NAASLAAPT\VS PVLEPFNLTSEPLDYASWNLSTFLQQH\ P AAF
2500	10551	A	3416	1623	2346	TFPSGAKPPLAASHHHRHRLDASRLWRG RSGGPSVTRRPTFLPSYPPAPAHAPASAP GPS\SDSCSPFSRRRSPTRTDCFVCRPVC PFPFIVPPGRAPSRMAEVLLLLLLLSLPSA AAKIQGYPSCPGPQLSRDILSSGDGWWA GLSGHHRVCGGPGVQEPQTTVHNATD GIKYIHHRLIHLTPADYDDFVNAIRSARS AFCLTPMGM MQFN DILQNLKRSKQTKE LWQRV SLEMATFSP
2501	10552	A	3417	256	657	KGLSLSKKAGENHYFYLPHSFPEKAPPG AIGHLSPRGTIEEALDLSARIVA EFIVLP ASHHPRHRLDASRLWRGRSGGPSVTRRP TFLPSYPPAPAHAPASAPGPS\SDSCSPF SRRRSPTRLARMRGLLG F
2502	10553	A	3418	294	573	SHLLGLHEPSRHNRA SPGSLFCTHRRGIH SASSKPSSPTSP*CKSPRPSPGAAPRRG*L E*AGLLGFSTGFRGFPNRARRPRRLGVAI AHQAP
2503	10554	A	3419	1	931	

2504	10555	A	342	462	1238	SFYETKLLISGSETLDSKDQYRINKYNH YFQTLHYTHLKFSSGLSSATQ*KLSWSK GNG*GERPVSPPLMAPSGQLLAHVWS EVKSVSSCFLSCQQGHVLTSPGSSFPQCO PAQCYLIPCSSEKYTNW/PPIPPSLGIQ SS/SSPGS*SGPISSSKYSGDAQVCFSSPNL FPSFRPVTGCIQSPPNISPGAEGCGLQPI PVHSFLTPSTFSPVSPi*RSRSTHPETHS MSHSSQSSPQAPSALPPSISLPLSP
2505	10556	A	3420	640	757	
2506	10557	A	3421	865	1314	TPLPSTTPPKQPNRGPSPGAESLETEEEE EEEKGSERPPPGRRSR\SLRPP\VRWRRGD P\GQ\QETGPP\KLRP\WDGAE\GVA\GH AAAFPH\ITEGRLVPLGG\GVRLTPSP\TL LRTGAGLLHYERLWNLVGP\CLHP\RQ DHTLGLGSWG
2507	10558	A	3422	2	310	ARDVHPLPLPFLGNSSLALGMQMRPQL LLSRCRLPATCASSCKCKECKCTS/TAR KKSCCSLNPCLVPKCAPRACICKRGHR RSASLLRLMTGTALLPTYK
2508	10559	A	3423	41	317	LLLKFFETGSHSFIQVGVQWCDHDSLD LPGSGDPSS/AS/RVAGTAGMHDHTWLIF VFLVRRWSLTVLLRLVFNWSAKVILHL GLPKGWGLQV
2509	10560	A	3429	781	949	LLCLGLAYRRHFEMSLWLGMAHVCNP SAWGGRRGGQIT/R/GQEFETSLVNMVKT CLY
2510	10561	A	343	2	384	
2511	10562	A	3430	3	1029	RAFRFDDTMAGGGCRAGPGATCSDGDA GSDQRQNEEIEAMAAIYGEEWCVIDDCA KIFCIRISDDIDDPTWTLCLHVMLPNEY CTAPPIYQLNAPWLKGQERADLSNLEEI YIQNIAESILYLWVEKIRDVLQKSQMT PGPDVKKKTEEDVECEDDLILACQPESS LKALDFEVSEARTEVEVEELPIDHGIPIT DRRSTFQAHLAPVVCQKQVKMGLSKLY ENKKIASATHNIYAYRIYCEDKQTFLOD CEDDGETVAGGRLHLMEILSVKDVGMG VRARWYVGMGLGPDRLFKNINCVARNIL VEKNYTSSLEESSKALGKNKKVRKDKK RNEH
2512	10563	C	3431	153	224	MVAHACNPSTLGDRGGRFTRSGD*
2513	10564	C	3432	20	58	MTQLTKRKETIL*
2514	10565	A	3433	837	1125	LDVTTSKNQFVLRWLKIPGNCYRRHFF FFETESCSVAQAGVQWHNLSSLQAPPPG SRHSPTSAS\QAAGTYRYPAHHAWPNFV FVFLVETGFHPC
2515	10566	A	3438	56	290	
2516	10567	A	3439	468	993	VLLACFWPGSDFWPRSRRKTYGTAPQSC YSFYVALDCGGVSRLVIFVSWRNPQVAP TSAHQNRPSRNPVSRPPNTQRVARRKHY ALADGYTERRWTNAPCRAESSFPNCPS AAPIPDSDYDK*PSRATLFTSHLTVEAFPV WSYLYPGETPRLHPRAHTRTPAAIRYP DRQTPNGLRGANTMHSQMDTLNGDGR THLAGQRARSPTARPQRQYRIHTTSDL PGLVRKYASGCCRLRIWYCCAWIERALSL QVGGGVFGDPLSEGOAECDHGST
2517	10568	A	344	2	624	SDSRASCKMLLILLSVALLALSSAQNLINE DVSQEEPSLIAGNPQGPSPQGGNKPQGP PPPGKPKQGPSPQGGNKPQGPSPGKPKQ PPPGDKSRSPSPGKPKQGPSPQGG* LQGPSPGGIKPKQGPSPGKPKQGPSPG SKSARAPPKPKQGPSPQEGNPNQGPSP AGGNPQQPQAPPAGQPGPSPGGRP SRPPQ
2518	10569	A	3440	1	3114	

2519	10570	A	3441	3	401	TSSLSLSGKSGRYIVFLRRSVGIQSPSAVA TVRLLLAGSDRRFAAGSAGCAVLSRAER S*EPGCCYRIRRSARLRAGSIGNRDKPV AWPDTGSGDNTEVYFRAHQAGILPDTVL AGPAQRVAVSGGTPVDW
2520	10571	A	3442	2874	3062	
2521	10572	A	3443	2766	3323	MPDLVEGREKSDKGAQPQPRTQSRSA RTNGSGVRILHSLWRIIGIPLLLGYSLVCSRV LLACFWPGSDFWPRSRRKTYGTAPQSCY SFYVALDCGGVSRLVIFVSWRNPQVAPT SAHQNRPSRNPVSRPPNTQVARRKH YALADGYTERRWTNAPCRAESSFPNCP L* RQYRIHIVDASVCGP
2522	10573	A	3444	968	1440	
2523	10574	A	3445	3	640	LSVVRSRIHMGVGVGVGCPVRYRNQDD HELQITHGNKILCGIVCDKGAQPQPRTQS RSARTNGSGVRILHSLWRIIGIPLLLGYSL VCSRVLLACFWPGSDFWPRSRRKTYGT VPQSCYSFYVALDCGGVSRLVIFVSWRN PQVAPSAHQNRPRNPVSRPPNTQVARR KHYPADGYTERRWTNAPCRAESSFPN CPSAAPIPDSYDK
2524	10575	A	3446	1	3140	MVYKMYRSQHPYSIKEKQMKSEVLSV KEKIGYGMGDAASHIIFDNVMLYMMFF YTDIFGIPAGFVGTMLFVARALDAISDPC MGLLADRTRSRWGKFRPWVLFALPGF IVCVLAYSTPDLSMNGKMIYAAITYTLLT LLYTVVNIPYCALGGVITNDPTQRISLQS WRFVLATAGGMLSTVLMPLVNLIGGD NKPLGFQGDLSPMFSTPEEIARPGPYEND VHVVGASSLAAGHKTLPELVRSAEQHM GTR
2525	10576	A	3447	750	1340	ILHAPAPPFSASASHEQPEWSDKGAQPQP RTQSRSA RTNGSGVRILHSLWRIIGIPLLL GYSLVCSRVLLACFWPGSDFWPRSRRKT YGTAPQSCYSFYVALDCGGVSRLVIFVS WRNPQVAPSAHQNRPSRNPVSRPPNTQ VARRKH YALADGYTERRWTNAPCRAESSFPNCP FAAPIPDSYDK*PFRIVS
2526	10577	A	3448	93	699	RASVQKKLSTDDKGAQPQPRTQSRSA RTNGSGVRILHSLWRIIGIPLLLGYSLVCS RVLLACFWPGSDFWPRSRRKTYGTAPQS CYSFYVALDCGGVSRLVIFVSWRNPQVAPT SAHQNRPSRNPVSRPPNTQVARRKH YALADGYTERRWTNAPCRAESSFPPE LPVPQVPNTGFIRQVTFRDCFVNTPQAA ASGFW
2527	10578	A	3449	1000	1530	QRYSDNPPNDKGAQPQPRTQSRSA RTNGSGVRILHSLWRIIGIPLLLGYSLVCSRVLL ACFWPGSDFWPRSRRKTYGTAPQSCYSF YVALDCGGVSRLVIFVSWRNPQVAPSA HQNRPSRNPVSRPPNTQVARRKH YALADGYTERRWTNAPCRAESSFPPE LPVPQVPNTGFIRQVTFRDCFVNTPQAA ASGFW
2528	10579	A	345	85	194	
2529	10580	A	3450	106	375	
2530	10581	A	3451	232	376	KKGVLSCVRRHSMET*NEKPALLKMSGI KIPSPVHHFVFHKQSEKGA
2531	10582	A	3452	481	781	IKDKKVSNSQLLCGYLVAMTDVETTYA DFIASGRTGRRNAIHDLVSSASGNSNEL ALKLAGLDINKTEGEEDAQRSSTEQSG EAQGEAAKSESLTPHF
2532	10583	A	3453	15	369	RVGEYDGYEAGPAPCPPRASLCQ/PGPD QGPPSCTQAIPAPRKPHPCPWPQGPKKL GELPGLCLQGSPTAGHPCCPPQETGAQG GAPASPWFSSQNNACGLICFPQPRIFL CINSNS

2533	10584	A	3454	201	711	KKMARTKQTARKSTGGKAPRQTAG/LA TKAARKSAPSTGGVKKPHRYRPGTVL REIRRYQKSTELLNRKLPFORLVREIAA GFSKTALRFQSARIRCACRLAKRYLVG LFEDNNLCAIHAKRVTHAPKTIQLARR DTGEKRALSEGSFYGVLLVKFLLKYFGLI C
2534	10585	A	3455	758	1188	GKLSGRGTGSLRGDALPRLQKTGCPKA GGNRPPAVSQSRGGAVRDEGLLAAQTA EGGPRVEEARPPQLPQARGSLPETPPPA PDAITPPPPSGSHISPSSAEGPSRPPVGA VDSGGAPQPQDPGPAPAPALLRHRHQT P
2535	10586	A	3456	2	297	
2536	10587	A	3457	1	1128	
2537	10588	B	3458	58	1282	MRTLLKNTVIVLLPYKSGSKLYGESSTE LNVEVLNCTASQFKCASGDKCIGVTNRC DGVFDCSDNSDEAGCPTRPFGMCHSDEF QQCEDGICIPNFWECDGHPDCLYGSDEH NACVPKTCPSYFHCNDCNCIHRWLC DRDNDCGDMSDEKDCPTQPFRCPSWQW QCLGHNICVNLVVCDFGIFDCPNGQMSP HFALVAAAVDWLSQDSKWLDQSHIVPD VKLCVVASAYRQSYQSLGNDISLGYRCQ PKFSRSIDPTGKAVQTADIRLSARATLWL GGSIEESPVLCSTLRLLLRPLTWTSP NRPTQPCTAQTQTNQSVGIAAPSAIRVIY PESVVLNAVILYLPDPEVSGLPRAFKRRF SVEVRLDCGTFKLLLVYCTHPGDIKVT CKTGALVAFRCFLPX*
2538	10589	A	3459	1	1870	MGKVPMRSEKPAHEVRASTISTPDLSSI ESFFSRGPESTNHTSIKGRPLTAEKLNKT NRAEEKIKKEELAISGVDEDDGGKGIKD TGDLVEMVDLAFRCDRHNDGCDYSDE GCLYQTCQQNQFTCQNGRCISKTFVCDE DNDGCGDGSDELMHLCHTPEPTCPPHEFK CDNGRCIEMMKLCNHLDDCLDNSDEKG CGEFIFRASSPGAILILIVAVSTIHAIITDPR LGNALPVRIVQPQYSWTPLTLKLWASR VSNCQGLLSAAKTHHTVQFSILMALPKG HLFSARLTGKCVAQVIVEGFFAGRDKFV CVLNVAFVPYQFVLSLVRTGTASKSTVG FYRNNISVITGFLIGFLCQSSALDLETFTV VSHFYFGINECHDPSISGCDHNCITDLTS FYCSCRPGYKLMSDKRTEVDIDECTEMP FVCSQKCEVIGSYICKCAPGYLREPDG KTCRQNSNIEPYLIFSNRYLRNLIDGY FYSLEGLDNVVALDFDRVEKRLYWID TQRQVIERMFLNKTNKETIINHRLPAAES LAVDWVSSALKGGFVHPLNGGSQHFTL LVD*VIKWLILISNSVPC*KRRWGLPVF WFGGKREMSWEMMGH*LVEGLCGCCH
2539	10590	A	346	617	711	
2540	10591	B	3460	1	2973	MEKQSINQQLPYPDQLPTQCSPLTGLNE YPLSGVSIPDES WDRKSKHSAAMTLRQV HQRHQNNFLDHNTNVEEYSAQMRIGT HCCCTSSSLLLLVASQNKIADSVTSQV HNIYSLVENGSYIVAVDFDSISGRIFWSD ATQGKTWSAFQNGTDRRVVFDSSILTET IAIDWVGRNLYWTDYALETIEVSKIDGS HRTVLISKNL TNPRGLALDPRMKLLYFM DSYLDYMDFCDYNGHHRQVIASDLGF EV

2541	10592	A	3461	257	3561	RHKKPFKKSMPNPGAG/MLYWSDDQGTDS GVPAKIASANMDGTSVKTLFTGNLEHLE CVTLDIEEQKLYWAVTGRGVIERGNVD GTDRMILVHQLSHPWGIAVHDSFLYYTD EQYEVIERVDKATGANKIVLRDNVPLNR GLQVYHRRITEP/CPN*PKTIKIGHYIKDK PTCSSE/AKWYLPHPGQM*IA/DKPEAQR GSRRLTDLEGGNNEIDWSISDCIYPSQ VFDLSAKIEGKVDKRTCCPSSFPKGYGPI
2542	10593	A	3462	1	10725	MAGAPPPASLPPCSLISDCCASNQRDSVG VGPSEPGVGYSLVVRRFLSRSEKRNIRV GVTRFSRELDPPLRFPEHLFFTDWRLGAI IRVRKADGGEMTVIRSGIAYILHLKSYDV NIQTGSNACNQPTHPNGDCSHFCFPVPN FQVCGCPYGMRLASNHLTCEGDPTNEP PTEQCGLFSFPCKNGRCVPNYLDCDGV DCHDNSDEQLCGTLNNTCSSAFTCGHG ECIPAHWRCDKRNDKVDGSDHNCNP T
2543	10594	A	3463	3	14105	SWRRCRPGKAFASGAAGAVCYARPPP GEGTARPGTIAEMDRGPAVACTLLAL VACLAPASGQECDSAHRFCGSGHCIPAD WRCDBGTKDCSDDADEIGCAVVTCCQGY FKCQSEGQCIPSSWVCDQDQDCDDGSDE RQDCSQSTCSSHQITCSNGQCIPSEYRCD HVRDCPDGADENDCQYPTCEQLTCDNG ACYNTSQKCDWKVDCRDSSDEINTEIC LHNEFSCGNGECIPRAYVCDHDNDQD GSDEHA
2544	10595	A	3469	2	230	WQDFYCQ*HIFGAFFTHPDGPSNWAFFS NFVMFCHCLPKCWDYRGESPRPAHFKIF VDQCTVVKKKKKIRKIKNFL
2545	10596	A	347	2	343	SSVRAVEFPEDASGGSSPSGTSKSDANR ASSGGGGGLMEEMNKLLAKRRKAAS QSDKPAEKKEDESQMEDPSTSPSPGTRA ATSHLTPQRLAGSPGSGATRWRSLCPRF CPG
2546	10597	A	3470	134	929	RTAARGCNGIPGAAWEEALPRRRPRR HPSVNPRSRAAGSPRTRGRRTTEERPSGSR LGDRGRGRALPGRLGGRGRGRAPERV GGRGRGRGTAAPRAAPAARGSRPGPAG TMAAGSITLTPALPEDGGSGAFPPGHFK DPKRLYCKNGGFFLRIHPDGRVDGVREK SDPHIKLQLQAEERGVSISIKGVVC/SNRY LAMKVEDGRLLASKCVTDECFFFERLESN NYNTYRSRKYTSWYVALKRTGQYKLG KTGPGQKAILFLPMSG
2547	10598	A	3471	1	2604	
2548	10599	A	3472	478	697	YLIYQSRFFLFSSIRYQMPMPMG/YCNP YAYGQYNMPYPPVYHQSPGQAPYPGTQ QPSYPPFPQPPQQSYYPQQ
2549	10600	A	3473	21	194	
2550	10601	A	3474	2	767	APLSPGAQLGRGAPTSAPPPAAEAHPA ARRGLRSPQLPSGAMSQNGAPGMQEEES LQGSWVELHFSNNGNGGSVPASVSIYNG DMEKILLDAQHESGRSSSKSSHCDSPAS SQTPQDTNRAFETDTHSIGREKQLTVLR EDDIERRKEVESILRKNSDWIWDWSSA GKIFPPKEFLFKTPGSRTATLSMRNTSVL KKGIFSAEFLKVFLPFSAAALIAWPGL GIYIGKASDQPSTSTFGWKEPGSLDLVR

2551	10602	A	3475	1	4220	MLNIVQDSALLEAIGCQMEMGGGENNL KSHSRTNSGISSASGGSTEPTTPDSEPA QALLRDYALNTDSAAGLLIRSIHLVTQRL NSQWRQDMSISLALELLSGLAKVKVM VDSGDRKRAISSVCTYIVYQCSRPAPLHS RDLHSMIVAAFQCLCVWLTEHPDMLDE KDCLKEVLEIVELGISGSKSKNNEQEVK YKGDKEPNPASMVRKDAAEATLTCLVN ETTLIKYSRLPTINKHSFRYFVLDNSVILA ML
2552	10603	A	3476	3	1676	HASDSFRYFVLDNSVILAMLEQPLGNEQ NDFFPSVTVLVRGMSGR LAWAAQQLCLL PRGAKANQKLFVPEPRPVKNDVGFKY VKHRPFPEEVDKIPFVKADLSIPDLHEIVT EELEERHRKLRISGMAQQIAYEIHLEQQS EEELQKRSFPDPVTDCKPPPAQEFQTAR LFLSHFGFLSLEALKEPANSRLPPLLALD STIPGFFDDIGYLDLLPCRPFDTVIFYMK PGQKTNQEILKNVESSRTVQPHFLELLS LGWSVDVGRHPGWTGHVSTWSINCCD DGEQSQQEEVISEDIGASIFNGQKKVLY YADALTEIAFVVPSPVESLTDSESNISD QSDSDNMDLMPGILKQPSLTLELFPNHT DNLNSSQRLSPSSMRKLPQGRPVPLGP ETRIVSVVWVERYDDIENFPLSELMTEIS TGVETTANSSTSLRSTTLEKEVLVIFIHPL NTGLFRIQIGATGKFNMVPLVDGMIVS RRALGFLVRQTVINICRRKRLESDSYSP HVRKQKITDIVNKYRNKQLEPEFYTSL FOEVGLKNCSS
2553	10604	A	3477	288	589	WCSRRRGWYLLLGFHNYWRSSTFLVRC TPSCPGGCCPRYGIYPVRSCPRLPGGVSR YGSIHSG/RWCSWSPSWPWLTSVTPRL YVALM*AVVCPVVGKQP
2554	10605	A	3478	1250	1909	GAGPDMVWDTELELALKISKGLQRPIKA HREEREDIGKHESRCVIYFGTAKKWILK DKNGRSRVDVISHRLKVSSGLCKTHEIG FDPLALKCPLRSRTAPWWPLDRVSFDLH HLVIGNFFVGNRKIFLDYLVYGFAHNNR WKLLVQSWSDGCVHRTFGLVKSFASKAS FCIFITKQRKSSDLALKIQICANTARVIL KLKHFHFVSYMCTFLFTCENGHL
2555	10606	A	3479	3	246	AAAMSALLILGLLTAVPPASCQQ/GEP AHMILTVGNKADGVLVGTDGRYSSMAA SFRSSEHENAYENVPEEKGVRSTPM

2556	10607	A	348	2	2355	WCDLGSLOPPPRFKQFCSLSLPRHS*TS Q*PQPPKTQLNFTVAIDFTASNGETRMSE KVGGNPLQPTSLHYMSPYQLSAYAMAL KAVGEIIQDYDSKLFPAVGFGAKLPPE GRISHQFPLNNNDEDPNCAGIEGVLESYF QSLRTVQLYGPTYFAPVINQVASNSWSS VTLGTDSEPAVEVPQYVGIRLLVEGFTIK KPMAMCHRRMGVRPAVPLLTQRGSSEG KDSGTPTHSLHTKAQLPSPHVLRHQGV LRRQHSKLVGKALSTTGKALRTLPTAK VFISLPPNLDKFAVPSILKPKRSIREDRNG RSQKTVHTEGDMNMNIKKIVKQATVLT FTTALLAGGATQAFAKENNQKAYKETY GVSHITRHDMLQIPKQQQNEKYQVPQFD QSTIKNIESAKGLDVWDSWPLQADGTV AEYNGYHVVFALAGSPKADDDTSIYMF YQKVGDNIDSWKNAGRVFKDSDKFDA NDPILKDQTQEWSGSATFTSDGKIRLFYT DYSGKHGKQSLTTAQVNVSKSDDTLKI NGVEDHKTIFDGDGKTYQNVQQFIDEGN YTSGDNHTLRDPHYVEDKGHKYLVFEA NTGTENGYQGEESLFNKAYYGGGTNFF RKESQKLQSAKKRDAELANGALGIEL NNDYTLKKVMKPLITSNTVTDEIERANV FKMNGKWYFTDSRGSKMTIDGINSNDI YMLGYVSNSLTGPYKPLNKTGLVLQMG LDPNDVTFTYSHFAVPQAKGNVVTISY MTNRGFFEDKKATFAPSFLMNIKGKNTS VVKNSILEPGQLAVN
2557	10608	A	3480	162	530	ELLQPMASALLILGLLTAVPPASCQQGL GNLQPWMQGLIAAAFLVLVAIAFAVN HFWGAKEEP/ESPAHMILTVGNKADGV LVGTIDGRYSSMAASFRSSEHENAYEN VPEEEGKVRSTPM
2558	10609	A	3481	4	409	NAATSLTANPDATTVNIEDPGETPKHQ GSPRSGGREEDDELLGNDDSDKT/EGTV SGNDSSEVNDTWPLPWGWKQANRPLLS LLAGQKKSSPFWTFEYYQTFFDVDTYQV FDRIKGSLLPIPGKNFVRLYIRSIV
2559	10610	A	3482	160	518	
2560	10611	A	3483	12	197	
2561	10612	A	3484	2	321	ARGVYGYSLFYIPTAILWIIPHKAVRWI LVQIALGISGSLLAMTFWPAVREDNRRV ALATIVTIVLLHMLLSVGCLACFFDAPE MDHLPTTTGTPNQTVAAAKSS
2562	10613	A	3485	187	1280	PLARLNCLCSSLSPSPLSNLSFLIGTSL GCTCSLKHSHKPCQIFFLIIGRRLTGRMA AVDDLQFEFEGNAATSLTANPDATTVNI EDPGETPKHQPGSPRSGGREEDDELLGN DDSDKTELLAGQKKSSPFWTFEYYQTFF DVDTYQVFDRIKGSLLPIPGKNFVRLYIR SNPDLYGPFWICATLVFAIAISGNLSNFLI HLGEKTYHYVPEFRKVSIAATIIYAYAW LVPLALWGFLMWRNSKVMNIVSYSFLEI VCVYGYSLFYIPTAILWIIPQKAVRWILV MIALGISGSLLAMTFWPAVREDNRRVAL ALIVTIVLLHMLLSVGCLAYFFDAPEMD HLPTTTATPNQTVAAAKSS
2563	10614	A	3486	112	563	LDSSHCCSCSTALFRTQTAAAVPRMVI RVYIASS\SGSTAI/RGKRQQDVLGFLEAN KIGFGRKDIAANGENRKWMRENVENS RPGTGYPPLPPQIFNESQYRGDYDAFFG RPEENNNAVYCLLRGLTAPPGVSKGRQE GAKPKAGQALTL
2564	10615	A	3487	105	335	GRLFPKVLVSYHSVGYLPLILFCHFLANC ILCCLMHFL*FFQSYRF*G*KFGFTQHHC HYIFHKQWPLLWKNFPEH

2565	10616	A	3488	993	1338	QNCLKPHFFFFFETRVSLLLPKREAMGTI STHCNLCPLPGFQGNPASASQGR/AGLH GMGPPCR/RGTFVFLIGDRGFLHVGSSWS WNSQPQVIRPVRPSPKCWGLQGMEATV PSP
2566	10617	A	3489	2	454	PLLPPALPGCHALAPSSYIPVAIRALEPPS PYHGQLKMQSIPGAPPQPRSFFLSSPLDVD SPQAPRHCTGLPAPSLSSPPWSCPTLFSW FFEASGVCHHWTSVIAASNSSPIFELPHP HPLRISAWLFPPWRDHSQDPLCRGATSP VLNS
2567	10618	A	349	1129	1821	AWGSGKQRRQEAQCEVAEFTPAWRR APDTPAPLVLEPARA*HTSPKKHPPMWC RFFFFRQS FALVPQIGVQWRNLGSLQPLP PRFKAIFSYPQPPSSWHYRHVPFVFS NFCIFNKRWGFMTLAKLVLNS*PHEIHP PGPSQSAGIMGVSHCTWLVFSFKVVLV DYFFEKFPN*GNRFEFYFLFETGSHSVN QAGVQR/PYHASLQPPQAQVSLPSSW DYRHVPF
2568	10619	A	3490	1109	1448	PRLISKCFLLLLFFRQSHFVAQAGVQWC DLRSVYHLPGLKRFSCSLSPSSWDYRH LPPCPANFCNFSRDRVSPCCPGWFRTPD PGDPPASASPKWWEYTL*PPGDHPKAF
2569	10620	A	3491	14	250	VLSVGLPTGDTGIGLSRKTSPAPVALIHS HSLKQAFP*LTLSRTGNIHAIYRGVLK YCNFICLGFMLRYQLVSPSF
2570	10621	A	3492	1	1065	
2571	10622	A	3493	90	1937	AGGNQRTQSPRKNFMAFQASHRPAWGK SRKKNWQYEGPTQKLFLKRNNSAPDG PSDPSISASSEQSGAQPPGLQVERIVDK RKNKKGKTEYLVRWKGYDSEDDTWEP EQHLVNCEEYIHDFNRRHTEKQKESTLT RTNRTSPNNARKQISRSTNSNFSKTSKA LVIGKDHESKNSQLFAASQKFRKNTAPS LSSRKNDLAKSGIKILVPKSPVKSRTAV DGFQSESPEKLDPVEQGOEDTVAPEVAA EKPVGALLGPGAERARMGSRPRIHPLVP QVPGPVTAAMATGLAVNGKGTSPFMDA LTANGTTNIQTSVTGVTASKRKFIDRR DQPFDKRLRFVSRQTESAYRYRDIVVRK QDGFTHILLSTKSENNSLNPVLEVVQS ALSTAAANDSKVVLPRVGSVFCCGLN FNYFKPRLPNARKRESIKMAEAI RNFN TFIQFKKPIIVAVNGPAIGLGASILPLCDV VWANEKAWFQTPYTTFGQSQEGCSPV MFPKIMGGSICILDAVLGDRNLTAQEAC GKGLVSRVFWPGTSPRKVMVRIKELASC NPVVLEESKALVRCNMKMELEQANERE CEVLKKIWGISAQGDGTRMLKVLCRGKI E
2572	10623	A	3494	2	572	WCLQHD/LGHASIFKKSWWNHVAQKFV MGQ/LKGFAHWWNFRHFQHHAKPNIF HKDPDVTVAPVFLGESSVEYGKKRR YLPYNQQHLYFFLIGPPLTLVNFEVENL AYMLVCMQWAVSGVAQDPGHTAAVA GGGASGDSTCP*RTGCTDLLWAASFY ARFFLSYLPFYGVPGVLLFFVAVRYGRE WR
2573	10624	A	3495	25	430	YKNNFPPILALGKCAMLTFPLPLSHQA QSQGHRAAEYTCEGRSPFPVGLPWGQ AAMRAGGWVGRTAECFSFGMESRPG*R VSGRGAGGQPRPSPGMSLGGPVPPAPSS PLLPPAGRCNPRTERTWNLPTRSWA

2574	10625	A	3496	821	1412	GSARASPQGPGLVVRVDHTDEPHQGD RPREAPGLGQLSAGSHLQRGALTFHQL VQRAPQLPDRAPPLQDAETQLQPGCPA CQVAVCQ\ARPQLR\SEALPHRAGGHR QVPEESLVTSCWTPTSISEGNTQAGREGL RAPATKPSPRDRIPPTPLTSLGVPCPLPS WYCCPLGLPTCVFSSPMALALGLMGQ G
2575	10626	A	3497	32	616	VLQCSHGCFSPSSGGVLTDEAASSCCSD ADPSTKDFLLQQTMLRVKDPKSLDFY TRVLGMTLIQKCDPFIMKFSLYFLAYE DKNDIPK\EKDEK\IAWAVSRKATLELTQ QFGALKDDATQSYHNGNSDPRGFGHIGI AVP\DVYSACK\RFEEELGVKFVKKPDDG KMKGL\AFIQDPDGYWIEILNPNKMATL M
2576	10627	A	3498	77	403	
2577	10628	A	3499	18	753	TQPQLTSTCYRAFASWRTRSLLEPATILP TTCCPAPAAMCRTLAAPTTCLERAKEF KTLGIFPHKSELGFDTGSTGKFEWGSK HSKGD\KTSQK\DLGWRESF\DLLSSK NGVAAFHAF\KTEFSEENLEFW\ACEE FKK\RSATKLASRAH\QIFEEFICSEAPKE VNIDHETRELTRMNLQTATATCFDAAQG KTRTLM\EKD\SPYPRFLKSPAYRDLAAQ ASAASATLSSCS\LDPSHT
2578	10629	A	35	45	819	RSLALSPRLECNGAISAHCKLRLPGSRHS PASASRAAGTTGAHHRARLFFVFLVET GFHRVSQDGLE/LPDL/DDPPASASQSAGI TGVTAAPSRACSFKLARGRACPGWDWA EELTGTSHTRRVHPGQALWGW\DWRRCS CGRSWQT*LQRCPAVLRGWLAC\LTQAQ EEQIGPYVSVSPVIPGAACCFIDVLR*KI SDKDVFKAGRGAQPKTFSFLR\KSL/NPV TQARVQWCDLSSLQLLP\PRFK*FSCFSLP SRTIT
2579	10630	A	350	325	608	LMPCNPRHFERLRQADHLRSGVPRPALV QHGETLSVLKIQKLGGHGSTCL*SQLRR LRQKNLLSLGGRGCSKLRSHHCTPAWV TEP\DSVSKKK
2580	10631	A	3500	28	342	PGSTHASADAWVHPKNI/SSVNALSPGPH CAQTEV/IVSPAPRCLCHRRGPRPSCCPN PVPSLTSLTRFPSLCRATLKNGRKACLN PASPIVKK\IEKMLNSDKSN
2581	10632	A	3501	1	274	MARATLSAAPSNPRLLRVALLLLLVA SRRAAGASVVTELRCQCLQTLQGIHLKN IQSVNATLKNGKACLNPA\SPMVQK\IE KILNNP
2582	10633	A	3502	1	893	MSSREVTTPGKDVARSRLRGSGSDPRRT ALGSR\ASSQAVISVSLRAAGSR\SRDS GQKENIPQLAGVTQDSQTRTSLVSAPTPL HPRGGAI\AFLPNSGSIWSSGNFPGPGLRA FQPQCIKGVR\RSR\ATEPGQAAPCQLS SSHRSRNL\SPMARATLSAAPSNPRLLR VALLLLLVAASRRAAGAPLATELRCQC LQTLQGIHLKNIQSVKVKSPGPHCAQTE VM*VSP\IAAAATAGVPDSPAAPNPVLS TSCLTRFPSLCRATLKNGQKACLNPA MVKK\IEKMLKK
2583	10634	A	3503	1	407	ATEPGPQAPPRQLFRSSH\SRQTRLLSPMA RAALSAAPSNPRLLRVALLLLLVAAGR RAAGASVATELRCQCLQTLQGIHPKNIQ SVNVKSPGPHCAQNEVHKHTQEMGGKA CLNPA\SP\IIK\IEKMLNSDKSN

2584	10635	A	3507	47	891	KQPFVWPAGGERLSGARPKKEARLLR WCPMSFKRNRSDRFYSTRCCGACCHVR TGTHLGTWYMVVNLLMAILLTVVTHP NSMPAVNIQYEVIGNYYSISERMADNA C/VFFFAVSVLKVYNPVPMLVYGSNFLY PSGVGWIPFFCYRLDFVLSICLVAISSLT YLPRIKEYLDQLPDFDKDDLRLALDSIS CLLFIVLVFFALFIIFKAYLINCWNCYK YINNRRN/VCPEIAVYPAFEAPPQYVLPY EMGREKWPEKEPHPLLTWPEGNSGLW TINP
2585	10636	A	3508	246	559	MPVAVMAES/AFSFKKLLDQCENQELEA PGGIATPPVYGQLLALYLLHN/GQRIWQR DFPGIYTTINAHQWSETVQPIMEALRDAT RRRAFALVSQAYTSIIADDF
2586	10637	A	3509	2	250	
2587	10638	A	351	3	218	
2588	10639	A	3510	2	119	
2589	10640	A	3511	197	921	GTWVGLAVRTVQRRGPAKMPVAVMA ESAFSFKKLLDQCENQELEAPGGIATP KVYQQLLALYLLHNDMNNARYLWKRI PPAIKSANSELGGIWSVGQRIWQRDFPG IYTTINAHQWSETVQPIYKGHFRDATR/ RDRAFAPGLLQAVYFQSIRPMIFAFAVG/ LPVEEAVKGILAEQGWQAIDSTRNGSC PGKPVCGRGPWDVFPFNKFISLYSEPAV/ PIIPNEQQLARLTDYVAFLEN
2590	10641	A	3512	3	354	
2591	10642	A	3513	1	179	
2592	10643	A	3514	63	386	LRTLISCHLVVLMMLFLHTGGDDGLLRG WDRVPGKFLFTSKR*PPKGQHSVPTPA PAFPGSPALPFGWVCVLDTGSEAAASAC RHTMGVCSIQSSPHREHILATGR
2593	10644	A	3515	1	147	
2594	10645	A	3516	450	1154	KSHVLEPLSSLALEEQCLALS LDWSTGK TGRAGDQPLKIHSSDSTGQLHLLMVNETR PRLQKVASWQAHQFEAW/TCCFQLPWH PEIVYSGGDDGLLRGWDTRVPGTFLFTS/ IKTHHGCVASIQSKPSSGAHPWPRESYDE THPTVDRNMKQPLADTPVQGGVWRIK WHPFHHLHLLAACMHSGFKILNCQKAM EERQEATVLTSHLTPDSL VYGADWSWL LFRSLQRAPLVVLS
2595	10646	A	3517	73	168	
2596	10647	A	3518	322	671	RLWASPAAPGKKKEMGNSMKSTPAPAE RPLNPEGLDSDFLAVLSDYPSPDINPPIF RRGEKLRVISDERGWKAI SLSTGRESY IPAICVARSYHGWLLRGPGKNMAEELL QLPD
2597	10648	A	3519	624	1580	KAATSENKHCCEWRTSQAALMLHRLW ASPAAPGKKKEMGNSMKSTPAPAERPLP NPEGLDSDFLAVLSDYPSPDISPPIFRGE KLRVISDEGGWWKAI SLSTGRESYIPGI CVARVYHGL/WLFEGLGRDKAEELLQL PDTKVGSFMI RESETKKGFYSLSVRHRQ VKTYRIFRLPNNWYYISPRLTFQCL AEDL VNHYSVADGLCCVLTPCLTQSTAAAP AVRACSSPVTLRQKTVDWRRVSRLQED PEGTENPLGVVESLFSYGLRESIASYLSL TSEDISSFDRKKKSISL MYGGSKRKSSFFS SPPYFED

2598	10649	A	352	319	1979	VPGVPAARPERECRAHPASFPFPPGGLDS GFVPSVQDFDKKLTADAYLQILIEQLKL F**QASK\RKEDQQRKKIETLKETTNSMV ESIKHCIVLLQIAKDQSNAEKHADGMIST IKSCRCNIPA*SLGTCDQAQCLPRLPYLQ NPLSCVSQSSVHLS*QVGPVLSYLGTSSD SNTQIVPGSGNFTNLAASLTPSQAMSTLS PNTVPEFSYSRQ*/EDEFYDAD/ENSIKVG SSPKRLIDSSGSASVLTHSSSGNSLKR PDT TESLNSSLNGTSDADLFDSHDDRDDDA EAGSVEEHKSVIMHLLSQVRLGMDLTK VVLPTFILERRSLEMYADFFAHPDLFVS ISDQKDPKDRMVQVVKWYLSAFHAGRK GSVAKKPYNPILGEIFQCHWTLPNDEE NKELVSEGPVPGVSKNSVTFVAEQVSH HPPIFSLFMLECFNKKIQFNAHIWTKSKF LGMSIGVHNIGQGCVSCLDYDEHYILTFP NGYGRSILTPVWVELGGECNINCSKTGY SANIIFHTKPFYGGKKHRITAEIFSPNDKK SFCISIEGEWNG
2599	10650	A	3520	24	688	VDHPPYKRTEKVRAQRSPKSQDIYLGLL VKLYRFSGPEEPNSNIQTRVVLKRLFMS RTNRPPLSLSRMIREDEAFLAGKKKNP AVVVGPKLIMCGVQKGTPKLKVCALG GTQAGPHKRNLARGQRSITFDQLALD/S PLRGCGTVLLASGPSKGREVYRHFGKAP GNPHSHTKPYVRSGRKFERRARGRRA SRGYKKLTLDPTLLYKKIFADSEKKKK
2600	10651	A	3522	195	391	PGVAGARHPLLGAAPKGRLEVLAVGFH GSAANQVWVSKSHPOFIPTDQIEGGDRA LKGTCLPLS
2601	10652	A	3523	112	492	AHSRTPARPENRAAASAPRKPRRAMSSP PEGKLETKAGHPPAVKAGGMRIQKHP HTGDTKEEKDKDDQEWESPPPKPTVFI SGVIARGDKDFPPAAQVAHQKPHASM DKHPSRPTQHIQPRK
2602	10653	A	3524	3	982	GTRVGVAWRSVRLLLGPGAGLRGGVVL KVSPSPCRGRRVPVRAEGARGRGRPN KVPGASSGAAVGAARLTAPLLAKAMAS KLLRAVILGPPGLGKGAPVCQRIQNF LQ\HLS\SGHFLRENIKAISTEVGEMANQV YREKVFLVPDHVITRLMMSELENRRGQ HWLLDGFPRTLGQAEALDKICEVDLVIS LNIPFETLKDGLNRRWIHPAPSGRVYNLA DFNPPHVHGIDVTGEPLVQEDDKPÆ AVAA\RLRQYKDVAKPVIEL\YKSRGVL HQFSGTETNKMWP\YVYTLFSNKITPIQ SKESILTLAQWEEPWNDVGHSTQ
2603	10654	A	3525	19	445	
2604	10655	A	3526	1	622	QAAWILKARALTEMVYIDEIDVDQEGIA EMMLDENAIQVPRPGTSLKLPGTNQTG GPSQAVRPITSHSEKPTGFLRPSTQSGRP GTMEQAIRTPRTAYTARPITSSSGRFVRL GTASMLTSPDGPFIN*SRLNLTKYSQKPK MAKALPEYIFHHENDVKTALELAALSTE HSQYKDWWWKVQIEKRYRLGMYREA EKQLISAMKQ

2605	10656	A	3527	1	1509	MKAEICKSRTVKDWHNHQKLGEKNKTD SPPQPSEGTNTANTLILDFWPLEMIACCW ETFPQRLTAELFMNPTHRRWHGYKNQSV GALRAPLGQGPSRRGLPGRVGRRLQFTF RPPLSWSAGPSLAAPAAMSSMEPLLLA WSYFRRRKFQLCADLCTQMLEKSPYDQ EPDPELPVHQAAWILKARALTEMVYIDE IDVDQEGIAEMMLDENAI/PSSTPITQAG RPITGFLRPSTQSGRPGTMEQAIRTPRTA YTARPITSSSGRFVRLGTLGMYREAEKQ FKSALKQQEMVDFTLYLAKVYVSLDQP VTALNLFKQGLDKFPGEVTLGCIARIYE EMNMSSAAEYYKEVLKQDNTHVEAIA CIGSNHFYSDQPEIALRFYRRLQMGYIN GQLFNNLGLCCFYAQQYDMTLTSFERA LSLAENEEEAADVWYNLGHVAVGIGDT NLAHQCFRLALVNNNNHAEAYNNLAVL GDAEG/RHVEQARALLQTASSISPHMYE PHF
2606	10657	A	353	27	749	STCCFQELVTL*GCKLCTFHPGRKWETR LAEPLQORDPSYRVVMLGELRGIVFLTGI VSPRTENDQEISEDTRSHGVLLGRFQKD ISQGLKFKEAYEREVSLKRPLGNSPGERL NRKMPDFGQVTVERS*PPGEREA/RKYN DFGNSFTVNSNLISHQRLPVG/DTRPHKC DECSKSFNRTSDLIQHQRHTGEKPYECN E/CCKAFSQQSHLIQHQRHTGEKPYECS DWGKTFSCSSDLILH
2607	10658	A	3531	1	174	
2608	10659	A	3532	1	189	MDAVAVYHGKISRETGEKLLLATGLDG SYLLRDSSEVPGVYCLCVL/FQKPDQGIV IPLQYPV
2609	10660	A	3533	3	210	CPRVHQAMD VAVYHGKISRETGEKLL LATGLDGSYLLRDSSEVPGVYCLCVL*V *YVCCEYDTPDCLWYLVMAA
2610	10661	A	3534	1	386	GISLAQFSSSACPRVHQAMD VAVYHG KISRETGEKLLLATGLDGSYLLRDSSEVP GVYCLCVLYHGYIYTYRVSQTETGSWS A/EAQKPDQGVIPVLPVEKKSSARST QGTGIREDPDVCLKAP
2611	10662	A	3535	224	751	LVPGCSSSGISLAQFSSSACPRVHQAMD AVAVYHGKISRETGEKLLLATGLDGSY LLRDSSEVPGVYCLCVLYHGYIYTYRVS QTETGSWSAETAPGVHVKRYFRKMKKS HFQHFQKQDQGVIPVLPVEKKSSARS TQGTGIREDPDVCLNAPLIKISPLRPLFS ITFNIC
2612	10663	A	3536	3	199	SIRAEMSRVALAVLALLSLSGLEAIQRT PKIQVYITSSSREWVKFPPELLCVWVSST PTLKLTY
2613	10664	A	3537	134	404	
2614	10665	A	3538	415	533	
2615	10666	A	3539	1	3349	MDQPEAPCSSTGPRLAVARELLLALEE LSQEQKRFHKLRLDVGPDGRSIPWGRL ERADAVDLAEQLAQFYGPEPALEVARK TLKRADARDVAAQLQERRLQRLGLGSG TLLSVSEYKKKYREHVLQLHARVKERN ARSVKITRFTKLLIAPESAAPPEALGPA EEPEPGRARRSDTHTFNRLFRDEEGRRP LTVVLQGPAGIGKTMAAKKILYDWAAG KLYQGQVDFAFFMPCGELLERPGTRSLA DLILD
2616	10667	A	354	69	378	KGGSLGAPRVEGPNFGLKDSPPKKRE FPALPPGGGN/KRAGPPCPGKFGFLKKK GVPPGGKRGLENRPQGDSSS*PPKGGGI TGGAPRPGKKRSFSLQKIL
2617	10668	A	3540	3	261	
2618	10669	A	3541	3	429	

2619	10670	A	3542	1	859	ALGKQKCEEWRISKY/EALK/ED/WRNLG AQHRELESQHLVLSKLQGADSRDLQM NQALRSLQNEHQQLQAKIECLQADRDL SLYTQDLQDQLKRSEAEKLTIVTRVQQL QGLLQNSLQLEQEKLTK/KRSANLL PQILRYCSFSYLPKSGMDYMTSWSPSQ FWEFC*VRDVWELFKD*SLALRTLQVLS LLS*DQALPVWSPKSPNEVEPEGTGKE KDWDLRDQLQKKTLLQAKEKECRELH SELDNLSDEYLSCLRKLQHCREELNQSQ QLPPRRQCGRWLP
2620	10671	A	3543	392	2016	AKRNRCLVIMISPDPRPSGLARGAESY EAKCERRQEIRSRRCRPNVTTCRQVGK TLRIQQREQLQARLQOFFRRRNLELEE KGKAQHPQAREQGPSRRPGQVTGTSSEV FPAQHPPPSGICRDLSDHLSQAGGLPPQ DTPIKKPPKHHRGTQTKAEGPTIKNDAS QQTNYGVAVLDKEIQLSDYLKEALQRE LVLKQKMMVILQDILLSTLIQASDSSWKQ LNEDKLKGLRSLENQLYTCTQKYSWP GMKKVLLEMEDQKNSYEQKAKESLQK VLEEKMNAEQQLQSTQSRSLALAEQKCE EWRSYEALKEDWRTLGTQHRELESQ HVLQSKLQGADSRDLQMNQALRFLNE HQQQLQAKIECLQGDRDLCSLDTQDLQD QLKRSEAEKLTIVTRVQQLQGLLQNSL QLQEKEKLLTKKDQALPVWSPKSPNEV EPEGTGKEKDWDLRDQLQKKTLLQAK EKECRELHSELDNLSDEYLSCLRKLQHC REELNQSQQLPPRRQCGRWLPVLMVVI APALAVFLANKNNLMI
2621	10672	A	3544	35	219	
2622	10673	A	3545	293	479	
2623	10674	A	3546	1	968	VKLPSCPDPMGTSLLCWMAICLLGAD HADTGVSQNPRIHNTKRGQNVTFRCPI SEHNRLYWYRQTLGQGPEFLTYFQNEA QLEKSRLSDRFSAPKPSFSTLEIQRTE QGDSAMYLCASSLAGLNQPHFGDGTR LSILEDLNKVFPEVAVFEPSEAEISHTQK ATLVCLATGFFPDHVELSWWVNGKEV HSGVSTDPQLKEQPALNDSRYCLSSRL RVSATFWQNPRIHNTKRGQNVTFRCPI DEWTQDRAKPVTQIVSAEAWGRADCGF TSVSYQQGVLSATILYEILLGKATLYAV LVSAVLVLMAMVKKRDF
2624	10675	A	3547	278	1283	GGIGEIKQRPSCLGRCPLSVLMNISL ELGSVFSAVISQKPSRDICHRGTSLTIQGG VDSQVTMMFWYRQQPGQSLTLIATANQ GSEATYESGFVIDKFPISRPNTFSTLTVS NMPSPEDSSIYLCVVEEQGFVGAETQYF GPGTRLLVLEDLNKVFPEVA/VLFEPSE AEISHTQKATLVCLAICFYLDHVELSWW VNGKEAHSGVSTDPQLKEQPALNDSRY CLSSRLRVSAITFWQNPRIHNTKRGQNV GLSENDEWTQDRAKPVTQIVSAEAWGR ADCGFTSGK\SYQQGVLSATILYEILLGK ATLYAVLVSAVLVLMAMVKKRDSRG
2625	10676	A	3548	151	286	
2626	10677	A	3549	28	177	
2627	10678	A	355	213	660	KPVILGYAEPAPGQFSRGP/WSRAE/WP GTASPLL/SCATSALL*SIKPGPDSHRGH QHGTPTKPSKPEKGTAGQLSRYITPQE KEIAPLNPPALKSPSKENRDPDLTGPGQ TSRALTVAPGCALGPQVEPMKALRRQM GGAVFPLGS
2628	10679	A	3550	422	671	RIYPALRMPSINTASIAQARKLVEQLFMF VANIDRIKVSAAAADLMAYCEAHAKEDP LLTPVPIASENPFKEKKFFCAHPLSL

2629	10680	B	3551	62	299	MFSLKKWNAVAMWSWDVECDTCAICR VQVMDEGIGVRNWSEALNLIYASEMGF DLDMGSQTSLSPLAHWLLNNLGWMNL X*
2630	10681	A	3552	1	602	ADVEDGEETCALASHSGSSGSKSGGDK MFSLKKWNAVAMWSWDVECDTCAICR VQVMDEGIGVRNWSEALNLIYASEMGF DCRSGSTALAVPSVSLASHQPCLDHR* QPIGSIQSSLF*RNSQVS*GRK*KVASYEL LKEGFCVNACLRCQAENKQEDCVVW GECNHSFHNCCMSLWVKQNNRCPLCQQ DWVVQRIGK
2631	10682	A	3553	2	428	SGGSTPLGLSAFPKPTSSAVGSGAAM ADVEDGEETCALASHSGSSGSKSGGDK MFSLKKWNAVAMWSWDVECDTCAICR VQVMDACFRCQAENKQEDFFVVLGECN HSFHNCCHVPCGSKQNNRCPLCQ\QDW VV\QRIGK
2632	10683	A	3555	3	378	
2633	10684	A	3556	2	299	LLNSRPRRRQQAQPSLEMQNDAGEFVD LYVPRKCSASNRIIGAKDHASIQMNVAE VDKVTGRFNGQFKTYAICGAIRRMGES HDSFLRMAKADGIVSK
2634	10685	A	3557	1	392	RRYLCRVTSCLSLSRVWWPARRSPAF EMQNGRRRSSDLYRARGKLSASNRIIG AKDHASIQMNVAEVDKVTGRFNGQFK TYAICGAIRRMGESDDSLRLAKADGIV FKELFDWREITDVGIFCHK
2635	10686	A	3558	1	415	FRDIVNENGEIEIQDEEEDGYDD\EMT GTGMKES*NSPWVMAG/HGGSNPQANR QTSDDSSAKMSTPADKVLRFENKINLD KLNVTDSVIYKATEKF/DTKGIKYVLDPT TRMILFKMLTRGIITDIDGCISTGREANV
2636	10687	A	3559	139	1914	AVPFHRAAASGGALQSWTTGGLMSR VVPQGQDDADSSDSENRLKTVKEKDDI LFEDLQDNVNENGEIEDEE/WKEGYD DD\EMTGTGMKELENSPRVMSGIGRKQP TGKSTD\PDSSSAKMSTPADKVLRFEN KINLDKLNVTDSVINKVTEKSQKEADM YRIKDKADRATVEQVLDPRTRMILFKM VTRGIITEINGCISTGKEANGYHASTANG ESRAIKIYKTSILVFKDRDKYVSGEFRFR HGYCRGNPRKMVKTWAEKEMRNLIRLN HSR/GYHCPEPIMLRHGLAMSFIGKDD MPATNFGKMFQLESKARELYLQVIQY MRRMYQDARLVHADLSEFNIMYHGGG VYIID\VSQSVEHDPHAEFLRKDCAN VNDFFMRHSVAVMTVRELFVTDPIPL HHENLDAYLSKAMEIASQRTKERTV/SS QDHVDEEVFKRSYIPRN\DEVKNYERD MDIIMKLKEEDMAMNAQQDNILYQTVT GLKKDLSGVQKVPALLENQVEERTCSDS EDIGSSECSDTDSEEQGDHARPKKHTTD PDIDKKERKK\EVKEAQREKRKNKIPKH VKRKEKTAKTKKKK
2637	10688	A	356	629	1007	KGTIYIKQERLENLRTNHLDKYYNPPMK QNYQKLCQKGMASRTHREESR*MRGNR CRLRITRNA*FEGENLQNKIAQGENLEKK PEPATYI*EA*ESKRDGV*KSYCVSSFPT MQ*KSD*SEYSYG
2638	10689	A	3560	129	567	SYKSRLARKSVTGGKAPRK\QLAYKKPA SQECGPLLGGLKKPHRYR\PGTVALREIR R\YQKSTELMIRK\LRFORLVREIAQDF KTDLRFQERSNQVALQEA\RRAYLVWP FLKDTNLVCLSMKRPVIMPKRHSSAR RHHVENVL
2639	10690	A	3564	194	338	

2640	10691	A	3565	197	522	GSAAMKVKIKCWNGVAHWLVVANDE NCGICRMAFNGCCPGCECSPSMLSERPR LQGAPATDCPAGCGGPVLPTCFQHALHP QVGLHAQQVQQALAPMLPPRIGKFKE
2641	10692	A	3566	1	6521	MLRKRKWLGVVAHACNPSTLGGQGH DKQPQVRRLLSAPGSRIAGQWVLDLKS PHLLKGENDKNSLSQKAFLYVAHVLD SERGVLVTMTTETGPDSEVKKAEQEAQ QPEAAAATTPVTPAGHGHPEANSNEK HPSQQDTRPAEQSLDMEEKDYSEADGLS ERTTPSKAQKSPQKIAKKYKSAICRVTL DASEYECEVEKHGRGQVFLDLVCEHLN LLEKDYFGLTFCDADSQKNWLDPSKEIK KQIRSE
2642	10693	A	3567	1	1232	GCTGTWGEALFIKEKGFFWSPATGPMA AVQMDPELAKRLFFEGATVVILNMPKG TEFGIDYNSWEVGPKLRGVKMIPPPIHFL HYSSVDKANPKEVGPRMGFFLSLHQRG LTVLRWSTLREEVDLSPAPESEVEAMRA NLQELDQFLGPYPYATLKKWISLTNFISE ATVKKLQPENRQICAFSDVLPVLSMKHT KDRVGNLPRCGIECKSYQEGLARLPEM KPRAGTEIRFSELTQMFPEGATPAEITK HSMDSLVALETVHNKQFPSPQDVLGEL QFAFVCFLLGNVYEAFEHWKRLNLLC RSEAAMKK/HATRLWINLISILHHQLGEIP ADFFVDIVSQHNFLTSTLQVFFSSACIA VDATLRKKAEFQAHLTKKFRWDFAE PEDCAPVVEELPEGIEMG
2643	10694	A	3568	2	166	
2644	10695	A	3569	56	1072	ARGGGAMEGLEENGGVVQVGELLPC CGRTFFPVALKKHGPICQKTATKKRKT DSSRQRAEGTDIPTVKPLKPRPEPPKPS NWRKHEEFATIRAAKGLDQALKEG/G KL\PPPP\PS\YDPGFIIQW/CPY\Q MENAADRHINFCKEQAARISNKRRTD TKGKPTSRTQVYKPPALKKSNSPGTASS GSSRVPPSGAG\KTVVGVP/SQGVSS SSSLG/NTKLQTLSPSHKGIAAPHAGANV KPRNSTPPSFARNPAPGVLTNKRKYT ESYIARPDGDCASSLNGGNIGIEGHSPG NFPKF\CHCEGKYPVEWAKFCECGIR RMIL
2645	10696	C	357	1	555	MLYVLIESERARIKKLQEEKTRNLESSRK LEPTIVSEHKGGLRTEQTDIDVLGQHLTK EHVSSHQSPIRDSQWFTLSPQEKYACSY ERKDPLIKRAFIIFYHRNAVSSHGNGPA VVLPISRFVLTPTTFESTLPFLSSRLAWGT SSKDPRIAAGQQSPLEKKILVSKLSSHHT VWNYTEKES*
2646	10697	A	3571	32	469	
2647	10698	A	3572	659	1149	EVTACRQPSVAFSTSLALALTLALLEEPF SLLHCESPLLGWASSCGGCAGSPSSAG PAGIVLK/SLAGPQLPPCRVGLGTCSLPY LSLPPAVGSFMARASLMSAAPCSMARVP STTQGLLSRTPQCGQMAQDWQAAPPAS PVQDPLEEASWAPESGDLENFYV
2648	10699	C	3573	361	501	MLFLRYAPLVGGSFCIWSHPLQFLTSIK VNFVETLFCFQSFKDIF*
2649	10700	A	3574	124	579	EPLPLAKAGAGSLSCSVRPCAAGASPT SATPCSIAPSPIDHPRAEECGRMVQDWQ AAPPAPRCGIHWVKPAGLLSLLMSMVR INMIVKLLVFVILLVT*FTVKVCLYIFQGL CCGLLFCILHGSPSHRPPKDLWHHCDL DVRHEVKGDH

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